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RESULT 7
ID Q00737
                                                                                                                                                                                                                         Query Match
Best Local S
Matches 1
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01-NOV-1996
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Q21484
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                                                                                                                                                                                                                                                                                                                       elegans.";
NATURE 368:32-38(1994).
NATURE 249128; El348188;
                                                                                                                                                                                                                                                                                                                                                                                             WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY J., COOPER J., COULSON OF CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCHURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MISG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 94150718.
MILSON R., AINSCOUGH R.,
BONFIELD J., BURTON J., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MCMURRAY A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
RHABDITINA; RHABDITOIDEA; RHA
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MYCOBACTERIUM LEPRAE.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q21484;
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                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Local Similarity 61.1%;
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F I N E R C
                                                                                                                                   F I N E Q C
TTYATHAAYGARCARTGY 1350
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NCE 517 AA; 57202 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                      Score 76; DB 5;
Pred. No. 2.39e+00
7; Mismatches
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  PRT;
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  1211 AA
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RESULTANCE OF SERVICE 
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Best Local (
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Q58652;
01-JUN-1998 (TREMBLREL, 0)
01-JUN-1998 (TREMBLREL, 0)
01-JUN-1998 (TREMBLREL, 0)
                                                                                                                                                                                                                        MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., BULT C.J., WHITE O., OLSEN G.J., ZHOU L.M., CLAYTON R.A., GOCAYNE J.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.B., REICH C.I., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., FURRMANN J.L., NGUYEN D., SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FURRMANN J.L., NGUYEN D., UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SANOW P.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M., KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C., COMplete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOSIS;
NP_BIND
DOMAIN
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-i- FUNCTION: INVOLVED IN CHROMOSOME SEGREGATION IN MITOSIS
-i- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

-i- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS

-i- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF THE CHROMOSOME SEGREGATION IN MITOSIS OF TWO PUTATIVE CENTRAL OF TWO PUTATIVE SEGREGATION IN MITOSIS OF TWO PUTATIVE SEGREGATIO
N-ACETYLGLUCOSAMINE.
EMBL; U67566; G1591889; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 398 AA; 46068
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DOMAIN
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SCIENCE 273:1058-1073(1996).
-!- SIMILARITY: TO E.
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EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES;
TRICHOCOMACEAE; EMERICELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998
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01-NOV-1998
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Aspergillus nidulans codes for a
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1 CTTCATTAATGAACGAT
F I N E R
                                                                                                                          FAECALIS UNDECAPRENYL-PP-N-ACETYLMURAMIC ACID-PENTAPEPTIDE
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YTTYATHAAYGARMGNY
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NEL. 06,
NEL. 06,
MJ1255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COILED COIL; NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 08, CREATED)

. 08, LAST SEQUENCE UPDATE)

. 08, LAST ANNOTATION UPDATE
PROTEIN SUDA (DA-BOX PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHANOCOCCALES; METHANOCOCCACEAE;
   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ATB/ASP-RICH (DA-BOX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
   4CAF01FF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitosis-defective bimD6 chromosome scaffold pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3E206D5F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 AA
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2.39e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UPDATE)
PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COILED-COIL REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLECTOMYCETES; EUROTIALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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WATERSTON R.,

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RESULP ACTOR OF THE SULP ACTOR
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Best Local
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Q45377; Q45399; PRELIMINARY;

O45377; Q45399; TREMBLREL. C

01-JUN-1998 (TREMBLREL. C

01-NOV-1998 (TREMBLREL. C

01-JAN-1999 (TREMBLREL. C
MEDLINE; 94150718.

MEDLINE; 94150718.

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

BONFIELD J., BURTON J., CONNELL M., COPSEY J., COUDSON A.

CRAXTON M., DEAR S., DU Z., DUDBIN R., FAVELLO A., FULTON L.,

GARONER A., GREEN P., HAWKINS T., HILLIER E., JIER M., JOHNSTON L.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

LIGHTNING J., LLOYD C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1131
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01-MAY-1997 (TREMBLREL 03,
01-JAN-1999 (TREMBLREL 09,
RUST RESISTANCE KINASE LR10
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                      CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F22G12.5 PROTEIN. F22G12.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00108; PROTEIN_KINASE_ST; 1. PFAM; PF00069; PKinase; 1. MENDEL; 13864; TRIAGe;1197;mn13864. SEQUENCE 636 AA; 71022 MW; B0058B4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEUILLET C., SCHACHERMAYR G., KELLER B.;
"Molecular cloning of a new receptor-like kinase
Lr10 disease resistance locus of wheat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRITICUM AESTIVUM (WHEAT).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P93604
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                                                                                                                                                                                                                                                                                                                                                                                                RHABDITINA;
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EMBL; U51330; G1680686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-LEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446
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RWSNTTYATHAAYGARG 1147
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TCATTAATGAACGATGC 19
I N E R C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCGTTCATTAATGAAG
S F I N E
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THATHAAYGARMGNTGY 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                                                                                                                                                       (MAR-1997)
                                                                                                                                                                                                                                                                                                                                                                                                RHABDITOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.8%;
52.9%;
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58.8%;
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                                                                                                                                                                                                                                                                                       EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                             RHABDITIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                      SECERNENTEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B0058B4B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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No.
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1.29e+01;
                                                                                                                                                                                                                                                                                                                                                                                             PELODERINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29e+01;
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                                                                                                                                                                                                                                                                                                                                                                                     RHABDITIA; RHABDITIDA;
ODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 636;
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                   SHOWNKEEN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                   ALD DRARAC PRICE PROPERTIES AND ARREST OF THE CONTRACT OF THE 
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Matches
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ULT 11
Q21980;
Q21980;
Q1-NOV-1996 (TREMBLREL 0
O1-NOV-1996 (TREMBLREL 0
O1-NOV-1998 (TREMBLREL 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BÜRTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DÜBBIN R., FAVELLO A., FÜLTON L.,
GARBUNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LICHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPEA A., ORUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z92831; E1346028; -...
EMBL; Z81066; E1346028; JOINED.
EMBL; Z81066; E1345723; -...
EMBL; Z92831; E1345723; JOINED.
SEQUENCE 2374 AA; 264800 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J. THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERST MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.; "2.2 Mb of contiguous nucleotide sequence from chromosome elegans.";
             WATERSTON R.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ
EMBL; U00046; G470361; -
PROSTTE; PS01186; EGF_2; 7.
PFAM; PF00008; EGF; 4.
                                                                                                                                             SEQUENCE FROM N'A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                             MILLER N.;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R13F6.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (OCT-1996)
                                                                                                                                                                                                                                SUBMITTED
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (APR-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHABDITINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KERSHAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM'N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE
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2 TICATITAATGAACGATG 18
F I N F B
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TTYATHAAYGARMGNWS
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                                                                                                                                                                                                                                (APR:1994)
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larity 52.9%;
Conservative
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1001,
                                                                                                                                                                                                                                EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                  EMBL/GENBANK/DDBJ
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LAST SEQUENCE UP
LAST ANNOTATION
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Mismatches
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No.
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                                                                                              DATA BANKS
                                                                                                                                                                                                                                DATA BANKS
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RHABDITIA; RHABDITIDA;

CAENORHABDITIS.

COULSON A.,

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Best Local Similarity
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Best Local
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       P2.";
P2.";
MOL. MICROBIOL. 22...
MOL. MICROBIOL. 22...
PURI.; Y08256; E384006;
T12 AA; 128
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01-MAY-1997
01-JUN-1998
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01-JUL-1997
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814 TTYATHAAYGARMGNWS 8

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2 TTCATTAATGAACGATG 1

F I N E R
                                                                                                                                        MEDLINE; 97055432.

SENSEN C.W., KLENK H.P., SINGH R.K., ALLARD G., PENNY S.L., YOUNG F., SCHENK M.E., GAASTERLAND RAGAN M.A., CHARLEBOIS R.L.;

"Organizational characteristics and information"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 13
P95858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 12
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SEQUENCE 2531 AA;
                                                                                               p2.";
                                                                                                                                                                                                                                                                                                                                                                    SULFOLOBUS SOLFATARICUS
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                                                                                                                                                                                                                                                                      STRAIN-P2
                                                                                                                                                                                                                                                                                                                                               ARCHAEA;
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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BL; U48851; G1912379; -.
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1 CTTCATTAATGAACG 15
F I N E
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(TREMBLREL.)
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7 (TREMBLREL. 04,
8 (TREMBLREL. 08,
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larity 52.9%;
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                                                                         22:175-191(1996).
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                           WW;
                                                                                                                    sequence
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LAST SEQUENCE ANNOTATION OF THE PROPERTY OF THE PROPE
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6; 1
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Pred. No. 1.95e+01;
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ANNOTATION UPDATE)
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No. 1.29e+01
                                                                                                                    information content from Sulfolobus soli
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RA MITCHELL W.P.
RA DAVIS R.W.;

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EUKARYOTA; METAZ
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SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; AE001282; G3328474; -.
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FILARIOIDEA; ONCHOCERCIDAE; BI
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Chlamydia trachomatis.";
SCIENCE 0:0-0(1998).
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6 (TREMBLREL. 01, LAST
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larity 61.1%;
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92) TO EMBL/GENBANK/DDBJ DATA BANKS
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FEATURES SOUTCE		TITLE JOURNAL COMMENT	REFERENCE	ACCESSION NID VERSION KEYWORDS SOURCE ORGANISM	LOCUS
For clone availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: T7 Class: BAC ends. Location/Qualifiers 1. 698	Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tlqr.org	Venter, J.C. Use of BAC End Sequences for Sequence-Ready Map Building (1998) Unpublished (1998)	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 698) Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,	AQ029367 93274498 AQ029367.1 GI:3274498 GSS. human. Homo sapiens	AQ029367 698 bp DNA GSS 21-AUG-1998 RPCI11-37N19.TV RPCI11 Homo sapiens genomic clone R-37N19, genomic survey sequence.

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REFERENCE
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CDNA Library Preparation: Raymond Lee. cDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

info@genomesystems.com) and Research Genetics, Huntsville, Alabama

(web address: www.resgen.com) (email contact: info@resgen.com) and

RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Waterston, R. and Wilson, R.
Washu Zebrafish EST Project 1998
Unpublished (1998)
On Jan 17, 1998 this sequence version replaced gi:1901040.
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1 (bases 1 to 359)
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Fax: 314 286 1810
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fbl3al0.xl zebrafish
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RPCI11 Human Male BAC L
/db_xref="taxon:9606"
/clone="R-37N19"
                                                                                                                                                                                                                                               /note-"Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; 1st strand cDNA primed with (GA)10ACTAGTCTCGAC(T)18, followed by second strand synthesis, and ligated to 5 adapter (5')-aattcggcacgag-3', 3'-gccgtgctc-5'. cDNA was cloned directionally (EcoRI/XhoI) into Stratagene Zap express contains the contains and contains the contains the
/map~"875B10; 20; 20p11.23-20q11.23"
/clone_lib~"zebrafish fin day0 regeneration"
/sex="mixed male and female"
                                                                                                                                                                       lambda phage arms. Mass invivo excision done to obtain inserts in pBK-CMV phagemid."
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/note="Vector: pBaCe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
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112 c 113 g 22
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survey sequence. AQ241183
                           AQ241183 663 bp DNA
RPCI11-68N14.TJ RPCI11 Homo
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Seq primer: M13 Reverse
Class: BAC ends.
                                           AQ241183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_GSSs: CITBI-E1-2509G23.TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1998)
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CalTech Human BAC Library D"
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/clone="2509G23"
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/note="Vector: pBeloBAC1
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/lab_host="E. coli XLOLR"
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                                                                                                                                                                                                                                                                                                                                                 в95213
g2977550
             Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                         Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 165)

Adams, M.D., Rounsley, S.D., Field, C.E., Ba
Golden, K., Berry, K., Granger, D., Suh, E.,
Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                  B95213 165 bp DI
CIT-HSP-2172JB.TF CIT-HSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
9712 Medical Center Dr., Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
For clone availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301 838 0200 Fax: 301 838 0208
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AQ241183.1
                                                                    Contact: Mark Adams
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                            human.
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                                                                                                          Unpublished (1997)
                                                                                                                                              Use of a random BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 663)
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larity 94.1%;
Conservative
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
/db_xref="taxon:9606"
/clone="R-68N14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Lymphocytes" 125 c 105 g 151 t
                                                                                                                                                                                                                                                                                                                                  GI:2977550
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                                                                                                                                          End Sequence
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Pred. No. 7:13e-02;
                                                                                                                                                                                                                                                                                                                                                                                                      Homo
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                                                                                                                                              Database
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                                                                                                                                                                            Bass,S., Lin., Wible,C.,
               20850, USA
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Best Local
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                                                                                                                                                                                                                                                        The ABI trace of this sequence can be viewed at http://www.sanger.ac.uk/Drugia/AFC/MBAFCZ5G02T3.html This is the full sequence of the cDNA clone. The polyA tail has been clipped and is excluded from this sequence Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes expressed in adult female Brugia malayi
Unpublished (1996)
On Apr 14, 1993 this sequence version replace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institute of Cell, Animal and Population Biology University of Edinburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones, S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blaxter, M.L., Waterfall, M., Daub, J., Lizotte, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Filarioidea; Onchocercidae; 1 (bases 1 to 168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brugia malayi
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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MBAFCZ5G02T3 Brugia malayi
malayi cDNA clone AFCZ5G02
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                                                                                                                                                                                                                                                                                                                                                                 Email: mark.blaxter@ed.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                       Tel: +44 131 650 6760 Fax: +44 131 670 5450
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ashworth Labs, King's Buildings, West Mains Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Blaxter ML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brugia malayi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.7%;
Similarity 93.8%;
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/Organism="Brugia malayi"
/Organism="Brugia malayi"
/Orde="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2
Xho I; Lymphatic filarial nematode parasite of humans.
mRNA was prepared from approximately 50 adult females
isolated from the peritoneal cavity of jirds and
converted to double-stranded cDNA
using reverse
transcriptase and oligo(dT) followed by RNase H and DNA
pol I. The library has 5 x 10E6 independent recombinants
and the average insert size is -900bp.The library was
constructed by
Michelle Lizotte-Waniewski. The
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/note="Vector: pBeloBAC11;
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="2172J8"
/clone_lib="CIT-HSP"
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28 c 35 g
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Pred. No. 1.25e+00;
0; Mismatches 1
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adult female cDNA (SAW96MLW-BMAF) Brugia
5', mRNA sequence.
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39 CTTCATTAATGATCTATG 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                           Fax: 314 200 1017
Email: mouseest@vatson.wustl.edu
Email: mouseest@vatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
On Sep 12, 1996 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 194)
                                                                                                                                                                                                                                                                                                  High quality sequence stop:
                                                                                                                                                                                                                                                                                                                  Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                  library is available from genome@smith.edu."
                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="B6D2 F1/J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
/lab_host="XL1-Blue MRF/"
18 c 30 g 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Brugia malayi adult female cDNA (SAW96MLW-BmAF)"
/tissue_type="blastocyst"
                                      /clone="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone-"
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/clone="AFCZ5G02"
                 'clone_lib="Knowles Solter mouse blastocyst B1"
                                                                                                                                                                                                                                                                               ocation/Qualifiers
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                                  'IMAGE: 978246"
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), 1.25e+00;
hes 2; Indels
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EST49800
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Zhu, H., Lall, Kupfer, D., Dunlap, J.C.
Two. Neurospora crassa EST Databases
Unpublished (1998)
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cDNA clone d3c08nm 3', mRNA sequence.
AI321054
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Seq primer: Universal Reverse Primer
High quality sequence stop: 118.
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Fax: 405 325 7762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
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                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBlueScript SK-; Site_1: xbaI; Site_2: ECORI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996. 5' end of cDNA cloned into XbaI site of pBluescript; 3' end of cDNA cloned into EcoRI.site of pBluescript" //db_xref="taxon:5141"
                 Gall
                                                                                                                                                                                                                                                                                               dark"
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/lab_host="DH10B"
47 c 43 g 52 t
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/strain="bd, frq7 A"
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d. No. 1.25e+00;
Mismatches 1;
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Z44153.1
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Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 377 (6547 Supres),
96026280
On Apr 14, 1993 this sequence version replaced gi:693512.
Other_ESTs: THC169726
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                      Z44153 318 bp mRNA
HSClTF031 normalized infant brain
                                                                                                                       c-1tf03,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Organ: gall bladder; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):145467"
/db_xref="taxon:9606"
                                                                                                                          mRNA sequence.
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IMAGE:2035627, mRNA sequence.
AI267326
                                Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 319)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jos Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.

IMAGE::molecular_integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI267326
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Similarity 88.9%;
16; Conservation
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1, rue de l'Internationale, BP60 91002 EVRY Cedex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 318)
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Unpublished (1997)
                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genexpress-Genethon
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/sex="Female"
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46 c 62 g 111
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Pred. No. 1.25e+00;
0; Mismatches 2;
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Best Local Similarity 88.9%;
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                                                                            Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 355)
Pih,K.T., Park,J.M., Jang,H.J., Kang,S.G., Piao,H.L. and Hwang,I.
EST of salt inducible mRNA in Arabidopsis thaliana
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1394805.
Contact: Kyeong Tae Pih
Department of Plant Molecular Biology
Gyeongsang National Univ., Plant Molecular Biology and
                                                                                                                                                                                                                                                                                                                                                                      OS172 NaC1-treated Arabidopsis subtraction library Arabidopsis thaliana cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGGGGGGGGGGGGGGT-3'), to be used as tester. Select Subtraction was performed using the Clontech PCR Select cDNA subtraction kit. Pool of two schizophrenics, male at 44 and female age 56 (S-116, S-118) subtracted by pool of two mentally normal male individuals ages 41 and 53 (S-124, S-141). Tissues were obtained from the Stanley Neuropathology Consortium (www.stanleylab.org). Library constructed and subtracted by Dr. Nancy Johnston [(410) 614-3918, nlj@welchlink.welch.jhu.edu]."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-*Organ: brain; Vector: pCR2.1-TOPO (Invitrogen);
Site_1: ECORI; Total RNA (purified with Trizol and DNAsed
before use) was reverse transcribed using a modified
oligo-dT primer containing RsaI and HindIII sites.
Double- stranded cDNA was digested with RsaI, resulting in
blunt ended cDNA of an average 0.1-2 kb in length.
Digested cDNA was split into two sets, one used as is as
the driver, the other set was split in half again and each
half linked to a different adaptor
[5'-TCGAGGGGCGGCGGGGAGGT-3' or 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2035627"
/clone=lib="Stanley Frontal SN pool 2"
/clone_lib="Stanley Frontal lobe (see description)"
/tissue_type="frontal lobe (see description)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
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/map="21q"
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Best Local Similarity 100.0%;
Matches 14; Conservative
                                                                   Matches
                                                                                                     Query Match
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  52 CTTCAATAATGAACGGTG 69
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                                                                                    Similarity
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Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditiddea; Rhabditidae; Peloderinae; Caenorhabditi
1 (bases 1 to 360)
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D73955
                                                                                                                                                                                                                                                                                                               Email: ykohara@ddbj.nig.ac.j
High quality sequence stop: 273.
Location/Qualifiers
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Tel: 82-591-751-5193
Fax: 82-591-759-9363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kohara, Y., Mitsuki, H., Nishigaki, A.,
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biotechnology Research Center
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    Conservative
                                                                                                     /clone="yk67a9"
/clone_lib="Yuji Kohara unpublished cDNA"
/1 c 77 g 101 t 1 others
                                                                                                                                                                               /note="dev_stage=varied, sex=Hermaphrodite
tissue_type=whole animal"
/db_xref="taxon:6239"
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                                                                                                                                                                                                                                                /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:3702"
/db_xref="taxon:3702"
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/dev_stage="7 day-old"
80 c 80 g 93 t 4 others
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/strain="Columbia"
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                       73.78;
88.98;
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Score 14; DB 32;
Pred. No. 1.25e+00;
0; Mismatches 2
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Pred. No. 1.25e+00;
0; Mismatches 0;
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1 CTTCATTAATGAACGATG 18

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REFERENCE
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AUTHORS
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JOURNAL
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Best Local Similarity 100.0%;
Matches 14; Conservative
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Fugu rubripes.

Fugu rubripes

Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Percomorpha;

Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;

Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.

1 (bases 1 to 380)

Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,

Williams,G. and Brenner,S.

Direct Submission

Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallaceeu.washington.edu
Sequence Tagged Connector
Plate: 3243 row: B column: 21
Class: BAC ends
High quality sequence stop: 367.
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Z90399
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High Throughput Sequencing Center
University of Washington
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Furlong,J.,
Shaker,R., Schmidt,S., Traicoff,R. and Hood,L.E.
Construction of a Characterized Clone Resource for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ231915 367 bp DNA GSS 25-SEP-1998
HS_3243_B1_A11_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3243 Col=21 Row=B, genomic survey
                                                                                                                                                                                                                            GSS; genome survey sequence.
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1 (bases 1 to 367)
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g3657144
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
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Search completed: Sat Nov 27 12:41:25 1999 Job time: 115 secs.
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                                                                                                                                                                                                                                                                                                                                          COMMENT
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Best Local Similarity 93.8%;
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1. .380
                                                                                                                                                                               /organism="Fugu rubripes"
/db_xref="taxon:31033"
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Staphylococcus aureus Caenorhabditis elegans Escherichia coli dehyd Bacillus thuringiensis Oreochromis mossambicu Homo sapiens mRNA for Escherichia coli K-12 Methanococcus jannasch Haemophilus influenzae E: coli genomic DNA, Ko Caenorhabditis elegans Drosophila melanogaste Homo sapiens clone GS3	Description	predicted by chance to have score of the result being protected score distribution	3:em_fun 4:em_htg 5:em_hum1 6:em_ :em_or 10:em_or 11:em_pat 12:em_ph 15:em_sts 16:em_vi 12:em_sts 16:em_vi 13:gb_htg1 20:gb_htg2 21:gb_in1 n 24:gb_ov 25:gb_pat 26:gb_ph 27:gr1 30:gb_pr2 31:gb_pr3 32:gb_ro s 35:gb_sy 36:gb_un 37:gb_vi	es	bases x 2		'.seg TATTTAATATGTTTATAATAGAG	MasPar time 2429.08 Se 1541.672 Million cell	iocomputing Research Usity of Edinburgh, U.K oxford Molecular Ltd using Smith-Waterman	
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Human DNA sequence fro	×		LW .	Rickettsia prowazekii	Caenorhabditis elegans	Homo sapiens chromosom	Plasmodium falciparum	Human DNA sequence ***		Arabidopsis thaliana D	Human DNA sequence fro	Caenorhabditis elegans	Plasmodium falciparum	Homo sapiens clone DJO	Arabidopsis thaliana '	Human DNA sequence ***	Drosophila melanogaste	Plasmodium falciparum	Caenorhabditis elegans	2	m .	Caenorhabditis elegans	Caenorhabditis elegans	Plasmodium falciparum	╗	ш.	m	Chromos	cilis DNA for	germline IgH ch	human STS CHLC.GCT3B06	
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## ALIGNMENTS

	CDS	gene		source	FEATURES		JOURNAL	TITLE	AUTHORS	REFERENCE	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	NID	ACCESSION	DEFINITION	RESULT 1 LOCUS
/gene="murc; /function="cell wall biosynthesis" /function="cell wall biosynthesis" /note="Murc; UDP-N-acetylmuramate-alanine ligase" /codon_start=1 /transl_table=11 /product="UDP-N-acetylmuramoyl-L-alanine synthetase" /protein_id="AAB87090.1"	1. 1314	11314	/organism="Staphylococcus aureus" /db_xref="taxon:1280"	11314	Location/Qualifiers	Hospital and Harvard Medical School, 181 Longwood Ave, Boston, MA 02115, USA	Submitted (11-NOV-1997) Channing Laboratory, Brigham and Women's	Direct Submission	Lowe, A.M. and Deresiewicz, R.L.	2 (bases 1 to 1314)	Unpublished	Cloning and sequencing of Staphylococcus aureus murc. a gene	Lowe, A.M. and Deresiewicz, R.L.	1 (bases 1 to 1314)	Bacillaceae: Stanbylococcus Bacillaceae: Stanbylococcus	Staphylococcus aureus	Staphylococcus aureus.		AF034076.1 GI:2642658	q2642658	AF034076		AF034076 1314 bp DNA BCT 26-NOV-1997

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ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT
                                                                                                                                       TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT
                                                                                                                                                                               TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                   TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTCAAA
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                                                                                                                                                                                                                       ATTGCTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAC
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WKGIKILPEDANNIKEDMVVIQGNAFASSHEEKARAHOMKLDVYSYNDELGQIIDQYT
SVAVTGAHGKTSTTGLLSHVMNGDKKTSFLIGGTGMGLPESDYFAFEACEYRHFLS
YKPDYALMTNLDEDHPDYFKDINDVEDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPI
YYYGFKDSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISY
LEKLDVTNIKEALETFGGVKRRENETTJANQVIYDDYAHHPEETSATLETARKXYPHK
EVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKIEG
ASILNEDSINVLEQFDNAVVLFKGAGDIQKLQNAYLDKLGMKNAF"
a 163 c 250 g 434 t
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99.3%;
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bin/display?db-wormaccasclass-Sequence & object = COIF6
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTIONS are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone COIF6. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
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268213.1 GI:1122764
HTG; Cytochrome P450; FEN
Caenorhabditis elegans.
Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                          Nature 368 (6466), 32-38 (1994)
94150718
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                            see:-
http://webace.sanger.ac.uk/cgi-
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2 (bases 1 to 31281)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Z82266. The true right 6
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m CO1F6} is at 9279 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
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/db_xref="FII:3873814"
/db_xref="STFREMBL:Q17559"
/db_xref="STFREMBL:Q17559"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-*cDNA EST EMBL:D35953 comes from this gene; cDNA EST EMBL:D33187 comes from this gene; cDNA EST yk445h11.3 comes from this gene; cDNA EST yk445h11.5 comes from this gene; cDNA EST yk455h11.5 comes from this gene; cDNA EST yk353f12.3 comes from this gene; cDNA EST yk310a7.3 comes from this gene; cDNA EST yk310a7.5 comes from this gene; cDNA EST yk310a7.5 comes from this gene; cDNA EST yk280d11.3 comes from this gene; cDNA EST yk296a2.3 comes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="C01F6.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(930. .972,1021. .1097,1153. .1254))
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/gene="C01F6.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QDRDHSPMRNLEKLTLKHSDGRLLVRQNYSYVDPSDLESSDVLAMIPIQMAQWKRMFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAA92434.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yk266c4.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="C01F6.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Caenorhabditis
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{\tt KEKIKKETKKSPQTMTLDEVQFDASSNFNIRPTMAPSPNVHTDSTQPSNRKSTGSDDS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="C01F6.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="C01F6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'chromosome="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rom this gene"
                                                                                                                                                                                                                                                                                                                                                                                                             .5575,5663. .5810,5860. .5985,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .31281) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"similar to RNA recognition motif. (aka RRM, RBD, RNP domain); cDNA EST EMBL:T00641 comes from this gene; cDNA EST EMBL:700642 comes from this gene; cDNA EST EMBL:D75485 comes from this gene; cDNA EST EMBL:D75485 comes from this gene; cDNA EST yk269c10.3 comes from the gene; cDNA EST yk269c10.3 comes from the gene; cDNA EST yk269c10.5 comes from the gene;
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ILVQKLCCLGADERVDVLSVIALCTLDIICETSMGIAJGAQLAENNEYVWAVHTINKL
ISKRINNPLMNNSFIYNLYGSFIINKENDYKHGGKLAFLDLLLENVNSGQMDETDVQA
ISKRINNPLMNNSFIYNLYGSFIINKENDYKHGGKLAFLDLLLENVNSGQMDETDVQA
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FFGKIQDIIQAQLGDSNILEATSDENLSEMSMYTESLMSSLAEIEPSFIETDVQEASE
TSSHCEPNLGAKQTYGNEQDADIVIDDSHLFAESENECSGSILVKGGQQKVLFRWTDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGNTFMLEGHDTTSTGLMWAVHLLGNHPDVQRKVQAELDEVMGDDEDVTIEHLSRMKY
LECALKEALRLFPSVLIITRELSDDQVIGGFNIPKGVTFLLNLYLVHRDPAQWKDPDV
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                                                                                                                               24126. .25095

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join(24126. .24194,24453. .24532,24780.

/gene="COIF6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13971. .1469:
/gene="C01F6
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AFYPPEYFWNEDESKYHTTFVVPRGTEFSKFYARRFHEALGMPPLENEIITVLDWLAK
LCILEIVYHTTIWCDITGFGGLPRIEHYRLAMENVEDIIFDLAIDDFSISRLQLQISP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(6798..6884,7346..7969,8083..828250..8346,8394..8428,8525..8737,8784..8876))
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                                                                                                                                                                                                                                                                                                                                                                                                                                            RRAPSNGRPAQRAPKRQNVKSGKPTGGAGAQKKLKAKKPKREAQPKKTLEELDAELDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
'note="similar to PDZ domain (Also known as DHR or GLGF).;
DNA EST EMBL:Z14584 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EISRYSPLDVSGYYETIKRKKDIEEYQNRFYEVHYSDDVRIMNVYATDCSRKR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SW: FEM3_CAEEL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oin(10227. .10297,10396. .10740,10786.
.1666. .11756,12137. .12369)
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                                                                                                                                                                                                      . 25095)
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RESULT 4
LOCUS
DEFINITION
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AUTHORS
TITLE
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KEYWORDS
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Best Local Similarity 100.0%;
Matches 21; Conservative
                                                                                                                                                                                                          Query Match
Best Local
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                           BACSKW01 4043 bp
Bacillus thuringiensis
D86064
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Submitted (08-OCT-1996) Botany and Plant (
California, Riverside, CA 92521-0124, USA
Location/Qualifiers
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Close, T.J. and Choi, D.-W.
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Eubacteria; Proteobacteria;
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Similarity 100.0%;
20; Conservative
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VTVLMAYLRNSAFKKDGYDYHVSADLTGQANHLAATIGADIVKOKMAENNGGYRAINY
GYTDDRVYSKLTSENPIDLVRYQLANCYMGRAGLINSGGAAGGETDLSDAVRTAVIIK
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3 571 c 589 g 507 t 2 others
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1. No. 3.01e+00;
1. no. 3.01e+00;
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                                                    promoter
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                                                                                                                                                                                                                       Submitted (06-MAR-1997) B. Sekkali, Universite de Liege (Ulg), Faculte des Sciences, Service de Genie Genetique, Institut de Chimie, Bat: B6, Sart Tilman, 4000 Liege, BELGIUM
                                                                                                                                                                                                                                                                                                                                                                         A gene encoding tilapia (Oreochromis mossambicus) growth hormone: Molecular analysis of the gene and functional test of its promoter region by transient expression in vitro and in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 5570)
Sekkali; B., Brim, H., Muller, M., Argenton, F.,
Colombo, L., Belayew, A. and Martial, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Per-Perciformes; Labroidei; Cichlidae; Tilapia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tigH gene; tilapia growth hormone.
Mozambique tilapia.
Tilapia mossambica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMTIGHGEN: 5570 bp DNA Oreochromis mossambicus tigH gene.
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                                                                                                                                                                                                                                                                                                                                            Unpublished
2 (bases 1
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578 c 751 g 120
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/clone="pgEM3.5tigH"
                                                                                                                                                                                                           1. .5570
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                                                    /tissue_type="testis"
1. .3679
/evidence=experimental
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                                   /gene="tigH"
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Pred. No. 3.01e+00;
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Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII SK plus clone:HH1779.
Homo sapiens
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Homo sapiens mRNA
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                                  KIAA0562 protein.
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/db_xref="PID:9325419"
/db_xref="PID:92243156"
/db_xref="GI:2243156"
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5328. .5333
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/gene="tigH"
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/gene="tigH"
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FSDFESSLQTEEQRQLNKIFLQDFCNSDYIISPIDKHETQRSSVLKLLSISYGLVESW
EFPSRSLSGGSSLRNQISPRLSELKTGILLLIRANQDEAENYDDTDTLQHAPYGNYYQ
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/gene="tigH"
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/gene="tigh"
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Prediction of the coding sequences of unidentified
The complete sequences of 100 new cDNA clones from
code for large proteins in vitro
DNA Res. 5 (1), 31-39 (1998)
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Escherichia coli.
                                              AE000299.1 GI:1788413
                                                                                                AE000299 U00096
                                                                                                                          genome
                                                                                                                                              Escherichia
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Similarity 100.0%;
20; Conservative
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IPSYLVQPLKANSSVHLAMSQMGLLARLLKDLGTGSSGFTIDNVMKFSVSALEHRVYE
VRETAVRIILDMYRQHQASILEYLPPDDSNTRRNILYKTIFEGFAKIDGRATDAEMRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HH1779"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:3043648"
/translation="MPHKIGFVVVSSSGHEDGFSARELMIHAPTVSGWRSPRFCQFPQ
EIVLQMVERCRIRKLQLLAHQYMISSKIEFYISESLPEYFAPYQAERFRRLGYVSLCD
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ALGIPDEHYLDNLCIFCGERSESFTEEGLDLHYWKHCLMLTRCDHCKOVVEISSLTEH
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REDALLALSKKLMEMPVGTPKEDLKNTLRASVFLVRRAIKDIVTSVFQASLKLLKMII
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ERKREAVQKERYDYAKKLKQAIADLQKVGERLGRYEVEKRCAVEKEDYDLAKEKKQOM
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>EQYRAEVYEQLELHSLLDAELMRRPFDLPLQPLARSGSPCHQKPMPSLPQLEERGTEN</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEKTGCKARELKSVYVDAVGQFLKLIFHQNHVNKYNIYNQVALVAINIIGDPADFSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="KIAA0562 protein"
/protein_id="BAA25488.1"
/db_xref="PID:d1026418"
/db_xref="PID:g3043648"
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}14. .3091
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This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director).
Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli Krizin MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coll K-12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 10036) Blattner, F.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (bases 1 to 10036) Plunkett, G. III. Direct Submission
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Blattner, F.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. col
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                                                                                                                                                           complement(181. .1305)
/gene="b2097"
                                                                                                                                                                                                                   /note="REP (repetitive extragenic palindromic) element;
contains 2 REP sequences"
                                                                                                                                                                                                                                                                                          /db_xref="taxon:562"
77. .153
                                                                                 /gene-"b2097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
/note="f374; This 374 aa ORF is 30 pct identical (9 gaps)
co 102 residues of an approx. 512 aa protein FLIC_SALMU
                                                                                                                                                                                                                                                                                                                                                    /sub_strain="MG1655"
                                                                                                                                                                                                                                                                                                                                                                                  /strain="K-12"
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Escherichia
                                                                'function="orf; Unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="orf, hypothetical protein"
/protein_id="AAC75160.1"
/db_xref="PID:91788416"
/db_xref="FID:91788416"
/db_xref="GI:1788416"
/translation="MKTERILGALYGQALGDAMGMPSELWPRSRVKAHFGWIDRFLPG
PKENNAACYFNRAEFTDDTSMALCLADALLEREGKIDPDLIGRNILDWALRFDAFNKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="b2099"
2764. .3768
                                                                                                                                                                                     /gene="b2100"
3765. .4730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="putative transport; Not classified"
/note="0425; This 425 aa ORF is 32 pct identical (30 gaps)
to 401 residues of an approx. 424 aa protein NUPG_ECOLI
SW: P09452"
                                                                                                                                                                                                                                                      3765.
                                                                                                                                                                                                                                                                                                                                                                              VLGPTSKIALNAIRDGKPVAELENNGVTNGAAMRVSPLGCLLPARDVDSFIDDVALAS
SPTHKSDLAVAGAVVIAWAISRAIDGESWSAIVDSLPSIARHAQQKRITTFSASLAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SW: P14300"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLFAMPLAFYYIFANGYLTEVGMKNATGWMTLGOFSEIFFMLALPFFTKREGIKKVLL
LGLVTAAIRYGFFIYGSADEYFTYALLFLGILLHGVSYDFYYVTAYIYVDKKAPVHMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MKTTAKLSFMMFVEWFIWGAWFVPLWLWLSKSGFSAGEIGWSYA
CTAIAAILSPILVGSITDRFFSAQKVLAVLMFAGALLMYFAAQQTTFAGFFPLLLAYS
LTYMPTIALINSIAFANVPDVERDFPRIRVMGTIGWIASGLACGFLPQILGYADISPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1308.
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GYTDDRVYSKLTSENP I DLVRYQLANCYMGRAGL I NSGGAAGGETDLSDAVRTAV I NK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="orf, hypothetical protein"
/protein id="AAC75158.1"
/protein id="AAC75158.1"
/db_xref="FID:91788414"
/db_xxef="GI:1788414"
/db_xxef="GI:1788414"
/db_xxef="GI:1788414"
/translation="MIARKRRARTIHSRYPIGIYGSIVMTDIAQLIGKDADNILQHRCMTPSDQLYLPGHDYVDRVMIDNNRPPAVLRNMQTLYNTGRLAGTGYLSILPVDQGVEMTPSDQLYLPGHDYVDRVMIVELAIEAGCNCVASTYGVLASVSRRYAHRIPFLVKINHN
ETILSYPNTYDQTLYASVEQAFNMGAYAVGATIYFGSEESRRQIEEISAAFERAHELGM
                                to 297 residues of an approx. 312 aa protein RBSK_ECOLI
SW: P05054"
                                                                                                                                                     3765. .4730
/gene="b2100"
                                                                                                                                                                                                                                                                                                                    <u>Ĺ</u>GGDTDT1GAMATA1CGALHGVNA1DPALKAELDAVNQLDFNRYATALAKYRQQREAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jelie Person (16 gaps)
/function="031; This 334 aa ORF is 27 pct identical (16 gaps)
/note="0334; This 334 aa ORF is 27 pct identical (16 gaps)
/note="0334; This 334 aa oRF is 27 pct identical (16 gaps)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAQGLITLCCQGFGSLLGYRLGGVMMEKMFAYQEPVNGLTFNWSGMWTFGAVMIAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIPLLITAGSSALLGVFAFFLPDTPPKSTGKMDIKVMLGLDALILLRDKNFLVFFFCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative nucleoside
/protein_id="AAC75159.1"
/db_xref="piD:91788415"
/db_xref="GI:1788415"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="b2099";
                                                                                       /function="putative enzyme; Not classified"
/note="0321; This 321 aa ORF is 26 pct identical (15 gaps)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="yegT"
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                                                                                                                                                                                                                                                                                                                                                 ETALKIVRNADGTESASEQLYQVVGAGTSTIESVPCATALVELAQTDPNRCAVLCAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor Sigma70; predicted +1 start at 2176792"
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DEFINITION
ACCESSION
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                                                                       REFERENCE
                                                                                                                                                               SOURCE
                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                             RESULT
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Matches 2
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Bult, C.J., White, O., Olsen, G.J., Zhou, L., Fleischmann, R.D., Sutton, G.G., Blake, J.A., FitzGerald, L.M., Clayton, R.A., Gocayne, J.D., Kerlavage, A.R., Dougherty, B.A., Tomb, J., Adam
                                                                                                                                                                                                                                                       U67574 11978 bp DNA
Methanococcus jannaschii section
U67574 L77117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.5%;
Similarity 100.0%;
20; Conservation
                                                                                                                  Methanococcus jannaschii
Archaea; Euryarchaeota;
                                                                                                 Methanococcus
                                                                                                                                                               Methanococcus jannaschii.
                                                                       (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="megahtqliaqlnerilaadntplyikfaetyknavrsgylehg
Nilpgerdlsqltgvsritvrkamqaleeegvvtrsrgygtqinnifeyslkeargfs
QQVVLRGKRPDTLWVNKRVVKCPEEVAQQLAVEAGSDVFLLKRIRYVDEEAVSIEESW
VPAHLIHDVDAIGISLYDYFRSQHIYFQRTRSRVSARWPDAEFQSHIQLDSKIFVLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(4704. .5450)
/note="b2101"
                                                                                                                                                                                                                 GI:1591978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="orf; Unknown"
/note="f275; This 275 aa ORF is 36 pct identical (21 gaps)
to 206_residues of an approx. 296 aa protein LYCM_STRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="yegx"
complement(5502. .6329)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="factor Sigma70; predicted +1 start at 2180843"
complement(5502. .6329)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5499. .5526)
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AGLASGLPLADAVLLGNAVASWVVGHRGGDCAPTREELLLAHKNV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSGARLHTLLPELTTRQSYMVVGAAVIDVIADAYALPWRGCDIE
LKQQSVNVGGCALNIAVALKRLGIEAGNALPLGQGVWAEMIRNRMAKEGLISLIDNAE
GDNGWCLALVEPDGERTFMSFSGVENQWNRQWLARLIYVAPGSLLYFSGYQLASPCGEL
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/protein_id="AAC75161.1"
/db_xref="PID:g1788417"
/db_xref="GI:1788417"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="orf, hypothetical protein"
/protein_id="AAC75163.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="PID:g1788418"
/db_xref="GI:1788418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative transcriptional regulator"
/protein_id="AAC75162.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="putative regulator; Not classified"
/note="f248; This 248 aa ORF is 30 pct identical (14 gaps)
to 217 residues of an approx. 272 aa protein YHFR_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="yegW"
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                                                                         to 11978)
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                                                                                                                                            jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                          2322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20; DB 18;
Pred. No. 3.01e+00;
0; Mismatches C
                                                                                                                       Methanococcales; Methanococcaceae;
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       Tomb, J., Adams, M.D.,
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Bult.C.J., White,O., Olsen,G.J., Zhou,L., Fleischmann,R.D.,
Sutton,G.G., Blake,J.A., Fitzgerald,L.M., Clayton,R.A.,
Sutton,G.G., Blake,J.A., Fitzgerald,L.M., Clayton,R.A.,
Gocayne,J.D., Kerlavage,A.R., Dougherty,B.A., Tomb,J., Adams,M.D.,
Reich,C.I., Overbeek,R., Kirkness,E.F., Weinstock,K.G.,
Merrick,J.M., Glodek,A., Scott,J.D., Geoghagen,N.S., Weidman,J.F.,
Fuhrmann,J.L., Nguyen,D.T., Utterback,T., Kelley,J.M.,
Peterson,J.D., Sadow,P.W., Hanna,M.C., Cotton,M.D., Hurst,M.A.,
Roberts,K.M., Kaine,B.B., Borodovsky,M., Klenk,H.P., Fraser,C.M.,
Smith,H.O., Woese,C.R. and Venter,J.C.
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Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii Science 273 (5278), 1058-1073 (1996)
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Center Dr. Rockville, MD 20850, USA
3, 1996 this sequence version replaced gi:1565379.
Location/Qualifiers
                                                                                                                                                                                                                                                                                    /product="H(2)-dependent methylenetetrahydromethanopterin dehydrogenase related protein "protein_id="AnaB99348.1"
/protein_id="AnaB99348.1"
/db_xref="pID:91591980"
/db_xref="pID:91591980"
/db_xref="GI:1591980"
/db_xref="GI:1591980"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene≖"MJ1338"
917. .1978
                                                                                    /gene="MJ1339"
2010. .2474
                                                                                                                                                                           GGAAAEGAIKRSARKLFEH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PID:48909 percent ide similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KASHPAYVRGFISEIDDNEVPKLIERDYKLKMPKYMVVKGETDYTIREEKIIDKIKEP
KIKAMECIGGTGDTLTEIVSSLISVDFKTEEALSLGCKINRKLGEIANVNPNTQITEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Methanococcus
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145. .840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MIGAVLKTLEYFDEKDVKVITTGDIGEGDGSLKIYDALKEIDDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to SP:P32440
PID:48909 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INAIPKALENTLK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MJ1338"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="GI:1592330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="MJ1337"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ′gene='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MJ1337"
   32.65; i
   SP:P04766 identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; identified by GeneMark;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                jannaschii"
GB:X04399 PID:39954 percent by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:U19363 GB:U19364 GB:X59547 29.09; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Research,
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gene

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/ note="hypothetical protein;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="MJ1342"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4078.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVEASKIIKDEIENAYFREFEGISVFIECDNPKNISKKINSLIKLDNRKSITTICPNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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WKQILGTNWPNNGLDLASWFFGLVFCATAATIVSGGVAERIKFSAYVLISLIITGLLY
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                                                                                                                                                                                                                                                                                                                                                    IKENGYCWFRIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="MJ1341"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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                                                                                                                                                                         codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            nii predicted
9.1"
                                                                                                                                                                                                                 SP:P54144 PID:2299143 : 35.64; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by GeneMark;
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                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                     VERSION
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                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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annotations omitted
                                                                                                  EINPNIPDAWNGKAIALEKLGKINEAIECYNRALDIYE'7553. .8917
                                                                                                                                                            LKLCRLEKSDLPVKYYTAFILKKLGEYDYALKIIDKILKKYPKSAIAWAEKGEILYRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(5750. .6088)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTANGIVAGLVAICSGTDVVSPIGGLIIGLIAGLQVPIVYKLVEKAGLDDVCGVVPVHGTAGGVIGAILTGILGLKIFGGAGGVSLIDQIIGAVFCIIYGTGLGYILAKIVGIALGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLFVYLGPWGASIVPWHDYAGSLVVHGLGGFLALGAIAALGPRIGRFVDGRPVPILGH
NIPMAVFGAFALAIGWYGFNVGSSLALGDISGLVCATTTMAMAGGGIGALIASRNDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to GP:1279429 percent identity: 59.82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(5750. .6088)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MJ1345"
/note="similar to GB:AI
identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTKEEGRDVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
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uence similarity; putative"
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1175 ATTTAATTGATAAAATTGGA 1194
                           2080 ATTTAATTGATAAAATTGGA 2099
                                                               1.5%;
Similarity 100.0%;
                                                       Conservative
                                                   Score 20; DB 18; Lo
Pred. No. 3.01e+00;
0; Mismatches 0;
                                                                                Length 11978;
                                                       Indels
                                                       0
                                                     Gaps
                                                       0
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12188 bp

09-SEP-1998

93212217 U32809.1 1 (bases 1 to 12188)

Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A.,

Kirkness,E.F., Kerlavage,A.R., Bult,C.J., Tomb,J., Dougherty,B.A.,

Merrick,J.M., McKenney,K., Sutton,G.G., FitzHugh,W., Fields,C.A.,

Gocayne,J.D., Scott,J.D., Shirley,R., Liu,L.I., Glodek,A.,

Kelley,J.M., Weidman,J.F., Phillips,C.A., Spriggs,T., Hedblom,E.,

Cotton,M.D., Utterback,T., Hanna,M.C., Nguyen,D.T., Saudek,D.M.,

Brandon,R.C., Fine,L.D., Fritchman,J.L., Fuhrmann,J.L.,

Geoghagen,N.S., Gnehm,C.L., McDonald,L.A., Small,K.V., Fraser,C.M. Haemophilus influenzae Rd Haemophilus influenzae Rd Haemophilus influenzae Rd section 124 of 163 of the complete Haemophilus. Eubacteria; Proteobacteria; U32809 L42023 GI:3212217 gamma subdivision; Pasteurellaceae;

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REMARK
COMMENT
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TITLE
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The H. influenzae sequence has been updated by R. Fleischmann. New database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. We gratefully acknowledge the work of Tatusov et. al. We have incorporated their annotation into the /notes fields of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-JUL-1995) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA 4 (bases 1 to 12188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tatusov,R.L., Mushegian,A.R., Bork,P., Brown,N.P., Hayes,W.S., Borodovsky,M., Rudd,K.E. and Koonin,E.V. Metabolism and evolution of Haemophilus influenzae deduced from a whole-genome comparison with Escherichia coli Corr. Biol. 6 (3), 279-291 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
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for (bases 1 to 12188)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"similar to SP:P09170 GB:X13270 PID:42218 PID:42222 PID:606107 percent identity: 67.44; identified by sequence similarity; putative" /codon_start-1
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288. 674
                                                                                                                                                                                                                                                        /gene="HI1289"
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                                                                                                                                                                                                                                                                                                                                   /gene="HII
674. .1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="ribosome binding factor
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                                                                                                                                                                                                                                                                                                                                                                                                     VEGMRMSNLVTNVVREDEKKHVEESN"
                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="marefkrsdrvaqeiqkeiaviiqrevkdprigmvtvsdvevss
DLSYAKIFVTFLFDHDEMAIEQGMKGLEKASPYIRSLLGKAMRLRIVPEIRFIYDQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clayton, R.A., Kerlavage, A.R. and Fleischmann, R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="HI1288"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="
                                                                                                                                                                                      transl_table=11/
                                                                                                                                                                                                            codon_start=
                                                                      'translation="MSRPRKRWRDVDGVFLLDKPQGMSSNDIMQKVKRLFQANKAGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGRFPERYEWLLEQIQIWGAKIYQTNATEHDHNMTYIQALRHFSTFANGLHLSKQPIN
LANLLALSSPIYRLELAMIGRLFAQDAELYADIIMDKSENLAVIETLKQTYDEALTFF
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DQTAENASPAWQVLYTTHLQSCSPIHSGENFAPIPLYKQLKNQPHLTQDLIKWQENWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / wore="nypothetical protein; identified putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NQPFTIGADIWTAYEISWLNEKGLPQVAIADIYLDYQSQNLIESKSFKLYLNSFNQSK
FADFNAVQQTMQRDLSECAQGDVKVRLNPMAVYDSQKIDHLQGDCIDEQDIEITSYEF
NANWLKDCVSDEIVEEKLVSHLLKSNCLITNQPDWGTLHIHYVGKKINQEKLLRYVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2838. .3677)
/gene="HI1291"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIYAPEREIAMLQARRLEAEKAGISADLIEDVLRRFMRESYANENQFGFKTINSDIHK
IVIVGGYGKLGGLFARYLRASGYPISILDREDWAVAESILANADVVIVSVPINLTLET
IERLKPYLTENMLLADLTSVKREPLAKMLEVHTGAVLGLHPMFGADIASMAKQVVVRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOLLAESFPLSELDRLLLPTDTAVSKLPALHLDAEQSKAIGFGQRVKFANEQOLSGOVRLSAENLFLGVLNRREYYSPTTINYTIRITSLPFL"
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                                                                                                                                                                                                                                                                     complement(4580. .4960)
                                                                                                                                                                                                                                                                                                                              complement(4580. .4960)
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                                                                                                                                                                                                                                                                                             /gene="HI1293"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRQHNEFHEQCVERIFCDLMHYAKPEKLTVYARYTRRGGLDINPFRSNFENLPENLRL
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                                                                                                                                                                                                                                      /gene="HI1293"
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translation="MIEQLKQAKNWEDRYRLIIQAGKNLPRPSDNELAQMQPITGCEA/

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REFERENCE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                               TITLE
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Local Similarity 95.2%;
les 20; Conservation
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Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S., Itch, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T.,
                                                                                                                                          Submitted (12-DEC-1996) to the DDBJ/EMBL/GenBank databases. Hirotada Wori, NARA Institute of Science and Technology, Res. & Edu. Center for Genetic Info.; 8916-5 Takayama, Ikoma, Nara 630-01, Japan (E-mail:hmoriégtc.aist-nara.ac.jp, Tel:81-7437-2-5660, Fax:81-7437-2-5669)
                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda miniset library clone:Kohara clone #359.
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D90848.1 GI:1736814 Complete and shotgun
                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                       Mori,H.
                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
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QARTQVKEWVHAEDKHAVIWTSGTTHAINLVANGLMPQLNAEDEILISQADHHANFVT
WHETAKKCGAKIQVLPILDNWLIDENALISALSEKTKLVALNFVSNVTGTEQPIKRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identity: 47.14;
putative"
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QYAISLAESVKVRLKSYENCRLFNSPQASTVVCFVFDGIDCSDLSTLLSEQNIALRVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WHETAKKCGAKIQVLPILDNWLIDENALISALSEKTKLVALNFVSNVTGTEQPIKRLI
QLIRKHSNALVLVDAAQAISHIKIDLQDLDADFLAFSAHKIYGPNGLGVLTGKLTALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(4957. .6270)
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complement(4957. .6270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="nuclease, putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(6104. .6640)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHCAQPYLARLGERTTLRLSFAPYNTQEDVEAFFTALDKALDLLQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QMWFQIMPKNDRTFQFSGFSEARIMNGLLWILFNQINGKTADELNTFDITVFFSELGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene-"HI1296"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="HI1296"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="G1:1574753"
/translation="MIRFIFKHKKMHKPKELVFGQTIIQLNQVNGADKRKLIWLLIIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="nifS protein, putative"
/brotein id="AAC22941.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to PID:882705 GB:U00096 PID:1789175 percent
identity: 47.14; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="HI1295"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identified by sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAC22941.1
/db_xref="PID:g1574753"
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing; IS5;
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clone #359(46.8-47.2 min.).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gatA; gatB;
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Members: (1995.4 - 1996.3)
Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saito, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, Yamamoto, Y. and Yano, M.
The systematic sequencing of the Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Information operator:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Headed by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Project:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Address: NARA Institute of Science Ikoma, 630-01; Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name: Takashi Horiuchi
Address: National Inst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T., Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,Y. and Yano,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Japan E.coli genome DNA sequencing group
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name: Hirotada Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kimura,S., Kitagawa,M., Kitakawa,M., Makino,K.,
Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1. .1003)
/gene="gatC"
                                                AILVNVAMLLTRMTRVVNVDIWNIWHMTFTGALLHLATGSWMIGMAGVVIHAAFVYKL
GDWFARDTRNFFELEGIAIPHGTSAYMGPIAVLVDAIIEKIPGVNRIKFSADDIQRKF
                                                                                                                                                                                                                 /transi_table=11
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(Phosphotransferase enzyme II, C component)."
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/db_xref="PID:d1016684"
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="ORF_ID:0358#2; similar to Number P37189]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Nucleotide position 2176551-2194463 from the initiation site of ThrA (0 min.).; This clone is frow Kohara lambda miniset library."
                                                                                                       /db_xref="pid:91736815"
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IGFVGIGLVIGLMLDSIGPAAKAMAENFDLNLHVVDVGWPGSSPMTWASQIALVAIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(<1. .1003)
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QARSRLQAKFGGQEFLIGLDPALLLGHTAVVSASLIFIPLTILIAVCVPGNQVLPFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="gatC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="46.8 min"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="Kohara clone #359"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .aist-nara.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E.coli genome DNA sequencing project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _lib="Kohara lambda
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                                                                                                                                                                                                                                                                                                                                                                                                                                              [SwissProt Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is from
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="IS5"
1605.
                                                                                                                                     /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1605. .2621
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                        complement(2659.
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                                                                       AEIHDGGAVRQGAIQG"
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GLMHLRIALLLFVLGRAGCLNDGGIDQGALSHHDACFGQPAIDGLEQLAGQLMLLQQV
                                                                                                                                                                                                                                                                                                                                 complement(1917. .2273)
/gene="IS5"
                                                                                                                                                                                                                                                                                                                                                                                   ERSH
                                                                                                                                                                                                                                                                                                                                                                                                                             ARLSLDSALPDRTT IMNFRHLLEQHQLARQLFKT INRWLAEAGVMMTQGTLVDATI I E
APSSTKNKEQQRDPEMHQTKKGNQWHFGMKAH IGVDAKSGLTHSLVTTAANEHDLNQL
GNLLHGEEQFVSADAGYQGAPQREELAEVDVDWL IAERPGKVRTLKQHPRKNKTAINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PWQNMVEVIEPFYPKAGNGRRPYPLETMLRIHCMQHWYNLSDGAMEDALYEIASMRLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAA15961.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ORF_ID:0358#4; similar to [SwissProt Accession Number P37187]; start codon is not identified yet"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1322. .2973)/gene="gatA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKRKIIVACGGAVATSTMAAEEIKELCQNHNIPVELIQCRVNEI
ETYMDGVHLICTTAKVDRSFGDIPLVHGMPFISGIGIEALQNKILTILQG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1007. .1291)
/gene="gatB"
/note="ORF_ID:o359#4; similar to
                                                                                                                                                                                                                                                                                                                                                                                                      EYMKASIRARVEHPFRIIKRQFGFVKARYKGLLKNDNQLAMLFTLANLFRADQMIRQ%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A91483]"
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/product="PTS system, Galactitol-specific IIB c/product="PTS system, Galactitol-specific IIB component)
(EIIB-GAN) (Galacticol- permease IIB component) (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ORF_ID:0358#3; similar to [SwissProt Accession
Number p37188]"
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                                                                                                                                                                                                                                                                                                           'note="ORF_ID:o359#2; similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="ORF_ID:0359#1; similar to [PIR Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Phosphotransferase enzyme II, A component) (EC
2.7.1.69)."
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(BIIA-GAT) (Galacticol- permease IIA component)
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Query Match 1.5%;
Best Local Similarity 100.0%;
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The sequence of C. elegans cosmid C17H12 (npublished (1998) 3 (bases 1 to 47045) Waterston, R.
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                                                                                                                                                                                          Nature 368 (6466), 32-38 (1994)
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Number P37191]"
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Note: remainder of
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E 1 (bases 1 to 209071)

Celniker, S. E., George, R. A., Galle, R. F., Hoskins, R. A., Svirskas, R. R., Harris, N. L., Agbayani, A., Arcaina, T. T., Baxter, E Blazej, R. G., Chev, M., Dolle, C. M., Farfan, D. E., Flanagan, J., Houston, K. A., Hummasti, S. R., Karra, K., Kearney, L., Kim, S. H., Lee, B., Lomotan, M. A., Mak, J., Mazda, P., Mok, M. S., Moshrefi, A. R., Moshrefi, M., Nixon, K., Pacleb, J. M., Park, S., Pfeiffer, B., Punch, E., Snix, E., Twomey, B., Wan, K. H., Whitelaw, K Yee, A., Zhang, R., Zieran, L. L. and Kimmel, B.

Sequencing of Drosophila chromosome 2L, region 26C1-26D2
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Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E.,

Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E.,

Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,

Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S.,

Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,

Moshrefi, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R.,
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HTG.
Submitted (15-JUL-1998) Berkeley Drosophila Genome Project, MS
                                                   Yee,A., Zhang,R., Zieran,L.L. and Kimmel,B.E. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    annotations omitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EYDKHITELKNOKISIRKPVVRRYEESSKYHQYSYMTISILLIFTIFLTGYLFGRCCC
VGNQDRNLYIQLDGSNIPTGHIVKNF"
Complement(26876. 29985)
/gene="C17H12:12"
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MVQVRVRVNNLLSKNVPAYLYEYTYPKHARHTDDLFYLMGVHRFEKDENEIELGKVYE
TIFMNFAKFGDPKEGFELANAENESYYEVYWDGETGERPQMKTKFEEKIINYWLKDMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILTFSSKINHDLSLFQQSICMSSGHDFETLEIQIQKTNRFAKHAGCTVPSIIEKKMTT
RQSDLYRMKCLQNKDALELLRVQRLLEDEGYPTYGYLVQREPLIQEIPYQEFMKSPKK
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LGIFSHFVVEDQSIAPTNLALYDILLGVEFVKNEIHNFGGNNQKNTIMGHSYGGSIVN
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HLFKHIPLAKPPIGKLRFQKPEPPEKWTGVRNAKAYGPACISNSSYSTSPQKWIDEDC
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/db_xref="PID:g2854165"
/db_xref="GI:2854165"
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Pred. No. 3.01e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Best Local Similarity 100.0%;
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and relationship to other sequences, please visit our sequence/new Web site (http://fruitfly.berkeley.edu/sequence/) email to drosophila@mbgc.lbl.gov. Library locations: 25-2, 137-57, 12-2. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64-121. Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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8
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Submitted (25-AUG-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                    In 1972. 1998 this sequence version replaced gi:3451378.

In Nov 22, 1998 this sequence version replaced gi:3451378.

In Nov 22, 1998 this sequence version replaced gi:3451378.

In Nov 22, 1998 this sequence record is sequence record is the process of the places is the not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence the place of the place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates; Catarrhini;
1 (bases 1 to 211037)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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be preserved
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2161
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16572
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a 45615 c 45383 g 58488 t
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/db_xref="taxon:7227"
/chromosome="2L"
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                                                                                                            2160:
16553:
16571:
                                                                          30233:
                                                               2142: contig of 2142 bp in length 2160: gap of unknown length 16553: contig of 14393 bp in length 16571: gap of unknown length 16571: gap of 13662 bp in length
   gap of contig
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Pred.
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No. 3.01e+00;
unknown length of 28770 bp in
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygil; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cooperative Human Linkage Center Unpublished (1995) Synonyms: GCT3806, CHLC.GCT3806.T11065 Contact: Dr. Jeffrey C. Murray
                                                                                                                                                                                                                                                                                                                                                     Primer A: ATTGACTTGGAGATGGATCG
Primer B: TCCTTAGGTCTTGGCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                              The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G09531.1 GI:941380
STS sequence; primer; sequence tagged site.
STS sequence; primer; sequence tagged site.
human vector=pUCP1 host=E.coli dut+ung+ (DH10B) Marker Selected
genomic DNA prepared from XX individual of French nationality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G09531 524 bp DNA STS human STS CHLC.GCT3B06.P11066 clone GCT3B06.
                                                                                                                       Buffer:
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Similarity 100.0%;
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59040
122512
122530
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                                         Location/Qualifiers
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/db_xref="taxon:9606"
/clone="GS308H05"
42490 c 42250 g 6088:
           organism="Homo sapiens"
                            . 524
                                                                                       MgCl2:
KCl:
                                                         PH:
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No. 3.01e+00;
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each 1.5 pmole
each 200 uM
0.3 units
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REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
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ACCESSION
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SOURCE
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chromosome 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Structural analyses of human developmentally regulated Vh3 genes Scand. \mathcal{J}. Immunol. 31 (3), 257-267 (1990)
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Human germline IgH chain (hv3005) V3-region
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Similarity 86.4%;
19; Conservative
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                                                                                                                 /note="G00-128-528"
/product="immunoglobulin heavy chain V-region"
2236. .2242
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                 /note="nonamer recombination signal; G00-128-528'
528 c 591 g 762 t
                                               /note="heptamer recombination
2266. .2274
/gene="IGHV@"
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/translation="MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGRSLRLSCAAS
GFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Homo sapiens"
/db_xref="taxon:9606"
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/tissue_lib="Y79-EMBL-3"
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                                                                                                                                                                    'gene="IGHV@"
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oin(1782. .1827,1929.
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Pred. No. 1.46e+01;
0; Mismatches 3
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             591 g
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如果也是是有人的现在分词,我们也有有的的,我们也有有的的,我们的人,我们的人,我们的人,我们的人,我们的人,我们的人,我们的人,我们	
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Sat Nov 27 14:14:48 1999; MasPar time 8.72 Seconds 460.971 Million cell updates/sec

Tabular output not generated.

Title: >US-09-103-287-1 (1-1351) from US09103287.seq 1351

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 ATGAGTAAGGAGTTTTATAT......TTAATATGTTTTATAATAGAG 1351
TACTCATTCCTCAAAATATA.....AATTATACAAATATTATCTC

Scoring table: TABLE jmetric

Gap 60

Nmatch STD: Dbase 0; Query 0

Searched: 1052 seqs, 1486975 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

HIV-NA8 1:H\_PRI 2:H\_UNA 3:H\_VIR

Statistics: Mean 10.393; Variance 2.033; scale 5.112

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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20	19	18	17	16	15	14	13	12	11	10	9	8	7	O	Մ	4	ω	Ŋ	1	Result No.
13	13	13	13	13	13	13	13	13	13	13	13	14	13	15	15	15	15	16	16	Score
1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.1	1.1	1.1	1.1	1.2	1.2	Query Match
341	324	324	324	324	323	320	320	319	312	305	302	273	253	9811	9468	9076	1459	10036	330	Length
ω	ω	ω	ω	ω	ω	w	ω	ω	w	w	ω	ω	w	ω	ω	N	ω	ω	ω	BB
HIVFLQ624	HIVFLPE21	HIVFLPE210	HIVFLPE22	HIVFLPE26	HIVFLQ7227	HIVFLQ7223	HIVFLQ7216	HIVMOM22	HIVFLQ626	HIVFLQ7214	HIVFLQ7229	HIVU08687	HIVBOS1	SIVCPZ	FIVPPR	HIVHAN	HIVVI69	SIVSABLC	HIVU04910	ID
Human immunodeficienc	Simian immunodeficien	Feline immunodeficien	Human immunodeficienc	Human immunodeficienc	Simian immunodeficien	Human immunodeficienc	Description													
8.65e+01	2.09e+01	8.65e+01	4.03e+00	4.03e+00	4.03e+00	4.03e+00	6.32e-01	6.32e-01	Pred. No.											

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9672 10271	9623	9597	9540	9215	8391	8344	7817	4549	4549	3201	2806	2589	2580	1462	1366	1116	675	371	371	367	352	345	343
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HIV2ST HIV2UC1	SIVAGM677	SIVSYK	HIVJRCSF	SIVMNDGB1	BIV106	EIAV	HIV2D205	HSPUENV	HSPUENV	HIVBAL2	HIVU08801	HIV2ALI	EIAVWU5	HIVLBV217	HIVSBB	SIVVER1E	HIVAT11S2	HIVFLPD28	HIVFLPC212	HIVFLPD214	HIVFLD25	HIVU08774	HIVELUZ4
Human immunodeficienc	=	Simian immunodeficien	Human immunodeficienc	Simian immunodeficien	Bovine immunodeficien	Equine infectious ane	Human immunodeficienc	Human spumaretrovirus	Human spumaretrovirus	Human immunodeficienc	Human immunodeficienc	Human immunodeficienc	Equine arthritis ence	Human immunodeficienc	Human immunodeficienc	Simian immunodeficien	Human immunodeficienc	Human immunodericienc					
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## ALIGNMENTS

				•	
ORGANISM	LOCUS DEFINITION ACCESSION SOURCE	nb 222 a.   Qy 1233 A.   RESULT 2	Query Mat Best Loca Matches	ACCESSION SOURCE REFERENCE AUTHORS COMMENT FEATURES CDS BASE COUNT ORIGIN	RESULT 1 LOCUS DEFINITION
Cocultured rames defined in its natural habitat of Senegal.  African green monkey captured in its natural habitat of Senegal.  Simian immunodeficiency virus  Viridae: ss-RNA enveloped viruses; Positive strand RNA virus;		agaacaatitgataat 237 	1.2%; Score 16; DB 3; Length 330; Best Local Similarity 100.0%; Pred. No. 6.32e-01; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Baltimore, U.S., partial env cds, C2V3 region.  U04910  Human immunodeficiency virus type 1 (HIV-1), isolate 662,  Baltimore, U.S.; cultured on PBMCs.  1 (bases 1 to 330)  NIAID/NIH DAIDS Variation Program.  This sample is part of a set of sequences generated through the NIAID/NIH DAIDS HIV variation program. The virus was derived from an asymptomatic individual, from Baltimore, U.S., whose route of infection is thought to be due to homosexual contact. The blood sample was taken in 1992. This env sequence clusters with HIV-1 B subtrype sequences. The full name of this sequence is HIV192US65DANIBA.OldilsED; it was presented in alignments in an abbreviated form in the April 94 Human Retro. AIDS compendium update as BJUS662D.OldilgED.  Location/Qualifiers <pre></pre>	HIVU04910 330 bp ds-DNA VRL 01-APR-1994 Human immunodeficiency virus type 1, isolate 662 from

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F., Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H. Mosaic Genome Structure of Simian Immunodeficiency Virus from West African Green Monkeys
EMBO J. 13, 2935-2947 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yirus sab-1 was derived from a wild female asymptomatic sabaeus virus sab-1 was derived from a wild female asymptomatic sabaeus African green monkey. She was caught in her natural habitat of Senegal and susequently exported to the United States. From the point of capture and throughout the study, she was housed in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was obtained as part of a study designed to determine the breadth of genetic variation of SIV infecting African green monkeys. With this aim in mind, Jin et al. PCR-amplified, cloned and sequenced the LTR and partial envelope region from 12 isolates (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1, tan-17, tan-40, and tan-49). These isolates were derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              different African green monkey species inhabiting various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retroviridae; Lentivirinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI gi: 466229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             individual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           710 of pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   staff_review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLSANLLETKEGYVKILSYLLPLYPTGSENLIALFNLCCYLACIHAEIKYKDTEEAKA
KVKEEYPAEMTESATATSSGQTKELQAKKKNEPTYTPSGGSRNYPIYSYNNQWYHQPL
SPRTLNAWYKYIEEKKESAEYYPMFSALAEGAIPYDINQMLNAYGEHQGALQIYKDVI
                                                                                                                                                                                                                                                                                                                                                                                                                              DCQKQVNFLGFGPWGRGKPRNFPLTSIRPTAPPMERDYSRPEENWYADRPPTRGPGPD
DPATALLKQYAVQGKRQKQQWQNHSPQQSPYEEAYSSLRSLFGEDQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEEAADWDLRHPPPQQPPAQGVLRDPQGSDIAGTTSTIQEQIEWTTRAQNAVNVGNIY
KGWIILGLQKCVKMYNPVNILDIKQGFKEPFKDYVDRFYKALRAGTDPAVKNWMYQS
LLIQNANPDCKTVLKGLGMNPTLEEMLTACQGTGGAQHRARLMAEAMTAAFQQQTWL
IFVQQGARPRGPLGGRGRPLNPNIKCYNCGKPGHLARFCKAPRRQGCWKCGSPDHOMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative TAR 1" 528..568
                                                                                                                                        /product="POL protein"
/translation="FFRVWPLGQRETQEFPSDLHQTNSSPNGTGLQQAGGKLVCRQTS
DQRTRARRSSNSPVKAVCCSGETAETAVAKPLATTEPLRGGLQLPQVSLWRRPWKTVY
IEGQKVTALLDTGADDSVIQGIELGDNWKPRIIGGIGGGINVKAYHNQEVKIEDKTCK
VQLGIPHPAGLQQREQITVLDIGDAYFSCPLDPDFQKYTAFTIPSVNNREPGIRYQYK
VLPQGWKGSPTIFQTTANKILQEFRQKNPDVDIYQYMDDMLIASDRPKAEHLVMVQQL
                                                                        ATILVGETPVNIIGRNVLAQLGVTLNLTQREIEPIKVHLKPGQDGPRIRQWPLSKEKI
EALKAICEDLEKQGHLERIGPENPYNTPVFAIRKKDKTQWRILMDFRQLNKSTQDFQE
                                                                                                                                                                                                                                                                                                                                                     /note="N-terminal uncertain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="GAG polyprotein"
/translation="MGASNSVLSGRKLDAFESVRLRPNGKKKYKLRHLVWASKELDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="NCBI gi: 466230"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="simian immunodeficiency virus"
/specific_host="African green monkey"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="sabaeus subtype"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="SIVagmSAB-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="SAB-1/MJ8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            putative TAR 2"
                                                                                                                                                                                                                                                                                                                                                 NCBI gi: 466231"
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KIRWNWYSYQEWYIPLKGGALIKVTNYHHLTPEKGWLETYATGIGYSKGEWFTELDPW
TADHIIHWSYFPCFTDRAVQQAIRGEKYLWCKHQVGHQPTGQVPSLQYLALRVYTNGL
RRVAFTSRRGSSGGSPQESQRRDTRMARNMGFAQRAVRRMAPRHYTGPQFRGPVPLPK
.ESPFPSLVEYCGRTSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANRTEIWOKNGNSNDSVIIRLNRYFNLTIRCRRPGNKTVLPVTIMAGLVFHSOKYNTR
LKQAMCWFGGKNRGAMKEVKETIVRLEPKKYSGTNDTINKIFLOKOMGDESEFFFINK
CGEEFFYCKNDWFLNYLLNKSVDPDHNNCAKNNTKPCNGRTYPPCHIROYNDWYTLSK
KTYAPPREGHLECNSTATALYVELNYNSKNRTINVTLSPQIESIWANELGDYKLVEIKP
IGFAFFKVRKTGPEROKRVPFVLGFLGFLGAAGAAMGAATALTVQSQOLLAGILQO
QKNLLAAVEQOQOMLKLTIWGYKNLNARVTALEKYLEDDARLNIWGCAFRQVGHTTVL
MKYNNTPDWENNTWQEWERQIEKYEANISRILEQAHEQEKNLDSYQKLVSWSDFWSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNWASQIYTGIKTKHLCRLIRGARPLTEIVQWTEEAELELEENROILRQKOQGGYYDP
ALPLRAKVLKLGDGQWGYOIVQPENKILKVGKYAKIKTAHTNELRMLAGLVQKIGKES
IVIWGQIPIMELPVERELWEQWWSDYWQVTWIPEWEMVSTPQLIRLWYKLVKDPIPGE
AVYYVDGAANKNSKEGKAGYLTDRGDGKVVALENTNOKAELEAILLAYKLVKDSGSKVNI
ITDSQYAMGIIAGEPTESDNNIVQQIIEELIKKEAVYIAWVPAHKGVGGNEEIDKLVS
OGIRQYLFLDRIEEAQEEHDKYHANWRSMQQEFGLPAIVAKEIVAACPKÇQIKGESVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCVKLSPMCIKMNCYRLEGGAATTTSPSTSTARPEVVSVGFNDSVIEQEMEKEQAMNC
SFAMAGYRRDVKKNYSTVWDDQEVVCEEGREKSNATHTVGCYMIHCNTSVIKEACDKT
YWDTFRLRYCAPAGYALLRCADTDYSGHKACRNVTVSACTRLINTTVSTGIGINGSYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MDQEQEARPQVWEELQEELHRPLQACDNTCFCKVCCFHCILCFH KKALGIRYYVPRPRASKKISHKQVSLHN"
join(6411.6474,8683..8918)
/note="NCBI gi: 466234"
                                                                             WCFKLVPVDLSEEAKNSENHCLLHPAQVAYEDDAWKETLVWKFDPLLAVDYVAWRLHP
EQVPSAQG"
                                                                                                                                                       /product="NEF protein"
/translation="MGGKSSKQQQRHSLMLMSKLRQAPVIQYDMLADPLLGQSSHIQE
ECAKSLROGLIRQGDSSTEEGVKMKHQGRQPSWYDEDEEEVGFPVRPCLPLRAMTYK
LAIDFGHFLKEKGGLEGIYYSERRKKILDLYALNEWGIYDGWQNYTDGPGTRYPKCFG
                                                                                                                                                                                                                                                                                                                                                                                                                                        FDLTKWFGWMKIAIMVIAGIIVARVLLVIIGILRKFRKGYAPLSSLPSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="REV protein"
/translation="MSLGQEELLRRERIIKFLYTTNPYPPGQGTARQRRARQRWAKQ
RQQYIHLAERILETPYSQIDHLAQEFDQLVLDNLQQPPSLPPGHPTENQTANSSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="VPX protein"
/product="VPX protein"
/translation="MASGGWLPPVGGDPPKDPPKNPREEIPGWLETWDLPREPFDEWL
/translation="MASGGWLPPVGGDPPKDPKNPREEIPGWLETWDLPREPFDEWL
RDWLQDLNSEAQCHPPRNLLFRLWWNIVEEPAIDHGQTRLEGWYKYCRILQKALFVHM
KGRCCKPKTHPAYGPGAGGPPPGLGGASGGAASAAPGL"
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ITQLHTDNGTNFTSQQVAAICWWGKIEHTFGVPYNPQSQGVVESMNKQLKEIIGQIRD
DAERLETAVIMAVHIHNFKRKGGIGGYSAAERLINIIHTELETKTLQQKISKIQNFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTNLWASTNCIPDDEPEGTIAEVPIPNITEKFDAWKNRNPLVGQAESNIHLLFESTLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="NCBI gi: 466236"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="TAT_protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YYREGRDPVWKGPAKLIWKGEGAVVIQEQGELKTIPRRKAKIIKDYGKALDSQAPLEG
                                                                                                                                                                                                                                                                                                                                                          'note="NCBI gi: 466237"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MKLLTVLLWLSGCWSLVWLVQYVTVFYGIPVWKNSSVQAFCKTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="NCBI gi: 466233"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="NCBI gi: 466235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product="ENV protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="VIF protein"
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n 1.2%; Similarity 100.0%; 16; Conservative

Score 16; DB 3; Le Pred. No. 6.32e-01; 0; Mismatches 0;

Length 10036; Indels

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Gaps

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ORGANISM
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                                                                                                              REFERENCE
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JOURNAL
STANDARD
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Best Local
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                                                                                                                                                                                                                                                                                                 TTTAGAGAAGCTAGA 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIVVI69 1459 bp ss-RNA VRL Human immunodeficiency virus type 1, isolate VI69 Rwandan national residing in Belgium, gag region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (HIV-1), Rwandan isolate VI69. Human immunodeficiency virus type 1 Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. The authors group the outlying V169 gag sequence with their subtype E. The naming of this subtype was made independently of envelope subtype studies, and so gag sequences in this subtype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Louwagie, J.J., McCutchan, F., Brennan, T., Peeters, M., Brennan, T., Sanders-Buell, E., Eddy, G., van der Groen, G., Fransen, K., Gershy-Damet, M., Deleys, R. and Burke, D.
Phylogenetic analysis of gag genes from seventy international HIV-1 isolates provides evidence for multiple genotypes
                  Sauermann, U., Schneider, J., Mous, J., Brunckhorst, U., Schedel, I., Jentsch, K.D. and Hunsmann, G.
Molecular cloning and characterization of a German HIV-1 isolate AIDS Res. and Hum. Retroviruses submitted, February 1990
                                                                                                                                                                              Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are not
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                                                                                                          HIV-1, isolate HAN-2, clones 2/2 and 2/3; infectious 1 (bases 1 to 9076)
                                                                                                                                                         genome.
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                                                                                                                                                                                                                                                                                                                                                                                      h 1.1%;
Similarity 100.0%;
15; Conservative
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*Aldpglletseggriigdepsplotgseelrslyntvavlytyhgkveykdtreale

*Kleebonksgokkogvadadkgvsgonypjvonlogomvhgaisprtlamkvkuteekap

*Spevipmfsalsegatpodlntmlntvgghqaamgmlkdtineeaaewdrlhpvhagp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPPGQMREPRGSDIAGTTSTLQEQIQMMTSNPPIPVGDIYKRWIILGLNKIVRMYSPV
SILDIRQGPKEPFRDYVDRFFKTLRAEEATQEVKGWMTDTLLIQNANPDCKTILKAMG
PGATLEEMMTACQGVGGPGHKAAVLAETMSQATNAAIMMQKSNFKGQRRTVKCFNCGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAPPAESFGFREEITPSPKQEQKDEGLSPPLASLKSX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGHVAKNCRAPRKKGCWKCGREGHQMKDCTERQANFLGKIWPSNKGRPGNFLQSRPEP
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/gene="gag"
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Pred. No. 4.03e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The PPR isolate is approximately 91% homologous to the previously characterized Petaluma isolate. The latter infected feline kidney cells and the G355-5 cell line but replicated less efficiently on feline PBL's. In contrast, PPR productively infects PBL's but not the ther cell lines. The authors point out interesting differences that the contrast of the contrast o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gottingen,
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                                                                                                                                                                                                                                                                                                             The small orfs include: orf 1, in size and position similar to vif but without statistically significant homology; orf 2 that is "tat" but without statistically significant homology; orf 2 that is "tat" but without statistically significant homology; orf 2 that is "tat" but without statistically significant homology; orf 2 that is "tat" but without significant homology; orf 2 that is "tat" but without significant homology; orf 2 that is "tat" but without significant homology; orf 2 that is "tat" but without statistically significant homology; orf 2 that is "tat" but without statistically significant homology; orf 2 that is "tat" but without statistically significant homology; orf 2 that is "tat" but without statistically significant homology; orf 2 that is "tat" but without statistically significant homology; orf 2 that is "tat" but without statistically significant homology; orf 2 that is "tat" but without statistically significant homology; orf 2 that is "tat" but without statistically significant homology; orf 3 that is "tat" but without statistically significant homology; orf 3 that is "tat" but without statistically significant homology; orf 3 that is "tat" but without statistically significant homology; orf 3 that is "tat" but without statistically significant homology; orf 3 that is "tat" but without statistically significant homology; orf 3 that is "tat" but without statistically significant homology; orf 3 that is "tat" but without statistically significant homology; orf 3 that is "tat" but without statistically significant homology; orf 4 that is "tat" but without statistically significant homology; orf 4 that is "tat" but with significant homology; orf 5 that is "tat" but with significant homology; orf 5 that is "tat" but with significant homology; orf 5 that is "tat" but with significant homology; orf 5 that is "tat" but with significant homology; orf 5 that is "tat" but with significant homology; or 5 that is "tat" but with significant homology; or 5 that is "tat" but with significant homology; or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kindly provided in computer readable form Research Foundation, La Jolla CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comparison of two host cell range variants of feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phillips, T.R., Talbott, R.L., Lamont, C., Muir, S., Lovelace, K.
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3 (AA at 7842)
2 (first expressed exon)
3 (AA at 7843)
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  AACAATTTGATAATG 1249
                                                                                                                                                                                                                                                                                                       Sequence kindly supplied in computer-readable form by T. Huet, pasteur Institute. Clone la is infectious.

The CPZ genome is more closely related to HIV-ls than to any other HIV or SIV, but it is more divergent from prototypical HIV-l than any other isolate, with possible exception of the partially characterized ANT70. CPZ is especially different with respect to the vpU gene product.
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                                                                                                        5'terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIVCPZ 9811 bp ss-RNA VRL Simian immunodeficiency virus from chimpanzee,
                                                                                                                                                                                                                                                                                                                                                                                                              Nature 345, 356-359 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetic organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huet, T., Cheynier, R., Meyerhans, A., Roelants, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Infectious clone)
1 (bases 1 to 9811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimpanzee immunodeficiency virus (CIV) proviral DNA,
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Similarity 100.0%;
15; Conservative
                                                                1.1%;
Similarity 100.0%;
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2353
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5236..5991
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/codon_start=6709
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tat, exon 3 (AA at 8
rev, exon 2 (first e
rev, exon 3 (AA at 8
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Pred. No. 4.03e+00;
0; Mismatches C
                                                                Score 15; DB 3; I
Pred. No. 4.03e+00;
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                                                                                                                                                                                                                                                                  gag polyprotein
pol polyprotein (NH2 terminus
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                                                                              Length 9811;
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8421)
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8420)
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                                                     Indels
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                                                                                                                                                                                                                                           242 aacaatttgataat 255
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                                                                                                                                                                                                                                                                                    Local Similarity 100.0%; es 14: Control 100.0%;
                                                           region.
M91149
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Human immunodeficiency virus
M27910
Human immunodeficiency virus type 1 a Florida local control (LCO3), DNA Human immunodeficiency virus type 1
                                                                                              HIVFLQ7229 302 bp ss-RNA
Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WHO Global Programme on AIDS.

This sample is part of a set of sequences generated through the WHO Global Programme on AIDS. The virus was derived from an asymptomatic individual, from Brazil, whose route of infection is thought to be due to homosexual contact. The blood sample was taken in 1992. This env sequence clusters with HIV-1 B subtype sequences. The full name of this sequence is allowed in alignments in an abbreviated form in the April 94 Human Retroviruses and AIDS compendium update as B2BR017W.01__19CR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIVUU8687 273 bp ss-RNA VRL
Human immunodeficiency virus type 1, sample
CC2V3_of:env cds.
                                                                                                                                                                                                                                                                                                                                                            811 bp downstream from the beginning of env cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atlanta. The sequence below, designated 1153-1, appears to be a major form of 11 sibling sequences taken from a Boston isolate A later (1 year) isolate from the same patient, represented by 12 clones of 1236, showed relatively small variation. Sibling sequences, are available (see 1989: I-A-185).

from to/span description 98 a 46 c 54 g 55 t
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1 (bases 1 to 253)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brazil; derived from a primary isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1 (HIV-1), sample 017 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1] kindly submitted in computer readable form by C.-Y. Ou, CI Atlanta. The sequence below, designated 1153-1, appears to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ou, C. -Y.
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Similarity 100.0%;
13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   129 a
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41 c 45 g 58 t
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Pred. No. 8.65e+01;
0; Mismatches 0
                                                                                                                                                                                                                                                                                Score 14; DB 3;
Pred. No. 2.09e+01
0; Mismatches
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                                                                                                   type

    viral

                    (HIV-1), M13 clone B29 of ID 5244.
                                                                                                                                                                                                                                                                                                                     Length 273;
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from Brazil,
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STANDARD
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                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                             AUTHORS
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V4C3V5-region sequences include sequences under the following v4C3V5-region sequences include sequences under the following accession numbers: M91084 - M91089 (dentist); M91090 - M91115 and M91121 - M91131 (dentist's patients); and M91132 - M91156 (Florida local controls). V3-region sequences used in [1] include: M90847 - M90853 (dentist); M90854 - M90912 (dentist's patients); and M90914 - M90966 (Florida local controls).

For related sequences, see also M90913 and M92100 - M92150.
                                                                                                                                                                                                                                                                                                                                                                                                                                            region. M91145
                                                                                                                                                                                               Ou,C.-Y., Ciesielski,C.A., Myers,G., Bandea,C.I., Luo,C.-C., Korber,B.T.M., Mullins,J.I., Schochetman,G., Berkelman,R.L., Economou,A.N., Mitte,J.J., Furman,L.J., Satten,G.A., MacInne.
                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1 (HIV-1), M13 clone B14 of a Florida local control (LCO3), DNA ID 5244.

Human immunodeficiency virus type 1

Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence in this entry is one of 12 clones over the V4C3V5 region obtained by the CDC from this Florida control sample. An alignment presenting all 12 clone sequences from the V4C3V5 region from this subject follows entry <HIVFLQ7227> in the March update to the 1991 Human Retroviruses and AIDS.

The sequences for the V4C3V5 region for this local control were generated by running the program "comp" and are the opposite sense strand of the sequences originally forwarded to the HIV Sequence
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full staff_review
Kindly submitted in computer readable form
Disease Control), Atlanta, GA.
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1 (bases 1 to 302)

Ou.C.-Y., Clesielski,C.A., Myers,G., Bandea,C.I., Luo,C.-C.,

Cuc.-S., Clesielski,C.A., Myers,G., Bandea,C.I., Luo,C.-C.,

Korber,B.T.M., Mullins,J.I., Schochetman,G., Berkelman,R.L.,

Economou,A.N., Witte,J.J., Furman,L.J., Satten,G.A., MacInnes,K.A.,

Curran,J.W., Jaffe,H.W., et al.

Molecular Epidemiology of HIV Transmission in a Dental Practice
                                                Kindly submitted in computer readable Disease Control), Atlanta, GA.
                                                                                                                                                    Curran, J.W., Jaffe, H.W., et al. Molecular Epidemiology of HIV Transmission in a Dental
                                                                                                Science (1992) In press
full staff_review
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Similarity 100.0%;
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please note that for this set of sequences, clone numbers from t
V3 region do not correspond with similar numbers from the V4C3V5
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                                                                                                                                                                                                                                                                               Retroviridae; Lentivirinae.
sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="env polyprotein (AA at 3)"
/codon_start=3
/codon_start=3
/translation="IVMHSENCGGEFFYCHTSQLFNSTWNDTKGPNYNBGNDTITLPC
RIKQIINLWQEVGKAMYAPPIKGQIRCSSNITGLLLTRDGGNTSRTNETFRPWGGD"
a 53 c 63 g 73 t
in
this entry is
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Pred. No. 8.65e+01;
0; Mismatches 0
one of 12
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LC03B14, V4C3V5
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the V4C3V5
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                                                                           (Centers
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COMMENT

full staff\_review
Kindly submitted in computer readable form
Disease Control), Atlanta, GA.

Ьy

the

CDC

(Centers

for

The sequence in this entry is one of 6 clone sequences over the V4C3V5 region obtained by the CDC from this Florida control sample. An alignment presenting all 6 clone sequences from the V4C3V5 region from this subject follows entry <HIVFL08225> in the March update to the 1991 Human Retroviruses and AIDS.

All the sequences for the V4C3V5 region for this local control were generated by running the program "comp" and are the opposite sense strand of the sequences originally forwarded to the HIV Sequence

local control were

Database by the CDC. Please note that for

V3 region

do not

for this set of sequences, correspond with similar nur

es, clone numbers f

from the

from\_the V4C3V5

V4C3V5-region sequences include sequences under the following accession numbers: M91084 - M91089 (dentist); M91090 - M9111

STANDARD

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CDS
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                                                                                                                                                                                                               Human immunodeficiency virus type 1 (HIV-1), a Florida local control (LC02), DNA ID 5242. Human immunodeficiency virus type 1
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For related sequences, see also M90913 and M92100 - M92150. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region from this subject follows entry <HIVFLQ7227> in the March update to the 1991 Human Retroviruses and ALDG. The sequences for the V4C3V5 region for this local control were generated by running the program "comp" and are the opposite sense strand of the sequences originally forwarded to the HIV Sequence
                      Korber B.T.M., Mullins, J.I., Schochetman, G. Economou, A. N., Witte, J.J., Furman, L.J., Sat Curran, J.W., Jaffe, H.W., et al.
Molecular Epidemiology of HIV Transmission
                                                                                                                                                                                                                                                                                                                                   \begin{array}{lll} {\tt HIVFLQ626} & {\tt 312~bp~ss-RNA} & {\tt VRL} \\ {\tt Human~immunodeficiency~virus~type~l,~viral~sample} \end{array}
                                                                                                                         90,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%;
Similarity 100.0%;
13; Conservation
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Science (1992) In press
                                                                                                                                                                     Retroviridae; Lentivirinae.
                                                                                                                                                                                              Viridae; ss-RNA enveloped viruses; Positive strand RNA virus
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V4C3V5-region sequences
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                                                                                                                 (bases 1 to 312)
C.-Y., Ciesielski, C.A., Myers, G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=3
/translation="IVKHSFNYGGEFFYCNTTQLENSTWKGTEGSNHTKGNDAITLPC
/TRIKQIINLWQEVEKAMYAPPIRGQIRGSSNITGLLLTRDGGTNGTNTTETFRPGGGN"
1 57 c 63 g 68 t
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Pred.
0; N
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d. No. 8.65e+01;
Mismatches 0;
                                                                                                Schochetman, G., Berkelman, R.L.,
                                                                                                                    Bandea, C.I., Luo, C.-C.
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                                                                       Satten, G.A., MacInnes, K.A.,
                           'n
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nbers from the V4C3V5
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                           Dental Practice
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LC02B6, V4C3V5
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RESULT 13
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CDS
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 Ou,C.
                                                  Human immunodeficiency virus type 1 (HIV-1), a Florida local control (LCO3), DNA ID 5244. Human immunodeficiency virus type 1 Viridae; ss-RNA enveloped viruses; Positive:
                                                                                                                                                              HIVFLQ7216
Human immu
                                                                                                                                                                                                                                                                                                                                                                                                                                ۸
                                                                                                                                                                                                                                                                                                                                                                                                                                                              An alignment of all 13 sequences with t paired infant (HIVTOT22) follows entry update of Human Retroviruses and AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence in this entry is one of 13 sequences region obtained from this patient. This sequence representative of the set on the basis of its close
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wolinsky,S.M., Wike,C.M., Korber,B.T.M., Hutto,C., Parks,W.P., Rosenblum,L.L., Kunstman,K.J., Furtado,M.R. and Munoz,J.L. Selective transmission of human immunodeficiency virus type 1 variants from mothers to infants Science 255, 1134-1136 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIVMOM22 319 bp ss-RNA VRL 14-FEB-1992
Human immunodeficiency virus type 1, partial env cds, V4V5 regi
clone CMW560-491R.
M76925 M76913 M76914 M76915 M76916 M76917 M76918 M76919 M76920
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For related sequences, see also M90913 and M92100 - M92150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1 (HIV-1) PCR amplified proviral DNA from peripheral blood, clone CMW560-491R.
                  Retroviridae; Lentivirinae.
1 (bases 1 to 320)
                                                                                                                            M91146
                                                                                                                                             region.
                                                                                                                                                                                                                                                                                                                              1.0%;
Similarity 100.0%;
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Similarity 100.0%;
13; Conservative
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                                                                                                                                                            Q7216 320 bp ss-RNA immunodeficiency virus
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> 319
a 47 c
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Ciesielski, C.A., Myers, G.,
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                                                                                                                                                                                                                                                                                                                                       Score 13; DB 3;
Pred. No. 8.65e+01
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   description
                                                                                                                                                          s-RNA VRL
virus type 1, viral :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          re 13; DB 3; Le
d. No. 8.65e+01;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       f 13 sequences over the V4V5
This sequence was selected sis of its closeness to the
Bandea, C.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1992.
                                                                                                                                                                                                                                                                                                                                                        Length 319;
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                                                                                                        clone
Luo, C.-C.
                                                                                                                                                            03-FEB-1992
LC03B16, V4
                                                    RNA
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                                                                                                                                                                                                                                                                                                                        0
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M91147
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The sequences for the V4C3V5 region for this local control were generated by running the program "comp" and are the opposite sens strand of the sequences originally forwarded to the HIV Sequence Database by the CDC.
The sequence in this entry is one of 12 clones over the V4C3V5 region obtained by the CDC from this Florida control sample. An alignment presenting all 12 clone sequences from the V4C3V5 region from this subject follows entry <HIVFLQ7227> in the Mar
                                                                                                                                                                   Ou.C.-Y., Ciesielski,C.A., Myers,G., Bandea,C.I., Luo,C.-C., Korber,B.T.M., Mullins,J.I., Schochetman,G., Berkelman,R.L., Economou,A.N., Witte,J.J., Furman,L.J., Satten,G.A., MacInnes,K.A., Curran,J.W., Jaffe,H.W., et al. Molecular Epidemiology of HIV Transmission in a Dental Practice Science (1922) In press full staff_review
                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1 (HIV-1),
a Florida local control (LCO3), DNA ID 5244.
Human immunodeficiency virus type 1
Viridae; ss-RNA enveloped viruses; Positive (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIVFLQ7223 320 bp ss-RNA
Human immunodeficiency virus
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                                                                                                                      Kindly submitted in computer readable Disease Control), Atlanta, GA.
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Similarity 100.0%;
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Pred. No. 8.65e+01;
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update to the 1991 Human Retroviruses and AIDS. The sequences for the V4C3VS region for this local control were generated by running the program "comp" and are the opposite sense strand of the sequences originally forwarded to the HIV Sequence Database by the CDC.

Please note that for this set of sequences, clone numbers from the V3 region do not correspond with similar numbers from the V4C3V5

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For related sequences, see also M90913 and M92100 - M92150. Location/Qualifiers
                                                                                                                                                                                                                                                   The sequence in this entry is one of 12 clones over the V4C3V5 region obtained by the CDC from this Florida control sample. An alignment presenting all 12 clone sequences from the V4C3V5 region from this subject follows entry <HTVFLQ7727> in the March update to the 1991 Human Retroviruses and AIDS.

The sequences for the V4C3V5 region for this local control were generated by running the program "comp" and are the opposite sense strand of the sequences originally forwarded to the HIV Sequence Database by the CDC.
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Ou,C.-Y., Clesielski,C.A., Myers,G., Bandea,C.I., Luo,C.-C.,

Korber,B.T.M., Mullins,J.I., Schochetman,G., Berkelman,R.L.,

Economou,A.N., Witte,J.J., Furman,L.J., Satten,G.A., MacInnes,K.A.,

Curran,J.W., Jaffe,H.W., et al.

Molecular Epidemiology of HIV Transmission in a Dental Practice
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Human immunodeficiency virus type 1, viral sample LC03B27, V4C3V5
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Human immunodeficiency virus type 1
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
Y4C3Y5-region sequences include sequences under the following accession numbers: M91084 - M91089 (dentist); M91090 - M91115 and M91121 - M91131 (dentist's patients); and M91132 - M91156 (Florida local controls). V3-region sequences used in [1] include: M90847
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V4C3V5-region sequences
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Copyright (c) 1993-1998 University
Distribution rights by Oxfor
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V99650;
17-MAR-1999
bacterial infections

Claim 2; Pages 3-4; 39pp; English.

Claim 2; Pages 3-4; 39pp; English.

The present sequence represents a MurC gene encoding a Staphylococcus aureus UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide). Host cell containing an expression system comprising the MurC gene can be us for the recombinant production of the polypeptide. Agonists or the MurC polypeptide are used to treat conditions requiring increased activity of expression of the polypeptide. Antagonists, inhibitory nucleic acid or
                                                                                                                                                                                                                                                                                                                                                                          UDP-N-acetylmuramate:L-alanine ligase (Murc polypeptide) encoding Murc gene; UDP-N-acetylmuramate:L-alanine ligase; Murc polypeptide bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine immunogen; drug; genetic immunisation; ds.
                                                                                                                  New isolated MurC polypeptide from nucleic acid - useful in diagnosis,
                                                                                                                                                           (SMIK) SMITHKLINE BEECHAM (SMIK) SMITHKLINE BEECHAM Burnham MKR, Wallis NG; WPI; 99-062655/06.
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30-JUL-1997; 100117.
07-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI I
Barash SC, Choi GH, Dillon
Rosen CA;
Polynucleotide(s) and proteins derived from Staphylococcus aure stored on computer readable medium and used in the production o anti-S.aureus vaccines Claim 1; Page 1287-1288; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA of the invention. The DNA sequences are recorded on a computer medium, preferably selected from a floppy or hard disk, random memory (RAM), read-only memory (ROM) or CD-ROM. Homology search the S.aureus DNA sequences allows putative functions to be assituated protein-encoding or regulatory regions of commercial, ther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus contig SEQ ID #392.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
Staphylococcus aureus.
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/note= "these bases represent a line of missing text in
/note= "the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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                                                                                      ATTCAAATTACGGATAAAGGTACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGAT
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                                                                                            Claim 2: Pages 4-5: 39pp; English.

Containing an expression system comprising the Murc gene can be used for the recombinant production of the polypeptide. Agonists or the Murc polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g.

Competitive polypeptide are useful for inhibiting the polypeptide e.g.

Competitive polypeptide are useful for inhibiting the polypeptide e.g.

Chacterial (especially S. aureus) infections. They are also useful against the Helicobacter pylori infections and related cancers, ulcers and gastrititis.

Claim 2: An antibacterial agents are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacterial to matrix proteins. The Murc polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to identify modulators or specific receptors; in rational carry design and as an immunogen for vaccines. The Murc gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant Murc gene; for chromosomal mapping; to determine bacterial serotype; and for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP-889123-A2.
07-JAN-1999.
26-JUN-1998; 305064.
03-JUL-1997; US-052720.
(SMIK ) SMITHKLINE BEECHAM C
(SMIK ) SMITHKLINE BEECHAM P
   sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated MurC polypeptide from Staphylococcus aureus and related nucleic acid - useful in diagnosis, treatment and prevention of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burnham MKR, Wallis NG; WPI; 99-062655/06.
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MurC gene; UDP-N-acetylmuramate:L-alanine ligase
bacterial; infection; H. pylori; cancer; ulcer;
immunogen; drug; genetic immunisation; ds.
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V80065;
17-MAR-1999 (first entry)
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immunisation. The present sequence represents a sequence (MurC ORF) of the MurC gene. Sequence 660 BP; 233 A; 83 C; 120 G;
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lcer; gastritis; vaccine;
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13-MAY-1998.
24-SEP-1997; 307485.
24-SEP-1996; US-027032.
24-SEP-1996; US-027032.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
A (SMIK) SMITHKLINE BEECHAM PLC.
NORTH BURNDHAM MKR, HODGSON JE, KR
New nucleic acid sequences from Staphylococcus aureus WCHU29 useful in vaccines and for treatment of bacterial infections respiratory tract and central nervous system Claim 1; Page 146; 390pp; English.
This sequence encodes a Staphylococcus aureus protein of unkn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; cardiac infection
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antimicrobial compound identification; broad spectrum antibiotic;
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PSDB; W77686.
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PD 1:

X13228; X13228;

standard;

19-MAR-1999

(first entry)

Enterococcus faecalis genome contig SEQ ID NO:291. Enterococcus faecalis; contig; detection; Enterocovaccine; attenuation; computer readable medium; ds

Enterococcal

infection;

Enterococcus 1 WO9850555-A2. 12-NOV-1998.

faecalis

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function, and represents a DNA Sequence of the invention. The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection.
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Similarity 99.8%;
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Pred. No. 0.00e+00;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecalis. Wo9850555-A2. 12-NOV-1998. U08985. U04-MAY-1998; U08985. 14-NOV-1997; US-046609. 16-MAY-1997; US-046655. 16-MAY-1997; US-046655.
             A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X1938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis genome contig SEQ ID NO:286.
Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAY-1997; US-VAVULLE (HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
WPI; 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides
New isolated Enterococcus for the detection of Enterococcus and for
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14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
                                                                                                                                                                                                                                                                                                                   New isolated Enterococcus faecalis polynucleotides and polypeptides used to develop products for the detection of Enterococcus and fo
                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
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                                                                                                                                                                                                                                                                                 nfection
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Local Similarity 100.0%;
les 32; Conservativo
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No. 7.78e-10;
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Best Local
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The invention relates to a UDP-N-acetylmuramate:L-alanine ligase (Murc polypeptide) encoded by the S. aureus Murc gene. Host cells containing an expression system comprising the Murc gene can be used for the recombinant production of the polypeptide. Agonists or the Murc polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. bacterial (especially S. aureus) infections. They are also useful against
immunogen;
Synthetic.
                       MurC polynucleotides amplifying primer.

MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide;
bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine;
                                                                                                                                                                                                                                                                            amplification of the Murc polynucleotides.
sequence (Murc ORF) of the Murc gene.
Sequence 19 BP; 10 %
                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The MurC polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to:identify modulators or specific receptors; in rational drug design and as an immunogen for vaccines. The MurC gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant MurC gene;
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V99652;
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                                                                        V99651 standard;
V99651;
17-MAR-1999 (fin
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MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide;
bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine;
immunogen; drug; genetic immunisation; PCR primer; ss.
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EP-889123-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacterial infections
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                                                                                                                                                                                                                                                                                                                                               for chromosomal mapping; to determine bacterial
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Similarity 100.0%;
20; Conservative
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               immunisation;
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3.60e-01;
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            PCR primer;
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The nucleic acid sequence can be useful in vaccines streptococcus pneumoniae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1216
                                                                        Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis Claim 1; Page 72; 118pp; English.
                                                                                                                                                       P-PSDB; W55120.
                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
Choi GH, Hromockyj A, Johnson
WPI: 98-272224/24.
                                                                                                                                                                                                                          07-MAY-1998.
30-OCT-1997; U19422.
31-OCT-1996; US-029960
                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae.
Key Location/
                                                                                                                                                                                                                                                                                                                                                                                                             detection; pneumonia; otitis media; meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae SP0070 nucleotide. Streptococcus pneumoniae; antigen; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunisation. The present sequence represents a primer used for amplification of the MurC polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated MurC polypeptide from Staphylococcus aureus and related nucleic acid - useful in diagnosis, treatment and prevention of
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03-JUL-1997; US-052720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence encodes a protein in nucleic acid sequence encoding the be useful in vaccines for inducing processes preumoniae, for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99-062655/06
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Similarity 100.0%;
19; Conservative
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                                                                                                                                                                                                                                                                                                  /product= "SP0070"
/note= "no stop co
                                                                                                                                                                                                                                                                                                                                       /*tag= a
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA; 1267 BP
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PLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene.
                                                                                                                                                                                       LS, Kunsch
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               rrom Streptococcus pneumoniae.
Streptococcus pneumoniae protein
protective antibodies against
                                                       from
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                                                                                                                                                                                       CA
   prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                 infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 T;
                                                                                                                                                                                                                                                                                                                                                                                                               ss.
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V43027 standard; DNA; 1822 ...
V43027;
09-NOV-1998 (first entry)
09-NOV-1998 (first entry)
109-NOV-1998 (first entry)
109-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleu empyema, endocarditis or infection of the cerebrospinal fluid. Sequence 1825 BP; 550 A; 385 C; 366 G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.

Sequence 1267 BP; 365 A; 269 C; 261 G; 372 T;
                                                                                                                                                                                                                                                                                                                                                                               1160 tgaaacgacgtttaacacc 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e pneumonia, bacteremia, meningitis or endocarditis Claim 1; Page 151-152; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas
Reid RH, 2arfos PN;
WPI; 98-3322654/28
P-PSDB; W62754, W63755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP.
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27-NOV-1996; US-031879
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Local Similarity 100.0%;
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Similarity 100.08;
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complement (731..868)
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 47; Pred. No. 1.57e+00; 0; Mismatches 0
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Pred. No. 1.57e+00;
0; Mismatches 0;
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V52194 stand V52194; 23-OCT-1998

standard;

DNA; 11864 BP

Streptococcus pneumoniae genome fragment Streptococcus pneumoniae; S. pneumoniae;

SEQ ID

NO:61.; diagnosis;

(first entry)

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Best Local
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Q36987 standard; [
Q36987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391; identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the
modification, for in-frame fusions with of the 5'-end of Ox VL cDNA. Sequence 67 BP; 16 A; 22 C; 1
                                                                                    Prod. of single chain fusion protein, pref. antibody - comprises transforming host cells, e.g. E. coli with expression constructs composed of proteins or domains, linked by spacer peptide(s) Example; Page 28; 56pp; English.

The sequence is that of the PCR primer VLI, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.

Sequence 11864 BP; 3440 A; 2668 C; 2183 G; 3573 T;
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30-OCT-1997; U19588.
31-OCT-1996; US-029960.
(HUMA-) HUMAN GENOME SCI IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
F19103434-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae
Claim 1; Page 524-530; 1409pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    computer readable medium; vaccine; pharmaceutical composition; ds Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                   WO9302198-A. (First N
17-JAN-1992.
16-JUL-1991; 913434.
16-JUL-1990; US-552751.
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                                                                                                                                                                                                                                                                           Alfthan K, Knowles JKC,
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nes 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide; secretable; single chain; fusion protein; antibody;
recombinant; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or a representative fragment or a sequence at least 95% ide
ID NO: 1 to 391. The nucleotide sequences depicted in SEQ I
(Y52134 to V52524) are genomic fragments from Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (first entry)
5'-end PCR primer.
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Dillon PJ, Dougherty BA, Fannon
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Best Local Similarity 100.0%;
Matches 18; Conservative
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Best Local
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V89109;
15-FEB-1999 (fi
EST clone BZ187;
WO9845436-A2.
15-OCT-1998.
10-APR-1998; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-S.aureus vaccines
Claim 1; Page 1907; 3271pp; English.
Claim 1; Page 1907; 3271pp; English.
This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so the S.aureus DNA sequences allows putative functions to be assigned so
                                                                                                                                                                                                                                                                                                                                                                                                                               1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that protein encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating
                                                                                                                gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                        receptor; ligand;
                                                                                                                                                                   Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (and their fragments) are useful as probable of any of the S.aureus DNA computer readable medium.

Sequence 154 BP; 42 A; 32 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V75600 standard; DNA; 154 V75600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1249 CATTATCAAATTGTTCT 1233
                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA;
WPI; 97-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JAN-1997; 100117.
05-JAN-1996; US-009861.
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            GCGTTTTAATATGTTTAT 1344
                                                                                                                                                                                                                                                                                                                 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SC, Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
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                                                                                                                                           thrombolytic;
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Dillon PJ, Fannon MR, Kunsch
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                                                                                                                                           anti-inflammatory; cadherin; anti-tumour;
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. 6.54e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contained on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA
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                                                                                                                                                                      haemostatic;
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Claim 1; Page 113; 618pp; English.

The present sequence represents a human expressed sequence tag (EST).

The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haemostatic and thrombolytic activity, receptor/ligand activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, activity. The polynucleotide may also be useful for gene therapy.

Sequence 458 BP; 152 A; 70 C; 74 G; 162 T;
                                                                               Query Match 1.3%;
Best Local Similarity 100.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.3%;
Best Local Similarity 100.0%;
Matches 17; Conservative
                                                                                                                                                       Example 4; Page 190; 500pp; English.

The Expressed Sequence Tag was isolated from a human brain cDNA
The Expressed Sequence Tag was isolated from a human brain cDNA
The Expressed Sequence Tag was isolated from a human brain cDNA
The Expressed Sequence Tag was isolated from a human brain cDNA
They can be used to facilitate
for human genes transcribed in vivo. They can be used to facilitate
tagging of most human genes, for mapping locations of expressed genes
on chromosomes, for individual or forensic identification, for mapping
locations of disease-associated genes, for identification of tissue
type, and for prepn. of antisense sequences, probes and constructs.
EST00527 has a "poor" coding probability as evaluated using the
coding-region prediction program CRM. See also Q59041-Q61440.
Sequence 474 BP; 155 A; 88 C; 75 G; 153 T;
1070 CATTTTTAAATGAATTT 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-1993.
12-FEB-1993. U01294.
12-FEB-1992: US-837195.
(USSH) US DEPT HEALTH & HUMAN SERVICE.
Adams MD, Moreno RF, Venter CJ;
WPI: 93-272882/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human brain Expressed Sequence Tag EST00527.

Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; ss
                                                                                                                                                                                                                                                                                                                                                                                                   markers for human gones of most human genes
                                                                                                                                                                                                                                                                                                                                                                                                                Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in vivo, facilitate tagging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q59532 standard; cDNA; 474 BP
Q59532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1217 ATCTTATTAATGTATTA 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M; WPI; 99-070077/06.
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(GEMY) GENETICS INST INC.
                        372 catttttaaatgaattt 388
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                                                                               Score 17: DB 8; Length 474; Pred. No. 2.60e+01; 0; Mismatches 0; Indels
                                                                                                                      Length 474;
                                                                                 0;
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PCT-US96-0	PCT-US95-0	PCT-US96-0	PCT-US96-0	5304637-21	PCT-US95-1	PCT-US95-0	5202236-12	PCT-US96-0	US-08-307-	US-08-307-	PCT-US96-0	5175383-1	<u>0</u>	US-08-565-	ò	US-08-920-	US-08-921-	-08	US-08-920-	us-08-167-	US-08-488-	US-07-919-	US-08-096-	PCT-US93-0	
1, Aç	Sequence 156, Applicat	<ol><li>Applica</li></ol>	1, A		50	Sequence 4, Applicatio	o. 5200	128	1, 2	14,	Sequence 5, Applicatio	О	5	Sequence 1, Applicatio	11	Sequence 11, Applicati	11	11	11, App	, Appl	19,	2, Appl	2, Ap	Sequence 2, Applicatio	
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0 0 0 0 0 0 0 0 0 0 0 0 0

## ALIGNMENTS

RESULT

ID US-08-695-736-2 STANDARD; DNA; UNC; 853 BP.

AC XXXXXX

DT

Sequence 2, Application US/08695736

CC APPLICANT: Au-Young, Janice

APPLICANT: Bandman, Olga

CC APPLICANT: Hillman, Jennifer L.

CC APPLICANT: Goli, Surya K.

CC APPLICANT: Holdman, Jennifer L.

CC APPLICANT: Holdman, Jennifer L.

CC APPLICANT: Bandman, Olga

CC APPLICANT: Holdman, Jennifer L.

CC CONSURY: Holdman, Jennifer L.

CC STREET: 3174 Porter Drive

CC CONSURY: U.S.

CC STREET: 3174 Porter Drive

CC STREET: J174 Porter Drive

CC STREET: J184 Porter Drive

CC STREET: J1845-4166

CC COMPUTER REDABLE FORM:

CC MAME: Billings, Lucy J.

CC REGISTRATION UNMBER: US/08/695,736

CC RECISTRATION UNMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0108 US

CC TELEPHONE: 415-85-0555

CC TELEPHONE: 415-85-0555

CC TELEPHONE: 853 base pairs

CC LENGTH: 853 base pairs

CC LENGTH: 853 base pairs

CC MOLECULE TYPE: CDNA

CC MOLECULE TYPE: CDNA GENERAL INFORMATION:
APPLICANT: AN-Young, Janice
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN PROTEOLIPID
NUMBER OF SEQUENCES: 4
CORRESSONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIT: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
COMPUTER FINDAMER: US
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION NUMBER: US/08/595,736
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION INFORMATION:
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TELECANDEDINESS: single
TOPOLOGY: 11near
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:

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                                         Query Match 1.3%;
Best Local Similarity 100.0%;
Matches 17; Conservative
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Best Local
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                          1345 GCTCAAAATATTCAAAT 1361
                                                                          LOCATION: 141..1649
SEQUENCE 1791 BP; 555 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. GENERAL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application Sequence 7, Application Patent No. 5693776
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Local Similarity 100.0%;
tes 17; Conservation
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APPLICATION NUMBER: US 0:
FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                    FEATURE:
                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                            STATE: George
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CLONE: 6
           GCTCAAAATATTCAAAT 728
                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                             NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.612
                                                                                                                                                                                                                                                       CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                                                                            NAME/KEY: CDS
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Regnery, Russell L.
RETHOUS AND COMPOSITIONS FOR METHODS AND COMPOSITIONS FOR FORTION: DIAGNOSING ROCHALIMAEA HENSELAE
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7 Peachtree Street, Suite 1200
                                                                                                                                                                             404/688-0770
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                                                                                                                                                                                                                                                                                                                                                                                                AND ROCHALIMAEA QUINTANA INFECTION
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US/08474499
                                                                           263 C;
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                                         Score 17;
Pred. No.
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Pred. No. 2.19e+00;
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                                                                           408 G;
                                          Mismatches
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. 2.19e+00;
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                                                                           565 T; 0 OTHER.
                                                                                                                                                                                                                                                                                       Version
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                                                          Length 1791;
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Best Local
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1345 GCTCAAAATATTCAAAT 1361
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|| 712 GCTCAAAATATTCAAAT 728
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LOCATION: 141..1649
SEQUENCE 1791 BP; 555 A; 263 C; 408 G;
                                                                                                            Sequence 7, Application Sequence 7, Application GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: Regnery, I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
                 TITLE OF INVENTION: ME
TITLE OF INVENTION: RO
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:

ANDRESSEE: NEEDLE & ROSENBERG, P.C.

ANDRESSEE: NEEDLE & ROSENBERG, P.C.

ANDRESSEE: NEEDLE & ROSENBERG, P.C.
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MEDIUM TYPE: Floppy disk
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Similarity 100.0%;
17; Conservation
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Russell L.
METHODS AND COMPOSITIONS
DIAGNOSING
                                                     METHODS AND COMPOSITIONS FOR DIAGNOSING ROCHALIMAEA HENSELAE AND ROCHALIMAEA QUINTANA INFECTION
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US/08245294
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Pred. No.
0; Misma
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2.19e+00;
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Local Similarity 100.0%;
hes 17; Conservat;
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                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                       APPLICANT: Regnery,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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CITY: A
                APPLICATION NUMBER:
                                                                                                                  COUNTRY:
                                                                                                                                                                    ADDRESSEE:
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LOCATION: 141..1649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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                                                                                                       30303
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US/08307279A
                                                                                                                                                                                                       Henselae and Rochalimaea Quintana Infection
                                                                                                                                                                                                                     Nucleic Acids of Rochalimaea Henselae and Methods and Compositions for Diagnosing
                                                                                                                                                                                                                                              Russell L
                                                                                                                                                                                                                                                             Burt E
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              US/08/307,279A
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Pred. No. 2
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XXXXXX
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                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2465 base pair
                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 310-788-5000
                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Oldenkamp, David J
                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Antigen Related to Inflammatory Diseases NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
MOLECULE TYPE:
                                                                                                                                        NAME: Oldenkamp, David REGISTRATION NUMBER: 2
                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                       TYPE:
                                                                                                                            REFERENCE/DOCKET NUMBER:
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                      STRANDEDNESS:
                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                         Los Angeles
California
                                    nucleic acid
                                               2465 base pairs
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2029 Century Park East,
                                                                                       310-277-1297
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Yamamoto, Karen K
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Floppy disk

US/08/421,661

Version

29,421

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Suite 3800

double

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1345 GCTCAAAATATTCAAAT 1363
                                                                                                               SEQUENCE 17,91 BP; 555 A; 263 C; 408 G;
712 GCTCAAAATATTCAAAT 728
                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                  Match 1.3%;
Local Similarity 100.0%;
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                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                              NAME/KEY: CDS
LOCATION: 141..1652
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   Spratt, Gwendolyn D. RATION NUMBER: 36,016
                                                                                                                                                                                                                  nucleic acid
                                                      Conservative
                                                                                                                                                                                                                              1791 base pairs
                                                                                                                                                                                                                                                                            (404) 688-9880
                                                                                                                                                                                         linear
                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                     double
                                                                     Score 17; I
Pred. No. 2
                                                      0
                                                                                                                                                                                                                                                                                                                       1414.624
                                                       Mismatches
                                                                                                                565 T;
                                                                                    DB 2;
                                                                      .19e+00
                                                                                                                0 OTHER
                                                       0
                                                                                 Length 1791;
                                                       Indels
                                                      0;
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Matches
                                               Matches
                                                         Query Match 1.2%;
Best Local Similarity 100.0%;
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                                                                                           MOLECULE TYPE: DNA (genomic)
SEQUENCE 373 BP; 117 A; 64 C; 56 G; 115 T; 21 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-967-101-17 STANDARD; DNA; UNC; 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 61..2054
SEQUENCE 2465 BP; 856 A; 488 C; 541 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
             325 ATGGTAATATTTTAT 340
                                                                                                                                                                         NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 248-7000
TELEPAN: (617) 248-7100
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191
 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 1.3%;
Local Similarity 100.0%;
hes 17; Conservative
                                                                                                     TOPOLOGY: 15
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 373 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Pitcher, Edmund R.
                                                                                                                                                                                                                                                                     FILING DATE: 10-NOV-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
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 ATGGTAATATTTTAT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACATAAAAGAAGATATG
                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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LOCATION: 61.
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                                              Conservative
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Application US/08967101
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High Street Tower - 125 High Street
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Pred. No. 2.19e+00;
0; Mismatches 0
                                                         Score 16; DB 3;
Pred. No. 1.05e+01
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           580 T; 0 OTHER
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                                              0;
                                                                     Length 373;
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Best Local :
                                                                   Sequence 20, Application US/08457648 Sequence 20, Application US/08457648 Patent No. 5639871
                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE; DNA (genomic)
SEQUENCE 415 BP; 127 A; 72 C; 74 G; 142 T; 0 OTHER.
                                                                                                                               US-08-457-648-20 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08474542A Sequence 20, Application US/08474542A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-474-542A-20 STANDARD; DNA; UNC; 415
                                                                                                                     XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
                     GENERAL INFORMATION:
APPLICANT: Bauer, Heidi M.
APPLICANT: Gravitt, Patti
APPLICANT: Greer, Catherin
                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Greer, Catherine E.
APPLICANT: Impraim, Chaka C.
APPLICANT: Manos, M. Michele
APPLICANT: Resnick, Robert M.
TITLE OF INVENTION: Detection of Human Papillomavirus by
TITLE OF INVENTION: Polymerase Chain Reaction
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bauer, Heidi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                      LENGTH: 415 base pairs
                                                                                                                                                                                                                            th 1.28;
Similarity 100.08;
16; Conservative
                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Jersey
        Gravitt, Patti E.
Greer, Catherine
Impraim, Chaka C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gravitt, Patti E.
Greer, Catherine E.
Impraim, Chaka C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Hoffmann-La Roche Inc
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                                                                                                                                                                                                                                                                                                              single
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                                                                                                                                                                                                                            Score 16; DB 1; Length 415; Pred. No. 1.05e+01; 0; Mismatches 0; Indels
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                                                                                                                                415
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APPLICANT:

Manos, M. Michele

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Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                    Sequence 288, Application Sequence 288, Application Patent No. 5527898 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
SEQUENCE 415 BP; 127 A; 72 C; 74 G; 142 T; 0 OTHER
                                                                                                                                                                                                                                                                                                XXXXXX
                                                                                                                                                                                                                                                                                                         US-08-474-542A-288 STANDARD; DNA; UNC; 467
                                                                                                                                                                                                                                                                                                                                                       612 TTTAACATTATGTGCC 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 9205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEPAN: (510) 814-2977
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      1.2%;
Local Similarity 100.0%;
Les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                58 TITAACATTATGTGCC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,648
FILING DATE:
CLASSIFICATION: 435
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: RESNICK,
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                        APPLICANT:
                                              STATE: New Jersey COUNTRY: U.S.A. ZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 07110
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STATE: New Je
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                 CITY: Nutley
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                                                                                                                                                                                                                        INFORMATION:
CANT: Bauer, Heidi M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Jersey
                                                                                                                                                                         Gravitt, Patti E.
Greer, Catherine E.
Impraim, Chaka C.
Manos, M. Michele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 Kingsland
                                                                                                                             Resnick, Robert M.

VENTION: Detection of Human Papillomavirus VENTION: Polymerase Chain Reaction EQUENCES: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoffmann-La Roche Inc.
0 Kingsland Street
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                                                                                                                                                                                                                                                           US/08474542A
US/08474542A
                                                                                                                                                                                                                                                                                                                                                                                                               Score 16; DB 1; Length 415; Pred. No. 1.05e+01;
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Best Local :
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RESULT

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MOLECULE TYPE: DNA (genomic)
SEQUENCE 467 BP; 140 A; 84 C; 91 G; 152 T; 0 OTHER
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                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 467 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                 84 TITAACATTATGTGCC 99
                                                                      / Match 1.2%;
Local Similarity 100.0%;
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 814-2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
TTTAACATTATGTGCC 597
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                2977
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                                                                                      Score 16; DB 1;
Pred. No. 1.05e+01
                                                                                                                                                                                                                                                                               288:
                                                                        0; Mismatches
                                                                                                           Length 467
                                                                        0; Indels
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Sequence 288, Application US/08457648 Sequence 288, Application US/08457648 Patent No. 5639871 US-08-457-648-288 STANDARD; DNA; UNC; 467 APPLICANT: Greer, Catherine APPLICANT: Impraim, Chaka C.
APPLICANT: Manos, M. Michele GENERAL INFORMATION:
APPLICANT: Bauer, Heidi M. APPLICANT: Manos, M. Michele APPLICANT: Resnick, Robert M. TITLE OF INVENTION: Detection of Human Papillomavirus by TITLE OF INVENTION: Polymerase Chain Reaction NUMBER OF SEQUENCES: 298

CORRESPONDENCE ADDRESS: ADDRESSEE: Hoffmann-La Roche Inc. the

STREET: 340 F CITY: Nutley STATE: New Jersey COUNTRY: U.S.A. ZIP: 07110 340 Kingsland Street

ZIP: 07110 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321 CURRENT APPLICATION DATA: APPLICATION NUMBER: US, FILING DATE: CLASSIFICATION: 435 US/08/457,648

TELEFAX: (510) 814-297
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 base pairs REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974 (510) 814-2977

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  Query Match
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Best Local
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                                                           TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                        MOLECULE TYPE: DNA (genomic) SEQUENCE 810 BP; 260 A; 127 C; 133 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXX
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TOPOLGCY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 467 BP; 140 A; 84 C; 91 G; 152 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 51, Application Sequence 51, Application
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                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ADDITORTON MUMBER: US 07/142 212
                                                                                                                                               APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIETCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
REFERENCE/TON INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as
TITLE OF INVENTION: Live Vaccine Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             612 TITAACATTATGTGCC 597
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Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 TTTAACATTATGTGCC 99
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                     TOPOLOGY: ui
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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2421 N.W. 41st Street, Suite A-1
                                                 unknown
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US/08307499
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  Score 16;
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Pred. No. 1.05e+01;
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                        290 T; 0 OTHER
 DB 1;
Length 810,
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Best Local S
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         Sequence 3, Application US/07803622E Sequence 3, Application US/07803622E Patent No. 5525497
                                                             T 14
US-07-803-622E-3
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                                                                                                                                                                                              SEQUENCE 1760 BP; 695 A; 243 C; 230 G;
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Sequence 117, Application US/08413118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5688920
GENERAL INFORMATION:
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                                                                                                          288
                                                                                                                   755 TTATAATGATTTTTTA 770
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                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1760 base pair
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET; STREET; YORK
                                                                                                        TTATAATGATTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US OF FILING DATE: 30-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 29-MAR-1995
                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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Similarity 100.0%;
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530 FIFTH AVENUE, 25TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                     (212) 840-0712
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                                                                                                                                                                                                                    ·linear
                                                             STANDARD;
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                                                             DNA;
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                                                                                                                                                              Score 16; DB 2; I
Pred. No. 1.05e+01;
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0; Mismatches 0;
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                                                             UNC;
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GENERAL INFORMATION:

Keller, Walter

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RESULT
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Matches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/803,622E
FILING DATE: 27-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 195/296
                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08070165F Sequence 7, Application US/08070165F Patent No. 5750365
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-070-165F-7 STANDARD; DNA; UNC; 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-489-1600
TELEPAX: 213-955-0440
TELEEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Local Similarity 100.0%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
                                                                                                                                                                                                                                          APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90017
COMPUTER READABLE FORM:
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LENGTH: 1821 base pair
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING Patrantin Release #1.0,
                                                                                                                                                                      STREET:
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                                                                                                                                  CITY: Columbus
STATE: Ohio
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                                                                                                 ZIP: 43210
                                                                                                             COUNTRY:
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                                                                                                                                                                                       E: Ing-Ming Chiu
S2052 Davis Medical Research Center, 480 West
                                                                                                                   USA
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Martin, Georges
Wahle, Elmar
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         Search completed: Sat Nov 27 14:17:01 1999
Job time :
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Best Local S
Matches 1
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AUTHORS: Poulin, Matthew I
RELEVANT RESIDUES IN SEQ ID NO: 7
SEQUENCE 1839 BP; 502 A; 400 C; 469 G;
                                     306 CAAAAACATCATTAAT 321
                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (614)-293-563
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                         Match 1.2%;
Local Similarity 100.0%;
nes 16; Conservative
                                                                                                                                                                                                                                                     CELL TYPE: Mesenchyme and Epithelium IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (614)-293-8093
                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                               POSITION IN GENOME:
UNITS: bp
                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE: ORGANISM: No. 5750365ophthalmus viridescens
                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                  CLONE:
                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: Adult
                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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                                                                                                                                                                                                                                               LIBRARY:
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104 secs.
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1135..1839
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                                                                           Score 16; DB 2; Ler
Pred. No. 1.05e+01;
0; Mismatches 0;
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                                                                                              Length 1839;
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RESULT 20 1 20 20 20 2 20 20 20 20 20 20 20 20 20 2	Pred. No score gre and is de	Database: Database:	**************************************
Match Length DB ID  1.5 244 31 D62295 1.5 351 31 H35671 1.5 429 26 AA956076 UI-R-E1-fh- 1.5 431 26 AA956542 UI-R-E1-fh- 1.5 435 21 AA943324 EST198823 1.5 436 21 AI013962 EST207517 N 1.5 637 38 H68124 CIT978SK-A- 1.4 196 13 AA480754 SWMFCA21338	ne number of results predicted than or equal to the score of t by analysis of the total score SUMMARIES	embl-est58 1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est2 6:em_est9 7:em_gss1 genbank-est111 8:gb_est1 9:gb_est10 10:gb_est11 11:gb_est12 12:gb_est. 13:gb_est14 14:gb_est15 15:gb_est2 20:gb_est2 7:gb_est2 18:gb_est2 21:gb_est2 21:gb_est2 21:gb_est2 22:gb_est2 23:gb_est2 24:gb_est2 22:gb_est2 23:gb_est2 23:gb_est2 23:gb_est2 23:gb_est2 23:gb_est2 33:gb_est2 33:gb_est3 34:gb_est2 36:gb_est3 31:gb_est3 32:gb_est2 33:gb_est2 33:gb_est3 34:gb_est3 35:gb_est4 32:gb_est5 33:gb_est6 33:gb_est6 33:gb_est6 33:gb_gss1 38:gb_gss2 39:gb_gss3 40:gb_gss4 41:gb_gss5 42:gb_gss6	**************************************
Description Pred. No. HUM253D09B Clontech hu 4.91e-06 EST105257 Rat PC-12 ce 4.91e-06 UI-R-E1-fh-b-08-0-UI.S 4.91e-06 UI-R-E1-fn-e-12-0-UI.S 4.91e-06 EST19823 Normalized r 4.91e-06 EST207517 Normalized r 4.91e-06 EST207540 Normalized r 4.91e-06 EST203406 Normalized r 4.91e-06 EST203408 Normalized r 4.91e-06 EST203408 Normalized r 4.91e-06 EST203408 Normalized r 4.91e-06 EST203408 Normalized r 4.91e-06	by chance to have a he result being printed, distribution.	4:em_est18 5:em_est2  11:gb_est12 12:gb_est13  16 16:gb_est10 2 0:gb_est20 2 24:gb_est24 27 28:gb_est24 37:gb_est5 33:gb_est6 37:gb_est5 33:gb_est6 37:gb_gss6 38:gb_gss2 42:gb_gss6	**************************************
FEATURES Source	TITLE FE COMMENT C	RESULT 1 LOCUS DEFINITION C ACCESSION C ACCESSION C VERSION S VERVORDS SOURCE ORGANISM E REFERENCE 1 REFERENCE 1 AUTHORS E	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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ALIGNMENTS	AA540 AA891 AI546 AQ282	AI535 AA825 AA937 AI145	AQ067 C5701 AQ057 AA569	2 AQ41527 2 AQ41527 2 AI05543 7 B67375 0 C89676 8 B54100 0 AA26213 0 AA88623	B8505 A1256 AA144 AQ139 AQ322	AQ195 AQ233 AA080 AQ115 AQ093 AQ303 AQ108
ENTS	3 ES 0 LD 1 RP	o od	B CCI B CCI	7 CO TO CO	5 ui 5 mr 7 HS	9 HSP 9 HSP 1 MBP 1 HSS 1 HSS
	9344.5prime LD Dros 195496 Normalized r 7843.5prime LD Dros 111-89E10.TV RPCI11	R-C3-sq-c-03-0-UI.s 7d04.sl NCI_CGAP_GC 3g09.sl Soares reti 8f08.sl NCI_CGAP_GC R-BTO-qf-c-02-0-UI. 8f09.yl Soares mous	2239_B2_A10_MF CIT 017 Yuji Kohara unp 017 Yuji Kohara unp 223 Yuji Kohara unp -HSP-2337K23.TF CIT -HSP-2337K23.TF CIT	CI-11-180011.TV RPCI au00004A01 Cotton Bol 4H9TF TAMU Arabidops 9676 Dictyostelium d 7-HSP-2014M4.TF CIT- 23b08.r1 NCI_CGAP_Ki	III-29M5.TV RPCIII 4f07.x1 Sugano mous 6h12.r1 Soares mous 3079.A2_D12_MF CIT III-11102.TJ RPCIII III-11102.TJ RPCIII	111-66E20.TK RPC111 2014_A2_C02_T7 CIT 2014_A2_C02_T7 CIT 80811.T1 Stratagene 111-57N20.TK RPC111 3020_B1_A12_T7 CIT 3113_B2_C07_MR CIT -HSP-2380119.TF CIT
	7.52e- 7.52e- 7.52e- 7.52e-	7.52e 7.52e 7.52e 7.52e 7.52e	7.52e- 7.52e- 7.52e- 7.52e- 7.52e-	2.10e-04 2.10e-04 2.10e-04 2.10e-04 2.10e-04 2.10e-04 7.52e-03 7.52e-03	2.10e- 2.10e- 2.10e- 2.10e- 2.10e-	2.10e- 2.10e- 2.10e- 2.10e- 2.10e- 2.10e- 2.10e- 2.10e-

## Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 244) Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y. Fujiwara et al. (1995) Unpublished (1995) Unpublished (1995) On Apr 14, 1993 this sequence version replaced gi:693074. Contact: Tsutomu Fujiwara Otsuka GEN Research Institute Otsuka Harmaceutical Co.,Ltd 463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan Tel: 0886-65-2888 Fax: 0886-37-1035. D62295 244 bp mRNA EST 29-AUG-1995 HUM253D09B Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-253D09 5', mRNA sequence. D62295 g966071 D62295.1 GI:966071 EST. Location/Qualifiers 1. 244 /organism="Homo sapiens" /db\_xref="taxon:9606" /map="13" /clone-"GEN-253D09" /clone\_lib="Clontech human aorta polyA+ mRNA (#6572)"

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On May 8, 1995 this s
Other_ESTs: TC797
Contact: Lee, NH
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H35671.1
EST.
AA956076 429 bp mRNA EST 07-FEB-1999 UI-R-E1-fh-b-08-0-UI.S1 UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1-fh-b-08-0-UI 3' similar to gi|2957159|gb|AC004404|AC004404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For clone availability please contact (tdbinfo@tdb.tigr.org) TC (Tentative Cassemblies of ESTs.
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Rattus sp.
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Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fuldner, R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 351)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nhlee@tigr.org
                                                                                                                                                                                                                                                                                                      note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
xhoI; poly(A)+ RNA was purified from untracted PC12 cells
cultured for 9 days. cDNA was constructed using an
oligo-dT primer and directionally cloned using the Lambda
CAP II Vector Kit by Stratagene"
/db_xref="ATCC (inhost):2000417"
                                                                                                                                                                                                                                                     /Clone_lib="Rat PC-12 cells, untreated"
68 c 80 g 87 t
                                                                                                                                                                                                                                                                                                                                                                                                                             ∕organism="Rattus sp."
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Pred. No. 4.91e-06;
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1348 TATTATAAACATATTAAAAC
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                                              32 TATTATAAACATATTAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult 12-Day-Embryo library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Iowa
451 Eckstein Medical Research Building Iowa
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9),
97044477
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AA955076
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                                                                                            1.5%;
Similarity 100.0%;
20; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heria; Rodentia;
(bases 1 to 429)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-E1
library is a subtracted library derived from the UI-R-E0
library is a subtracted library consisted of a mixture of
individually tagged normalized libraries constructed from
8, 12 and 18-day embryo. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-GT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-E1) was constructed as follows: PCR
amplified cDNA inserts from a pool of UI-R-E0 clones from
which 3' ESTs had been derived was used as a driver in a
hybridization with the UI-R-E0 library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
                                                                                                                                                                                                                                                                      /map="18p11.1-g11.2"
/clone="UI-R-E1-fh-b-08-0-UI"
/clone_lib="UI-R-E1"
/dev_stage="adult"
                                                                                                                                                                                                                     /lab_host="DH108 (Life Technologies)"
84 c 93 g 120 t
                                                                                                                                                                                                                                                                                                                                                                                                                                               bacteria (Life Technologies) to generate the UI-R-E1 library. This procedure has been previously describe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                               Score 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult 12-Day-Embryo library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Program for Rat Gene Discovery and Mapping University of Iowa
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AA956542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
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h 1.5%;
Similarity 100.0%;
20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: msoares@blue.weeg.uiowa.edu
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                                                                                                                                         134
                                                                                                                                                                                                                                                                                                                                             of origin of a clone within the mixture. The subtracted library (UI-R-EI) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-EO clones from which 3′ ESTs had been derived was used as a driver in a hybridization with the UI-R-EO library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the UI-R-EI library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                individually tagged normalized libraries constructed from 8, 12 and 18 day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-off track which allows identification of the library of origin of a clone within the mixture. The subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/Strain="Sprague-Dawley"
/Strain="Sprague-Dawley"
/note-"Vector: pT773D-Pac (Pharmacia) with a modified
/note-"Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-E1
library is a subtracted library derived from the UI-R-E0
library. The UI-R-E0 library consisted of a mixture of
                                                                                                                                                                                      /clone="UI-R-E1-fn-e-12-0-UI"
/clone_lib="UI-R-E1"
/dev_stage="adult"
                                                                                                                                   /lab_host="DH10B (Life Technologies)"
83 c     95 g     119 t
                                                                                                                                                                                                                                                                            /map="11q23"
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Score 20; DB 26; Le Pred. No. 4.91e-06; 0; Mismatches 0;
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                                                     Length 431;
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                                                          AUTHORS
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                                                                                       Eukaryota;
Eutheria; R
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EST207517 Normalized
RSPBC29 3' end, mRNA
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RBRAI23 3'
AA943324
Gene Index
Unpublished (1998)
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On Apr 14, 1993 this sequence version replaced gi:716993
                             1 (bases 1 to 460)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
                                                                                                                    Rattus sp.
                                                                                                                                                                AI013962.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 9712, Medical Center Drive, Rockvi. Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: nhlee@tigr.org
Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus sp.
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Normalized rat brain, 85 c 102 g 114 t
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/db_xref="taxon:10118"
/clone="xBRA123"
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/note="Organ: brain; Vector:
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Normalized rat brain,
' end, mRNA sequence.
                                                                                        Rodentia;
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                                                                                     Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                        sequence.
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Pred. No. 4.91e-06;
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                             Rat EST (REST) Catalog & Rat
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                                                                                     Mammalia;
Rattus.
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Best Local Similarity 100.0%;
Matches 20; Conservative
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Rattus sp.
Rattus sp.
Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 571)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Genome Project: Generation of a Rat EST (REST)
                                                                                                                                                                                                                                                                                                                                                                                                                            The Institute for Genomic Research 9712, Medical Center Drive, Rockville, Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
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EST220540 Normalized rat ovary,
ROVBY77 3' end, mRNA sequence.
AI176934
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The Institute for Genomic Research
9712, Medical Center Drive, Rockville,
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On Jan 19, 1998 this sequence version
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Fax: (301)-838-0208
Email: nhlee@ttigr.org
Seq primer: M13-21.
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Site_2: NotI"
(db_xref="ATCC (inhost):2031607"
/db_xref="taxon:10118"
/db_xref="taxon:10118"
/clone="ROVBY77"
/clone_lib="Normalized rat ovary, Bentcation of the state of th
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/note="Organ: spleen; Vector:
Site_2: Not1"
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/clone="RSPBC29"
/clone_lib="Normalized rat spleen,
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Pred. No. 4.91e-06;
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B68124.1
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                                                            1 (bases 1 to 667)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Kim, U.-J., Shizuya, H., Simon, M. and Venter, J.C.
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Unpublished (1997)
                                      Use of a human BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                  B68124
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Seq primer: M13-21.
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Tel: (301)-838-3529
Fax: (301)-838-0208
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On Jun 15, 1998 this
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1 (bases 1 to 633)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
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/note="Vector: pT7T3Pac;
/db_xref="taxon:10118"
/clone="REMBG04"
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CONTACT: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                       Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                Genes expressed in microfilaria of Brugia malayi Unpublished (1995) On Sep 12, 1996 this sequence version replaced \sigma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA480754 196 bp mRNA EST 23-JUN-1997
SWMFCA2133SK Brugia malayi microfilaria cDNA (SAW94LS-BMMf) Brugia
malayi cDNA clone SWMFCA2133 5', mRNA sequence.
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Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
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Class: BAC ends.
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Seq primer: SP6
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Clones are available from Research Genetics (info@resgen.com). BAC
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Similarity 100.0%;
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                                                                                                                                                                                                                                      genome@smith.edu
            /note-"vector: lambda Unizap XR; Site_1: EcoR I; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from microfilariae of Brugia malayi isolated from jirds and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNASE H and DNApol I. The library had 3.5 x 1025
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/note="Vector: pBAC108L; Site_1: HindIII; Site_2: HindIII;
CallTech Human BAC Library A"
/db_xref="taxon:9806"
/clone="A-802H9"
                                                                                                                                   /organism="Brugia malayi"
/strain="TRS Labs"
                                                                                                                                                                                             Location/Qualifiers
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150 c 150 g 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="CIT978SK"
independent recombinants and average insert size was 900
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Pred. No. 4.91e-06;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 19; Conservative
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Best Local :
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589
                  112 GGAATGCATCAAAAACATC 130
                                                                          y Match 1.4%;
Local Similarity 100.0%;
hes 19; Conservative
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GGAATGCATCAAAAACATC 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPCI11-66E20.TK RPCI11 Homo sapiens genomic clone R-66E20, genomic
                                                                                                                                                                                                                                                                                                                                                                                                 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                              For clone availability, please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 232)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mail: mdadams@tigr.org
                                                                                                                                                                           77
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                                                                                                                                                                                                                                                   /Organism="Homo sapiens"
/note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI;
RPCII1 Human Male BAC Library"
/db_xref="taxon:9606"
/clone="R-66E20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome@smith.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          base pairs. The library was constructed by Lori Saunders. The library is available from Dr. S.A. Williams, email genome@smith.equ "
                                                                                                                                                                       /cell_type="Lymphocytes"
50 c 34 g 7
                                                                                                                                                                                                                  /sex="Male"
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/map="19q13.3"
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31 c 29 g 75
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Pred. No.
0; Misma
                                                                          Score 19; DB 39; L
Pred. No. 2.10e-04;
0; Mismatches 0;
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d. No. 2.10e-04;
Mismatches 0;
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                                                                        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                         mn88e11.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:551180 5', mRNA sequence.
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2014 row: M column: 4
Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ233339 332 bp DNA GSS 25-SEP-1998 HS_2014_A2_G02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2014 Col=4 Row=M, genomic survey
                                                                                                                                                                                                                                                                                                                                                                    AA080511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High Throughput Sequencia
University of Washington
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                                         The WashU-HHMI Mouse
                                                                                                                                                                                                                                                                        AA080511.1 GI:1619483
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Similarity 100.0%;
19; Conservative
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1 (bases 1 to 332)
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                                                                                                                                                                                                                                    louse mouse.
                                                                                                                                                       Cheria; Rodentia; (bases 1 to 376)
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/note="Organ: sperm; Vec
E-Coli DH10B"
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/clone="Plate=2014 Col=4 Row=M"
/clone_lib="CIT Approved Human (
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Pred. No. 2.10e-04;
0; Mismatches 0;
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Matches 19; Conservative
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survey sequence.
AQ115573
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1 (Dases 1 to 383)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
MGI:331972
                                                                                        Class: BAC ends
                                                                                                                                                                                                             The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                         Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 346.
Location/Qualifiers
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                    Email: mdadams@tigr.org
For clone availability, please contact Pieter de Jong
[pieter@dejong.med.buffalo.edu]. Clones may be purchased from
[pieter@dejong.med.buffalo.edu]. BAC end search page:
Research Genetics (info@resgen.com). BAC end the page:
                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
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                                                                                                       ittp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
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/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/lab_oc 67 g 139 t 1 oth
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1 (bases 1 to 399)

Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E. Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ093108 399 bp DNA 26-AUG-1998 HS_3020_B1_A12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=23 Row=B, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
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AQ093108.1 GI:3464555
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Sequence Tagged Connector
Plate: 3020 row: B column: 23
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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## ALIGNMENTS

	CDS	gene	source		JOURNAL	AUTHORS	REFERENCE	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	SION		ACCESSION	ITION	RESULT 1
<pre>/gene="murc" /function="cell wall biosynthesis" /function="cell wall biosynthesis" /note="MurC; UDP-N-acetylmuramate-alanine ligase" /codon_start=1 /transl_table=11 /product="UDP-N-acetylmuramoyl-L-alanine synthetase" /protein_id="AAB87090.1"</pre>	/gene marc	/db_xref="taxon:1280"  1. 1314		02115, USA	Submitted (11-NOV-1997) Channing Laboratory, Brigham and Women's	Lowe, A.M. and Deresiewicz, R.L.	2 (bases 1 to 1314)	Unpublished	Cloning and sequencing of Staphylococcus aureus murC, a gene involved in cell wall biosynthesis	Lowe, A.M. and Deresiewicz, R.L.	1 (bases 1 to 1314)	Eubacteria; Firmicutes; Low G+C gram-positive bacteria;	Staphylococcus aureus	Staphylococcus aureus.		AF034076.1 GI:2642658	Q2642658.	(murc) gene, complete cas. AF034076	UDP-N-acetylmuramoyl-L-alani	AF034076 1314 by DNA RCT 26-NOV-1997

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lekldyinikealeteggykrffnerigtangvivddyahhpreisatietarkkyphk
evvavfqhftfsrtqaflafelssikalryelceifgstrentgaltiqdlidkieg
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Pred. No. 0.00e+00
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Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a smale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M., Bonfield,J., Burton,J., Connell,M., Copsey,J., Cooper,J., Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A., Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M., Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,M., Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B., O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A., Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E., Staden,R., Sulston,J., Thierry-Migy,J., Thomas,K., Vaudin,M., Vaudhan,M., Watchen, R., Sulston,J., Thierry-Migy,J., Thomas,K., Vaudin,M., Vaudhan,M., Watchen,M., Smith,A., Sonnhammer,E., Vaudhan,M., Watchen,M., Smith,A., Sonnhammer,E., Vaudhan,M., Watchen,M., Smith,A., Sonnhammer,E., Vaudhan,M., Watchen,M., Smith,A., Vaudin,M., Vaudhan,M., Watchen,M., Watchen,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone CO1F6.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
2.2 Mb of contiguous nucleotide sequence from chron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The end of this sequence (31178. .31281) overlaps with the start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                start of this sequence (1. .104)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence Z82266.
The true right end of clone ZC410 is at 2893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neighbouring submissions.

The true left end of clone CO1F6 is at 1 in this sequence. The true right end of clone CO1F6 is at 9279 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94150718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     jes@sanger.ac.uk or rw@nematode.wustl.edu
2 (bases 1 to 31281)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(930. .972,1021. .1097,1153. .1254))
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/note-"cDNA EST EMBL:D35953 comes from this gene; cDNA EST EMBL:D33187 comes from this gene; cDNA EST yk445h11.3 comes from this gene; cDNA EST yk445h11.5 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Caenorhabditis elegans'/db_xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SPTREMBL:062023"
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/gene="C01F6.9"
                                                                                                                                                join(1955. .1992,2059. .2244,2332. .2818,2866. .2969,
3189. .3435,3482. .3609,3655. .3817,3868. .3945,3992.
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/db_xref="GI:3873821"
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                                                                                                                                                                                                                                                                                       955. .4099
'gene="CO1F6.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .1254)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from this gene; cDNA
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complement(join(6798. .6884,7346. .7969,8083. .82
8250. .8346,8394. .8428,8525. .8737,8784. .8876))
/gene="COlf6.3"
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TSSHCEPNLGAKQTVGNEQDADIVIDDSHLFAESENECSGSILVKGGQQKVLFRWTDE
KPTTVDSVTLTGSFFGWNMNIPMKRNELKMFEVCIELPDGMHDYLINVYRFD"
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GGRLIILLIASPLAPCSLEIVGKVPDYYSQFLRIRESGNYLHSSSDVIPLQLYYILSIP
TEERTIMLYKESEMLRETKYPEWAAFSIPLFLLNYFNESSIQLHYYNYYPUHDDQLVGH
CTTTLTQLQQGVGHFNSYMLMEPNGKRIHEKTCIELKELSLENGPTFFQMMENNVKIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLITKPDPEGFMNQVIGMGYLYPDPRMCLLWIGPFPCLMLYSGDLVEAIFSSTKHLNR
ILVQKLCCLGADETVVLSVIALCTLDIICETSMGIA IGAQLLAENNEYVWAVHTINKL
ISKRTNNPLMWNSFIYNLYGSFINKENDYKMEGRLAFLDLLLEMVNSGOMDETVDVA
EGNTFMLEGHDTTSTGLMWAVHLLGNHPDVQRKVQAELDEVMGDDEDVTIEHLSRMKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6798. .8876)
/gene="CO1F6.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(4953. .5032,5081. .
6033. .6264,6332. .6585)
/gene="CO1F6.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTSAIDLTASNGNPVNQSSLHYIHPHQPSPYLEALLQTVPPLLAYLPNPQNPHIGALG
FGAKVQVPGGALQLSHCFCLNGTPTDPRVEGLGGLLSAYRTAVMGLQPFAPTDFSEVI
YFMSKFAKAESRRHVGLYFVLIIYSDGGPANALNMKRSIDAIVDASPHPMSIIGVGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LECALKEALRLFPSVLIITRELSDDQVIGGFNIPKGVTFLLNLYLVHRDPAQWKDPDV
FDPDRFHPENSIGRKSFAFIPFSAGSRNCIGQRFALMEEKVIMAHLLRNFNIKAVELM
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/db_xref="PID:e1343692"
                                                                                                                               /note="Identity with sex-determining protein FEM-3
(SW:FEM3_CABEL)"
                                                                                                                                                                                                                               /gene="fem-3"
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                                                                                                                                                                                                                                                               join(10227. .10297,10396. .1
.1666. .11756,12137. .12369)
                                                                                               codon_start=
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                                          Sasaki, Hokkaido University, Applied life science; NSH Hokkaido 060, Japan (E-mail: JSSK@al.hines.hokudai.ac.Tel:81-11-706-2402)
                                                                                                                                                                                                  Submitted (17-JUN-1996) to the DDBJ/EMBL/GenBank databases.
                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis
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21; Conservative
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GYERNDEITRFVEQRTMKTIVTYCNFMYDLARRNGKVQITRFEDDLIHRDEFREYMY
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AFYPPEYFWNEDESKYHTTFVVPRGTEFSKFYARRFHEALGMPPLENEIITVLDWLAK
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/gene="C01F6.6"
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/db_xref="PID:e1343694"
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/gene="CO1F6.5"
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/gene="CO1F6.6"
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bred. No. 2.86e-01;
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Submitted (27-SEP-1997) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
The H. influenzae sequence has been updated by R. Fleischmann. New database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. We gratefully acknowledge the work of Tatusov et. al. We have incorporated their annotation into the /notes fields of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann, R.D., Adams, M.D., White, O., Clayton, R.A., Rikness, E.F., Kerlavage, A.R., Bult, C.J., Tomb, J., Dougherty, B.A., Merrick, J.M., McKenney, K., Sutton, G.G., FitzHugh, W., Fields, C.A., Gocayne, J.D., Scott, J.D., Shirley, R., Liu, L.I., Glodek, A., Kelley, J.M., Weidman, J.F., Phillips, C.A., Spriggs, T., Hedblom, E., Cotton, M.D., Utterback, T., Hanna, M.C., Nguyen, D.T., Saudek, D.M., Brandon, R.C., Fine, L.D., Fritchman, J.L., Fuhrmann, J.L., Geoghagen, N.S., Gnehm, C.L., McDonald, L.A., Small, K.V., Fraser, C.M., Smith, H.O., and Venter, J.C.
                      5 (bases 1 to 12188)
White, O., Clayton, R.A.,
Peterson, J., Hickey, E.,
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                                                                                                                        corresponding H. influenzae genes
                                                                                                                                                                                                                                                                                                                                                                                                                                     Medical Center Dr, Rockville,
4 (bases 1 to 12188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-JUL-1995) The Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96398784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95350630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eubacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus
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Similarity 100.0%;
20; Conservative
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/db_xref="taxon:1428"
578 c 751 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clayton, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Bacillus thuringiensis"
/strain="SKW01-10.2-06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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influenzae
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Pred. No. 1.47e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rd Rd
                             Kerlavage, A.R., Dodson, R. and G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kerlavage, A.R. and Fleischmann, R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NA BCT section 124 of 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20850,
                             ., Fleischmann, R.D., Gwinn, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deduced from
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The whole genome was shifted by 588 nucleotides for a new start
On Jun 12, 1998 this sequence version replaced gi:1574746.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-MAY-1998) The Institute for Genomic
                                                                                                                                                                                                                                                                                                                                   /db_xref="gil:q1574749"
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IvivggygkloglearylraasgypisJldredwavaesilanadvviysvpinutlet
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Dgrfperyemlleqiqimgakiyqtnatehdhnmtyiqalrhfstfanglhlskqpin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="trna pseudouridine 55 synthase (truB)"
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PID:606106 percent identity: 58.44; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="ribosome binding factor A (rbfA)"
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                                                    sequence similarity; putative"
                                                                                                                                                                                                                                              ENNDRQGFIDAFHKVRDWFGDYSEQFLKESRQLLQQANDLKQG"
complement(2838. .3677)
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288. .674
                                                                              PID:1789158
                                                                                                                                                                                   complement(2838. .3677)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PID:43345 percent
                                                                                    /note="similar to PID:882689 GB:U00096 SP:Q46920
PID:1789158 percent identity: 61.59; identified by
                                                                                                                                                                                                                                                                                                            LANLLALSSPIYRLELAMIGRLFAQDAELYADIIMDKSENLAVIETLKQTYDEALTFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein_id="AAC22939.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="chorismate mutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="similar to SP:Q02287"
D:43345 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="HI1290"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="HI1290"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOLLAESFPLSELDRLLLPTDTAVSKLPALHLDAEQSKAIGFGORVKFANEQQLSGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="HI1289"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="HI1288"
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/db_xref-"taxon:71421"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LESAENLELGVLNRREYYSPTTINYTIRITSLPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'transl_table=11
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ID:606107 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:M74135 GB:X60420 PID:415010 58.86; identified by sequence
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: 67.44; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prephenate dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to PID:882705 GB:U00096 PID:1789175 percent identity: 47.14; identified by sequence similarity; putative"
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YLAEEDGAGGFANTON CONTENTAL TOTO TOTO TRANSHIFTON TRANSHIFTO
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                                                                                                                              /note="similar to SP:P29769 percent identity:
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CDS gene

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Note: remainder of annotations omitted

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Gaps
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AL Submitted (23:5EP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (Dases 1 to 177411)

RES diren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Donelan, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., Karattas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., Karattas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nahf, R., Naylor, J., Nilef, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Jiect Submission Gage,D., Gardyna,S., Geralgery,K., Grant,G., Hagos,B., Heaford,A.,
Herena,L., Horton,L., Howland,J.C., Jacotot,L., Jones,C., Kann,L.,
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Severy,P., Stange-Thomann,N., Stilwell,J., Stojanovic,N., Stone,C.,
Subramanian,A., Tesfaye,S., Tichovolsky,N., Torruella,Miller,I.,
Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,Y., Wyman,D., AC005696 g3819097 Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Location/Qualifiers
1. .177411 Submitted (01-NOV-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 1, 1998 this sequence version replaced gi.3818406. Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone hRPK. 74\_E\_22 All repeats were identified using Green, P. (1996-1997) Ye,W.J., Zhao,J. and Zody,M. Direct Submission Unpublished Homo sapiens AC005696.1 Homo sapiens chromosome Primates; Catarrhini; 1 (bases 1 to 177411) Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; AC005696 177411 bp GI:3819097 Hominidae; Homo DNA 17, prI 01-NOV-1998 clone hrpk.74\_E\_22, complete sequence RepeatMasker:

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/rpt_family="THEIC"
                                                                                                                                                                                                                                                              /rpt_family="AluSg" 22393. .22709
                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="L1M4" 21751. .21996
                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="(TA)n"
complement(20950..21228)
rpt_family="Alusg1"
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/rpt_family-"Alusx"
complement(16784..17170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="AluJo"
complement(18744. .18870.)
/rpt_family=""."
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/rpt_family="MER20"
complement(17403..17565)
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/rpt_family="L1MC4"
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complement(15778. .16043)
/rpt_family="Alusg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (19195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(18880.
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/rpt_family="L1MC4"
                                                                                                           rpt_family="(TAAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="AluSg"
complement(1910c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="AluJb"
complement/18800
                                                      rpt_family-"L1M4"
                                                                                                                         rpt_family="AluY"
3328. .23354
                                                                                                                                                                                                                                                                                                               'note="Single-stranded coverage."
1997. .22274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="MER46B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="AT_rich"
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5, .19801
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5, .17040
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lement(17200
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3.0%;
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                                                                                                                                                                                                                                                                                                                                                             family="AluSx"
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                                                                                                                                                                                                                                                                                                                                                 21851
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                                                                                                                                                                                                                        .ly="AluSg"
Score 20;
DB 31; Length 177411;
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14-AUG-1995

0;

Gaps

0;

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VERSION
KEYWORDS
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TITLE
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STS size: 229
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Reopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
1 (bases 1 to 351)
2initi,J., Jackson,D.G. and Fishman,M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g4494300
G47692.1
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G47692
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: fishman@mgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
Primer A: TCTGAGCCTTAGCAGGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 6177265806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G4/692 351 bp DNA STS 23-MAR-1999 Z25793 1 Zebrafish AB Danio rerio STS genomic clone Z25793 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G47692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mark C. Fishman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zebrafish
                                                                                                                                                                                                                                                                                                                                                                                              dNTPs:
Taq Polymerase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Denaturation: Annealing:
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                                                                                        /note="Vector: ml3MP19 with added BstXI site; V-type: Phage; Genomic DNA from a single adult Zebrafish of AB strain was digested with AluI. CacoBI HaeIII, NlaVI, or RsaI. Fragments in the range of 250-500 bp were gel purified and a BstXI linker was added. The fragments were cloned into a modified Ml3mp19 vector and transformed into E. Coli DH5alpha. Microsatelllite sequences were screened with labeled d(CA)15 and d(GT)15 oligonucleotide
                                                                              probes.
                                              /db_xref="taxon:7955"
/clone="Z25793"
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:4494300
                               /clone_lib="Zebrafish AB"
                                                                                                                                                                                                                        /strain="AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTGTGCTCTGCGGATCTT
/dev_stage="Adult"
                                                                                                                                                                                                                                      ∕organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                   MgCL2:
KC1:
                                                                                                                                                                                                                                                                                                    Tris-HC1:
                                                                                                                                                                                                                                                                                                                                                                              10 ng
each 375 nM
each 200 uM
: 0.034 units/ul
10 ul
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94
58
72
27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.47e+00;
0; Mismatches 0;
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50 mM
10 mM
8.3.
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                           primer_bind
primer_bind
BASE COUNT
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KEYWORDS
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primer_bind
BASE COUNT
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Best Local
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                                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                                                         Primer A: ATTGACTTGGAGATGGATCG
Primer B: TCCTTAGGTCTTGGCTTCCT
STS size: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 524)
Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G09531 524 bp DNA STS
human STS CHLC.GCT3B06.P11066 clone GCT3B06.
G09531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synonyms: GCT3B06, CHLC.GCT3B06.T11065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STS sequence; primer; sequence tagged site.
human vector=pJCP1 host=E.coli dut+ung+ (DH10B) Marker Selected
genomic DNA prepared from XY individual of French nationality.
                                                                                                                                                                                                      Buffer:
                                                                                                                                                                                                                                                                                                              Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The University of Iowa
Department of Pediatrics, Iowa City,
Tel: (319) 356-3508
Fax: (319) 356-3347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Dr. Jeffrey C. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cooperative Human Linkage Center Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                            PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.9%;
Similarity 100.0%;
19; Conservative
                               73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       jeff-murray@uiowa.edu
                               ω
                             complement(211. 101 c 110
                                                           /organism="Homo sapiens" 90. .230 90. .109
                                                                                                                    Tris: 10mM
pH: 8.3.
Location/Qualifiers
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3. .27
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94 c 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:941380
                                                                                                                                                                                                                                                                                                                                                                           denature: annealing:
                                                                                                                                                                       MgCl2:
KC1:
                                                                                                                                                                                                                                  Taq Polymerase:
Total Vol:
                                                                                                                                                                                                                                                                                               Template:
                                                                                                                                                                                                                                                                                                                                extension:
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PCR cycles:
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Pred. No. 7.20e+00;
                                                                                                                                                                                    1.5mM
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<sup>ე</sup> g
                                          .230)
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75
15
27
                                                                                                                                                                                                                                                                                                                                                                           seconds
                                                                                                                                                                                                                               30ng genomic DNA
each 1.5 pmole
each 200 uM
0.3 units
10 ul
                                                                                                                                                                                                                                                                                                                                                            seconds
                                                                                                                                                                                                                                                                                                                             minutes at 72 degress
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                                                                                                                                                                                                                                                                                                                                                         s at 94 degrees
s at 55 degrees
s at 72 degrees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IA 52242,
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356 AACAATTTGNTAATGCTNTTNT 377
                                                                                                                                                                                                wore than 870,477 bases have been sequenced by the genomic walking technique and assembled into 372 non-overlapping contigs (Accession numbers Z33005 to Z33376) covering 214,528 base pairs. The length of the contigs varies from 63 base pairs to 2049 base pairs with an average length of 658 base pairs. The data consists of 13,091 bases (64%) from one pass fluorescent sequencing and 201,437 bases (94%) produced by genomic walking. Of the latter, 155,805 bases (77%) have multiple coverage on at least one strand and 112,621 bases (56%) are covered on both strands. There is a total of 968 ambiguous nucleotide assignments in the data set (0.5%). We have compared 8,868 bases of our data with Mycoplasma capricolum sequences already stored in the public databases and note less than 0.7% difference between the two data sets (1 including ambiguous calls, insertions, deletions and mismatches).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The tga codon is read as Tryptophan in Mycoplasma capricolum Coding sequences below were putatively identified by Peer Bork using the program Genequiz at the EMBL.

EMBL, Meyerhofstr.1, 69012 Heidelberg, Germany

E-mail bork@embl_heidelberg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-SEP-1994) Mycoplasma capricolum Genome Project, Harvard University, Cambridge, MA 02138 Prokaryotic Genomes Project Institute for Computational Sciences and Informatics George Mason University, Fairfax, Virginia, USA, 22030-4444 E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gillevet,P., Ally,A., Barton,F., Brenner,S.E., Clark-Whitehead,R., Dolan,M., Douglas,N., Hsu,E., Purzycki,M.S., Richter,B., Russo,S., Sartell,J., Smith,S.W., Wang,C., Williams,J. and Gilbert,W. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bork,P., Ouzounis,C., Casari,G., Schneider,R., Gilbert,W. and Gillevet,P.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MC097 2057
M.capricolum DNA
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Similarity 86.48;
19; Conservet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gillevet@uranus.nchgr.nih.gov 3 (bases 1 to 2057)
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1 (bases 1 to 20
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Mycoplasma capricolum
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                     complement(<3. .>224)
/note="ORF identified by homology to SwissProt entry
swiss|P23539|KIPF_ECOLI; Probablity 6.0-11"
                                                                                     /organism="Mycoplasma capricolum"
/strain="ATCC 27343(Kid)"
/db_xref="taxon:2095"
                                                                                                                                                                               Location/Qualifiers
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Pred. No. 7.20e+00;
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Query Match 2.9%;
Best Local Similarity 100.0%;
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Vertebrata; Eutheria;
1 (bases 1 to 2650)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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/note="ORF identified by homology to SwissProt entry
/note="ORF identified by homology to SwissProt entry
/note="15082|GUTR_ECOLI; LACR_LACLA; Probablity 2.0-15"
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/note-"~~
                                                                                                                                                                            /map="14q32.33"
1649. .1656
/note="G00-128-528"
join(1782. .1827,1929.
                                                                                     /gene="]
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/cell_line-"Y79 retinoblastoma"
/tissue_lib="Y79-EMBL-3"
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YKFATNLELELIED"
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STTYYLAKILDPNLDLKIVTNSILNVQELSKNNHQNIYLLGGKYQVVTSSILGYQAVN
                                                                                                                                                          /gene="IGHV@"
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/gene="IGHV@"
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join(1782. .1827,1929. .1939)
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/codon=(seq:"tga",aa:Trp)
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Eutheria; Primates; Catarrhini; Hominidae; H
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ne IgH chain (hv3005) V3-region
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Pred. No. 7.20e+00;
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Matches 19; Conservative
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Direct Submission
Submitted (02-NOV-1998) The Institute for Genomic Submitted (02-NOV-1998) Rockville, MD 20814, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE001383 14459 bp DNA INV 06-NOV-1998 Plasmodium falciparum chromosome 2, section 20 of 73 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 14.
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4;282(5395):1827]]
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Location/Qualifiers
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/db_xref="taxon:5833"
/chromosome="2"
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528 c 591 g 762 t
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/note="G00-128-528"
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)oin(635. .728,878. .978,1130. .1213)
/gene="PFB0255w"
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/codon_start=1
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note="identified by sequence similarity;
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Pred. No. 7.20e+00;
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CIIECSVYAALSLGLVFVGSQNREIAEYIIDTVLEKEKINNSLDTPIAKLYAVALGLL
FLCSREKCEATLSALEIIKHPISKYMIATVEGMAFAGSNDVLKVQKMLQVLVEKRGDK
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YQSKIEDFFPLLEKKRKTVDDLIDHIRANNKQKRQKNKTVHI
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ISNYNTEMLEISETLKYHENKFKQHLNYLDENNSTPVYMNNLKNINYKNNDLIEGG
EKKSFINLINYDSCYSSSNSRLENDERIERGKIMKFINDEKSININYKNNNNNNNN
NNNDNMDNNDVIIEHNKNNNNIYDNKYNYECSSEKINDNGISNKNINILELPNNLDT
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SSKNYVEDNLDQCVAILNIALIALTDDISSDMTTRIIDHFLQYSNVNQKKAVPLALAL
LFTSFPKPNIVDILSKLTHDQDPDVALHAIISLGFVGAGTNNSRIAILLRQLSAFYCK
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LIFECNDILICKOIALICSRHCHIOFTEERKVTHLNUNEISTLTSGEHLSPIFLK
LIFECNDILICKOIALICSRHCHIOFVEERKVTHLNUNEISTUNAFVNAAFCKDKLMTV
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NSSLMIFKNKDYGLMSATASMGLLLMWNLDEGLSQIDKFQYSSDQYVKAGALMAFGLA
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TVIKNFFNKKKTVEVYEKKAIEEKLGLYQEELINISLLCGCDYTIGVHGIGIVNALEI
IKAFPNFEDLKILKDIVSNPFRKIDKNMYNEEIQQFLNTHKNYKLNWIFPNNFPDREV
                                                                                                                                                                                                             DLENNY ISYSSDMKTNVSKNNITCYKENKVDKTNNEYDKKGDDGVIEISFEDSHKLE
ESKFDDNNNIYDNDDELEKNLSKDYISDVDKNHVNNIYNIEGEDEREWEFVENKIQS
TESHKSNEFICTENKSLRKQYMSKEDISNVRILKSDDINNLSKONYFEILLDKKOVM
NFOMNIGONDKLKEDKLDBGAYFEYLEDNKIIDSYIKETNKENEELIKEYKKLKKNN
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DSNKYTFIKIENEFKKDLLLDDSQIFGDSLLADIKEYNYTADNLDNNERKSLYEDGE
NFTFRNEPIINEYEEKNIIIYISDSCOKYNEEDLIFKDDKIKEKEKNNDYTSSDDFENSCY
QEKIYVNEKIEEYNNKNDDKSSSSSSIILEEIKYKKEKKDELVSPNLCVLLDEFEHSN
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IKAIKSKDDMDVFSQVQLETYVRMIKTDFEIEKLKIKMAENIQSVEGELLINKDLSKN
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RNKDENNLSYSINYNKVQDVNNNNDDDKDKDKENINEVRRDQKNYVYKNKENINNIYL
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KYHYLLYHLVPCIYPRMLVTVNEKLESLPVSVRVGQAVDIVGQAGKPKTITGFQTHVT
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NGLITTSTTSNKLVTINHIYDIVNIVVPYCFAHNTEYEAIDLLIEVDKINDIYLYVDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="PFB0265c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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/protein id="AAC71841.1"
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LOCUS
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-FEB-1992) U. Arnason, Dept of Mol Genetics, Univ of Lund, Box 7031, S-220 07 Lund, SWEDEN
Users are requested to refer to the citation of this entry as well as the accession number in their publications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion Phoca vitulina
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Carnivora; Pinnipedia; Phocidae; Phoca.
1 (bases 1 to 16826)
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1966. .2038
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                                                               note="anticodon"
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/db_xref="GI:13434"
                                                                                                                                                                                                                             complement(6139.
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MLLPMTPMMSILE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FMHNSSTTTLSLSNTWNKLPLMTSLILMLMMSLGGLPPLSGFAPKWMIIQELTKNDMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="NADH dehydrogenase subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="NADH dehydrogenase subunit 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene-"tRNA-Trp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:13432"
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                                                                                            codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="tRNA-Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tRNA-Met"
                                                                                                                                                             .6273)
                                                                                                                                                                                            .6273)
                                                                                                                                                                                                                                                                                                                                                                            .6106)
                                                                                                                                                                                                                                                                                                                                            .6106)
                                                                                                                                                                                                                             .6205)
                                                                                                                                                                                                                                                                                                                                                                                                         .6032)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         6032)
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                                                                                                                                                                                                                                                                           replication"
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Db. 3254 CTAATTGATCCAAAAATTT 3272
                                                                                                                       Note: remainder of
                                       Query Match 2.9%;
Best Local Similarity 100.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trna
                                                                                                                         annotations omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="memnrmlestnhkdigtlyllegamagmygtalslliraelgop
gallgdooiynvivtahafvmiremynemingiggminydymigapdmafermnmse
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aineittiinmkppamsoyotelefwsvlitavllllslpvllaagitmiltdrnintt
erdpagagsdpilyohlewefghebyxililpegramishivtyxgakkbefgxkamvma
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spamlmalgeitlefyggatldotmakihtimfygvnmtefpohelglsgmprrysdypdayttm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="anticodon UCN" complement(7817. .126: /gene="tRNA-Ser"
                                                                                                                                                            9555. .>10337
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SLYLHDNT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="tRNA-Lys"
8644. .8712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAYPLOMGLODATSPIMEELLHFHDHTLMIVFLISSLVLXIISL
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QWYMSYEYTDYEDLMEDSYMLFTOELKPGELRHLEVDMRYVLPMEMTIAHLISSEDVL
HSWAVPSLGLKTDAIPGRLNQTTLMTMRPGLYYGQCSEICGSNHSFMPIVLELVPLSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(7817.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8875.
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/db_xref="PID:g13436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="cytochrome c
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7959. .8642
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7892. .7958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTVSSMGSFISLTAVMLMVFMIWEAFASKREVAAVELTTTNIEWLHGCPPPYHTFEEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEKWSTSML'
                                                                                                                                                                                                                                                                                            [QQWLIQLTSKQMLSIHNRKGQTWALMLISLILFIGSTNLLGLLPHSFTPTTQLSMNL
                                                                                                                                                                                                                                                                                                             /db_xref="SWISS-PROT:Q00521"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNSAPWEEKWTKIYSPLSLPLQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3714. .8917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SWISS-PROT:Q00528"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="tRNA-Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                           transl_table=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="GI:13436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transl_table=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene-"tRNA-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=
                                       Score 19; DB 23;
Pred. No. 7.20e+00;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .12618)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .7887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c oxidase subunit II"
                                         0
                                                                                Length 16826;
                                       Gaps
                                       0
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                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    459 CTAATTGATCCAAAAATTT
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                                                                                                                       sequence
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Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hiller,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Wilkinson-Sproat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bin/display?db-wormace&class=Sequence &object=K08H2
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a smale
                                                                                                                                                                                                                                                                                                                                                                                                                                 once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone K08H2 is at 1 in this sequence. The true right end of clone K08H2 is at 7075 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone K08H2.

It may be shorter because we only sequence overlapping sections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coding sequences below are predicted from predictions from Genefinder (P. Green, U. available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-MAR-1996) Louis, MO 63110, Ujes@sanger.ac.uk or rw@nematode.wustl.edu 2 (bases 1 to 3653)
Wilson,R., Ainscough,R., Anderson,K., Bayı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z70210.1 GI:1229075
HTG; Murine modifier 2 pro
II elongation factor like;
                                                                                                                                                                                                                                                                                      true right end of clone R12H7 is at 15206 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                             sequence Z50742.
The true left end of clone K09All is at 36436 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 36539)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                              end of this sequence (36436. .36539) overlaps with the start of
                                                                                                                                                                                    Z5074
/db_xref="taxon:6239"
/chromosome="X"
                                                                           /organism="Caenorhabditis elegans"
                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36539 bp
tis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein like; Protein kinase;
ike; Steroid hormone receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA cosmid K08H2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secernentea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    computer analysis, using Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditia; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
for a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA;
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gene

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complement(16114. .17283)
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                         complement(join(16114.
16887..17163,17257...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGVIPIFYKIARFADMORNDGIPMEYEEEDPIGTGLEYSĒRAEGEFIELVNTWFFHED
VDGQQPGREDFDPAAEQENSEDPEVVEPKSVDRNLALFLGEMYLTMQPHTDVYPPAPK
PGDĪYIPIGGLAKCECSPGCTRELPQPAYRIIDEAERRWFPKDNNKLRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="Sptrembl:Q21366"
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MYAKSIKPHVDVFPSAAEEKVNVETGHKKKKSKGKKVAKE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="predicted using Genefinder; Similarity to Human RNA polymerase II elongation factor like protein (PIR Acc. No. S55509); CUNA EST EMBL:D72393 comes from this gene; CDNA EST EMBL:D75263 comes from this gene; CDNA EST yk374f9.3 comes from this gene; CDNA EST yk374f9.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="predicted using Genefinder; cDNA EST yk375c12.3
comes from this gene; cDNA EST yk375c12.5 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:Q21368"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:Q21367"
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FRLEIVGLLDVACRAVSIMLGRTLNEVKLMLRVGGVESPSDEEDSLEDVLELEVDVDE
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/db_xref="PID:e1347977"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(9283. .9576,9654. .9962))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(9283. .9962)
/gene="K08H2.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1139. .1669)
/gene="K08H2.1"
                                                                                                                                                                                                                                                                                                         /protein_id="CAA94151.1"
/db_xref="PID:e1347980"
/db_xref="PID:g3878388"
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/gene="K08H2.4"
join(13656. .13700,13828. .13911,14596. .14685,14744. .14953)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEEDDVEIEIPAISAA"
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/db_xref="PID:e1347978"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1139. .1669)
/gene="K08H2.1"
  'note="Similarity to Mouse CLK protein kinase
                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="K08H2.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="K08H2.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(12427. .12726,12816. .13121,13172. .13369)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene-"K08H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="K08H2.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'protein_id="CAA94150.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="predicted using Genefinder"
                                                         4. .16302,16348.
.17283))
                                                                                   .16605,16651.
  RESULT
LOCUS
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                                                                                                                                                                    В
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                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                        Matches
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                                                                                                                                          6091 CAATAACTTGATTTGCAAT 6109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                                                263
                                                                                                          CAATAACTTGATTTGCAAT 245
  CEF41D3
                                                                                                                                                                                                                  2.9%;
Similarity 100.0%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       '/protein_id="CAA94154.1"
/db_xref="pID:e1347983"
/db_xref="pID:g3878391"
/db_xref="GI:3878391"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SPTREMBL:Q21370"
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TSSSAELQPSTSDEWACKTLKTIIGITKAPGELHFLCKFSDDSVHLIPLREANVRFPS
QVIKTYETRLYLQGYSPTIPGGMS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"predicted using Genefinder; Similarity to Mouse modifier 2 protein (SW:MOD2_MOUSE); cDNA EST yk432cll.: comes from this gene; cDNA EST yk432cll.5 comes from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="Sptrembl:Q21371"
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ENKTITAGYGNQSEPCDIVQQAFVGENLVRITPSNTPTGILCQCSDQVSFLPVVKSI
DTATRLTFFAEMLRFQTTSQFTRQRQIIRKVCFRSKIMSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="G1:3878392"
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TITPASPCKLIDYGYGKFERNRRGWYYKNRFORDVNFKEGGHYSWNVMAGGYBNLKDE
FSSLMFLGLKISGISSLEIGSVSEVRHQKMIFELDPSRFLRSVPWLLKVACVIVDSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAA94153.1"
/db_xref="PID:e1347982"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(22268.
23180. .23323,23372. .2
/qene="K08H2.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(26779. .26805,26969.
28677. .28754,29203. .292
30903. .31004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(22268. .23431)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA94152.1"
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join(20433. .209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKFNYAGVFNAIKQGFPFDEEEIINHSYLQGSLKVY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAA94155.1"
/db_xref="PID:e1347984"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="Similarity to steroid hormone receptors'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="K08H2.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="K08H2.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="PID:g3878389"
/db_xref="GI:3878389"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="K08H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="K08H2.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="K08H2.
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39030 bp
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                                                                                                                                                                                                               Score 19; DB zı, __
Pred. No. 7.20e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .20525,20601. .20684,20738.
  DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .29286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .22360,22742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .27032,27236. .27382,28474
5,29340. .29431,29900. .30
                                                                                                                                                                                                                                                                            Length 36539;
  ANI
                                                                                                                                                                                                                        Indels
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  23-NOV-1998
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gene

CDS

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from this

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Gaps

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gene

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REFERENCE
AUTHORS
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ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                            SgS
                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a sma overlap between neighbouring submissions.

IMPORMANT: This sequence is not the entire insert of clone F41D3. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is NOT necessarily the entire insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B., O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A., Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E., Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M., Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Consell,M., Copsey,T., Copper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neighbouring submissions.

The true left end of clone F41D3 is at 29177 in sequence 281502.

The start of this sequence (1. .107) overlaps wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Mar 30, 1997 this sequence version replaced gi:1665953. Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans cosmid F41D3, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-NOV-1996) Louis, MO 63110, USA. jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bin/display?db=wormace&class=Sequence &object=F41D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 368 (6466),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z81537.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence Z81502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 39030)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 39030)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             start of this sequence (1. .107) overlaps with the end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z81553
                        /protein_id="CAB04372.1"
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                                                                                                                                                                                                      /gene="F41D3.1"
join(723. .747,868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:1914230
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                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                 organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      this sequence (34757.
                                                                                                                                                                                                                                                                                                                                                                                                                      .3903
_xref="PID:g3876985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32-38 (1994)
                                                                                                                                                                                                         .1011,1057. .1122,1177. .1361,1411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .39030) overlaps with the start of
                                                                                                                 C4 type (two domains)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
for a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ი
                                                                                                                                                                                                            .1842,
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complement(join(9773. .10036,10080. .10290,10401. .10528,
10740. .11077,11126. .11292,11505. .11760,11808. .11946,
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TKLPAKLHNPYYTIIGLASYLFFHFSPAPVAFNSVLARIWQFIIGMLIYNIGCSKLKR
HYKIITDQEEKCKLQESYKSYLFTHFSPAPVAFNSVLARIWQFIIGMLIYNIGCSKLKR
HYKIITDQEEKCKLQESYKSYLFLHAFTIMAFFPIPLDASIIRFUVTIGTGCLMLTCE
GNPMLSNKIITYLGDISYSYLYIFHAPTYAYWKHZCNGDSSLLICALISSTULAIVFFE
TFEKWYLKLSNPNLSILVALLFASSGLAIEKIEISNQIYMYRHNIKTLDSVTSNMTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(9773. .12447)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:3876987"
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8387 .8588,8647 .8721,8774 .8821)
/gene="f4183.3"
/note="similar to Zinc finger, C4 type (two domains)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKYKIAVFGNSWAANHGEMIHQECGHKAKIIIQGSANACDPLYFSPDSVPCRKNFTDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPLYTIGTGCLMLTSEGNPILSNKILSYIGDISYSLYLIHWPIYAYWKLTCKGDSILL
ICALISSIYLAIFTFETFEKWYLKISNSSLIILVTLLFVSNGGLIKKNQISNEIYMYQ
RNITSLDDITSNMTVDDAIRLNYQWNVDDGPNLFVSYCVYESDTGPFGWCNHTGLSPS
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ISIEYNGKSATRALFFVSNRFSSLÓDDYFSMLSMAIDIFTHTWSLSVEVGFYILVDFM
FLIVTRLÞAFHTASFAILGITSLLHENESPAPIAFNSVFARVWOFILGMLVYLKGS
MLKRDYTILSDKEEDCKFSKELAKSHSYFNNVQASSYSSLAVLIILTFLPFTLSSSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="meatsqurgpcpvcssmdrtrrhfgiiactacaaffrrsfgqqy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IYKEMVRLYRQMGV"
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MNAFPRIDQPSVEMIAKWLKNGTSPEEVDKRLFNSKDAVIEQQSYELTRERYAQLEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAB04373.1"
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LFALGRSNLNNLNSLNNMNNTNQELSEFISLVKSTLVSPLSRLRLDITEFAAFKAIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="PID:e1346781"
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/db_xref="SPTREMBL:045506"
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/gene="T41D3.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WALRKYYKESTNMTEVEIAARIGDITLQLLTVSDIFHDMIKLYHQVGISF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFDFLHQVRSTLGSSLVRLNLNIFEYAAFKSFCIWNLKFFGTSTAMKIVAEEHHIGIT
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                                                                                                                                                                                                                                                                                                                                                                     'db_xref="SPTREMBL:045508"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="F41D3.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MNSMNRQEPSKRLDLQGIRGLAILAVLGFHFFPGAFPNGYLGVD"
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  SOURCE
                        KEYWORDS
                                                                                        ACCESSION
                                                                                                                      LOCUS
DEFINITION
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                                                                                                                                                                RESULT
                                                 ERSION
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 1
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                                                                                                                                                                                                                                                           1538 TGCTCAAATATTTCAAATT 1556
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                                                                                                                                                                                                                                                                                                                      2.9%;
Local Similarity 100.0%;
res 19; Conservat****
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                                                                                           CELF47D12 41275 bp
Caenorhabditis elegans
U22831
Caenorhabditis elegans strain=Bristol N2
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complement(join(15179. .15442,15488. .15698,15745. .1585
complement(join(15179. .15442,15488. .17643,17092. .17891. .16036,16093. .16412,16877. .17943,17092. .17293,17486. .17624,17673. .17937,17991. .18115))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAPSSTFGWWIGYLSKNOSAVYYRDIRETKDQVOLOMTKEDFYPPTWNKLLTRGTFRR
RDVYLNGGRPHGGGGGGGGGGGGGGGGTIAKNLFKGFPSGSFORGQRILLYARPKTG
PNASQMTVNLYAYNONILEHFNPRPEENVVVRSTSIGGVWQAADRDGGYPFATGVRFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQVISVPIEPSETTRFAISSDCCRYELSDNHLADESKFLVIEGHYFQSYKYFADMKL
SIKEWLKPEDPEKFRMMISKTESQRHKTCVHVRRGDFLTDEQHAGTDSNYTISAIDHL
RSLYHGVIFIMSNDPKWVKVHIADHLDYQKDIRIMKTLMEDAIDDLHFSQIYCDSVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(18969. .19208,19259. .19543,19800. .19853,
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21084. .21244,21298. .21405,21468. .21534))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVLLILLNYFLINKEHFKMGPKEKEEVEKNYALNYDDAILKNHOWDLNDQOSICVSYC
NYEAYAPLGWCNHTSLSPSGKYKISVIGNSWAANHGAMVHEECGSKANTILQGSMASC
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LTDGASYEMARRRYAALVKDCDGRCVLVDYKPVFYNSTIKSYRIFDNSGYSYLTTPKH
LTPRGLEHVRHVMKDVCATL"
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YVSYLPLESIIFINALPYLSTDFVRPFVTLVTGFLMMISENNMLLSNKCLAYIGNS
YSLYLIHMPVYAYMKLTCEGDQNLLLIALLSSIVLAVIVHEFFEKMYLKLCSTSIGLV
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LTFPMTTIVYKGGLGNQLFEVLSLLGIARKLKRIAVFNSSDPVLQSNLEFLNQKLPRI
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VLSGFLMCMLLKRAESDSTCTLITLFYSKRFKRILPLYLLIILLSMISLYTIFPDTSI
                                              GI:722352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F41D3.7"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTIVNEAAGLQMYVNRNFFGAYRHRTENPFRAYVSVSASGAMDIFGLVVV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAB04377.1"
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/db_xref="PID:g3876990"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to Vertebrate galactoside-binding lectins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F41D3.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oin(22341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SPTREMBL:045510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start≈1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F41D3
                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 21;
Pred. No. 7.20e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .22360,22407. .22494,22546. .22758)
                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                   cosmid F47D12
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                               Length 39030;
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TITLE
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Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hiller, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, M., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaudhan, K., Watson, A., Weinstock, L., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The C. elegans genome project: Contiguous nucleotide sequence of over two megabases from chromosome III Nature (1994) In press 2 (bases 1 to 41275)
                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                              Waterston, R.
                                                                                                                                                                                                                                                                                                                                                        The sequence of C. elegans Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                         Taich, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
1 (bases 1 to 41275)
                                                                                                                                                                                                                                                            rect Submission
                                                                                                                                                                                                                                                                                                                         (bases 1 to 41275)
                                                                                                                                                                                                                             (14-MAR-1995)
Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England e-mail: rw@nematode.wustl.edu and
                                                                                        Department of St. Louis, MO
                                                                                                                                                                Genome Sequencing Center
                                                                                                                                                                                               Submitted
                                                                                                                                                                                               by:
                                                                                               Genetics, Washin
63110, USA, and
                                                                                                                                                                                                                                                                                                                                                                                              cosmid F47D12
                                                                                                                          Washington University
jes@sanger.ac.uk
```

# NEIGHBORING COSMID INFORMATION:

The 5' cosmid is C18F10, 399 bp overlap; 3' cosmid is C31H11, 200 bp overlap. Actual start of this cosmid is at base position 200 of CELF47D12; actual end is at 41076 of CELF47D12

#### NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green and L. Hillier, ms in preparation).

```
SATURES
Location/Qualifiers
source
// 1. .41275
// db_xref="Caenorhabditis elegans"
// db_xref="taxon:6239"
// map="III"
// strain="Bristol N2"

gene="r47D12.4"

CDS
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// note="coded for by C. elegans cDNA CEESS77R"
// codon_start=1
// protein_id="AAA64316.1"
// db_xref="pID:9722356"
// db_xref="FID:9722356"
// db_xref="FID:9722356"
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KRALSAFFFYSQDKRPEIQAGHPWKVGQVAQEUGKWKLVPQETKDMYEQKAQADKD
RYADEMRNYKAEMQKMSGMDHYDDNIHTVHVEDINSQNIS"
complement(1459. .4677)

gene="F47D12.5"

CDS
. 3923,3975. .4240,4367. .4488,4596. .4677))
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complement(12410...14864)
/gene="F47D12.7"
complement(join(12410...12529,12577...12871,13010...1321 13277...1348,13545...13635,13681...13834,13881...13979,14028...14116,14167...14251,14291...14393,14440...14534,14679...14864))
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YLDISETNVPNISGISSLKNLESLIMRSVELECFEQFVDLFNLTGLRILDVSRSMYKH
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FIATKOFNISLWTI FESLLKLLESSLKPMSVERVCRIAGLGIVCKLLDGVVNNGRL
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17YKNGILKKILKDSREDGSLLWALLVIKSSMEQDKSFVNLLTTEMSNLNTNSEIIMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MDICDISASQLATSPPPRTAIDFNSSIEESPVKRVKFSPELTKS
FEETLSPTVTLVLRNREVIFDRYLLST'SNY FRVLFSKFFRONSTHRIRLISASD
LHFLLTIFRAFEOGIKR NITLOKA IELLEPAAFLOMSIALDVISDIICKNLTHENIK
IFRLALLYHTTLAVRVWRSMVRKFQTLFATNVYLSLKENELIGLLTDKHLNLKSEDET
TVVVNNK KHNSPLOSDRITOFAQRNFSRFOQPDATK VEVIRTROPMDAIVCFGGWASR
GVAOKIEVCNYRSDRWOTCNENVD IPAIHRAVHGIEVVEDKLIVYGGFBGIKOFOTU-
LFDLSTKEWRRSDRWODKRCYVTSARVNDSYGRPLVFACGGMNGVSRLKTAEMYDYRA
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complement(join(18812. .19005,19378. 20307. .20565,21091. .21375,21422. .2/gene="F47D12.9"
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/db_xref="GI:722359"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entire protein; weakly similar to M. musculus MIPP prote (SP:MIPP_MOUSE, P28575)"
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                                                                                                                                                                /translation="MVNELSFNCEDAWLNLFVGGEMYPVQVKTLMNPTTCGSYFRDVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DQWTEVANMTQMRSDGAVVTIDNKIVAIGGFDGRNIHQGGEVYDDVLDLWHPLSSNMR
TRRIGCTAVSIMNQVCMIIGGFNGNRRLDSAEIYDMREGLWHPEPTLQTARSNFSACQ
MDTCYVYVAGGFDGQTTTKESERLDLRSKMWQALPDMAEAKSALRMVTLSDHPFLDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MDNIQTFFDQYYHLPSEISSKHDHAYIILILLSVILILLLLICN
LCICYFIRQRRRRELIDYPSNTLQYIPFPRNVRKPYRTESGTSSSNRMMLPPRQHV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDIPDDTGIVTSW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MVLKKHCLESLGIGDLDYIGYYYRDLIDDNTIDIFELLKAILNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=
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                                  8. .19946,20005. .20244
.21512))
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gene

CDS

gene

SgS

gene

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CDS

CDS gene

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SOURCE
                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                            DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: remainder
                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                  VERSION
                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6287 AACGATACAAGATTTAATT 6305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                      complete
AB018112
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                         AB018112 70475 bp
Arabidopsis thaliana
                                                                                                         clone:MAB16
                                                                                                                               Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                                                                                  AB018112.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.9%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of annotations omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MDFTKDNEIVRPPTPPDDNTYSNPNFSMISEQLTNGFSRQEPSSVIERESTAPCVSPEPSHASLENEFNENHHAHFKPELSLPFIDADSVSSMVGHDDLRRA
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YVQFWTNPYLNWGMYISYYWTTLFYMLYLYWGIYRAAKKLALKSDQKTKRLALLTEMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNIWSVGWNAPQMSIGFGLESCFRVENLLTDRSFLMSSRKRNVLNHCFSADGNLVYMG
LRNDNVIKSDLRMNRDHITGQLNGACNTTFVRVLEKTRPECVVTEGFDSIIRIWDFRW
PKNPMMEMHGHSNNCNRLNVFFDKEERFVFAAGSDGYVRGWSLTSGDMLCSVKTPNHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IEHYDVSGCEFLDVSETGDRI VGTFTVNPNGVAAKHSAVYVFEVDSIGDTIQSESSRR
EAYQLLPIRSRSNNAGFNTLGLTVRPMLRDDGFSDEPSYLDYAVTRYNSFIVDQTLAR
VDADVTCMLTVTANDTITRNGNVCSYCTVHLEPLAELSDPEAMFTLNSPIYNKSNREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPEVSVRTSDAGNSSSDSPNDTSNSSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serotonin receptor, and other G-protein coupled receptors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28435.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSIRISRSVSMQGTARATPVIEIVENLEEALKICENLEELREDENKNEEEKQKNGLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
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38345. .38629,39333. .39617)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPIFPRAVYSDCWGGRPGNSAIIMAVGDSMRVHSLEL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLEDQPYEGGPLNMTGFMYHPRTKKYYKMTQDPTMPQGFSKSDLDRMEKAREAKFQAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="G1:722360"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="AAA64320.1"
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                                                                        Nakamura,Y.
Structural Analysis of Arabidopsis thaliana Chromosome 5. IX
Unpublished (1998)
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Submitted (06-007-1998) to the DDBJ/EMBL/GenBank databases.
Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of Gene Structure 2: 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, 7ax:+81-438-52-3934)
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Nakamura, Y.
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                                                                                                                                                                                                                                       /organism "Arabidopsis thaliana"
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/db_xref="taxon:3702"
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/clone=lib="Mitsui P1"
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Feline Simian 687 Human 774 Human 05 Human 05 Human Human 1 Human 1 Human 1 Human Panthe Panthe Panthe Panthe	910 Human immunodeficienc 2 Human immunodeficienc 2 Human immunodeficienc 1 Simian immunodeficienc 10 Human immunodeficienc 73A Human immunodeficienc 74 Human immunodeficienc	UMMARIES  Description	lance 1.741; scale 5.672 results predicted by chance to hav to the score of the result being of the total score distribution.	A 3:H_VIR	summaries	0 175 bases x 2		103-287-3 from US09103287.seq ATTTAAAGATTCGGATGACAGCGTTTTAATATGTTTATAATATGTTTATAATTATTTAATATGTTTATAATA	search, using Smith-Waterman al:37 1999; MasPar time 4.11 Seco	Collins, Biocomputing Research Unit. 98 University of Edinburgh, U.K. rights by Oxford Molecular Ltd	
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## ALIGNMENTS

	REFERENCE
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus; Retroviridae: Lentivirinae.	
SM Human immunodeficiency virus type 1 (HIV-1), Clone 1, AUC Sample F.	ORGANISM
	SEGMENT
	ACCESSION
	DEFINITION
	RESULT
7 AGAACAATTGATAAT 562	Qy 547
	Db 222
Query Match 2.4%; Score 16; DB 3; Length 330; Best Local Similarity 100.0%; Pred. No. 7.65e-02; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query M Best Lo Matches
/note="envelope (AA at 1)" 142 a 43 c 61 g 84 t 835 bp downstream from beginning of env cds	BASE COUNT
<1>330	CDS
·Location/Qualifiers	FEATURES
SUBTYPE sequences. The full name of this sequence is HIV192US662DAIBA.Oldi1sED; it was presented in alignments in an abbreviated form in the April 94 Human Retro. AIDS compendium update as B2US662D.Oldi1qED.	
sample was taken in 1992. This env sequence clusters with HIV-1 B	
an asymptomatic individual, from Baltimore, U.S., whose route of infaction is thought to be due to homosevial contact. The blood	
This sample is part of a set of sequences generated through the NIAID/NIH DAIDS HIV variation program. The virus was derived from	COMMENT
	AUTHORS
E 1 (bases 1 to 330)	REFERENCE
	SOURCE
N U04910	ACCESSION
Human immunodeficiency virus type 1, isolate 662 f	DEFINITION
	Locus
1 .	RESULT

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                                                                                                                                                                        with primary infection
Science 261, 1179-1181 (1993)

RD full staff_review
This sample has been taken from patient M, one of the seven patients (A, M, L, F, C, V, R), in the study(1). All patients had acute, patients (A, M, L, F, C, V, R), in the study(1). All patients had acute, patients (A, M, L, F, C, V, R), in the study(1). All patients had acute, self-limited symptomatic illness with measurable viremia followed by seroconversion. Patient M was a chronically infected male who subsequently transmitted the virus to patient F. The authors report that the sequences in this study are found to be uniformly macrophage-tropic and non-syncyrlum-inducing. The sequence for sample M clone 6, along with other patient M clones 1, 2, 7-9, 11, 12, 14, 15, 17-23, and 32-34, is shown in alignment following the printed text entry. These env sequences cluster with HIV-1 B subtype sequences. See also L21224-L21591 and L24161, L24162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhu, T., Mo, H., Wang, N., Nam, D.S., Cao, Y., Koup, R.A. and Ho, D.D. Genotypic and phenotypic characterization of HIV-1 in patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (HIV-1), clone Human immunodeficiency virus type 1
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Science 261, 1179-1181
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/codon_start=1
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PSNNTRRSIHIGLGRAFYTTGDIIGDIRQAHCNISREKWNNTLKKIVTKLREQYENKI
                                                                                                   /product="envelope glycoprotein"
                                                                                                                                                     Location/Qualifiers
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PSNNTRRSIHMGLGRAFYTTGDIIGDIRQAHCNISREKWNNTLKKIVTKLREQYENKI
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                                                                             /gene="env"
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453 GATCCAAAAATTTCAC 438
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This sequence was obtained as part of a study designed to determine the breadth of genetic variation of SIV infecting African green monkeys. With this aim in mind, Jin et al. PCR-amplified, cloned and sequenced the LTR and partial envelope region from 12 isolates (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1, tan-17, tan40, and tan-49). These isolates were derived from different African green monkey species inhabiting various
                                                                                                                                                                                                                                                                                                                                                                              phylogenetic analysis suggests that each AGM species is infected with a distinct subtype of SIVagm. Interestingly, the sabaeus virk genome seems to be a mosaic of many viruses infecting different primate species [1]. Virus sab-1 forms a distinct lineage in the send of gag, clusters closest to the HIV2/SIVsm group in the 3 gag and 5 pol regions, and clusters closest to the other SIVagm lineages in the 3 pol, env and nef regions [1]. This feature was demonstrated for two viral sabaeus strains, sab-1 and sab-D37 (sequenced only over the 5' end of the pol gene). Jin et al. conclude that an ancestor of the sabaeus virus was a recombinant with two breakpoints: one roughly at codon 310 of gag and the other at the sabaeus virus was a recombinant of the pol gene of the sabaeus virus was a recombinant of the sabaeus virus was a viru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIVSABLC 10036 bp ss-RNA VRL 25-MAY-1994
Simian immunodeficiency virus (SIVagm) complete genomic sequence,
African green monkey isolate SIVagmSAB-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   geographical regions.
Virus sab-1 was derived from a wild female asymptomatic sabaeus African green monkey. She was caught in her natural habitat of Senegal and susequently exported to the United States. From the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jin, M.J., Hui, H., Robertson, D.L., Mueller, M.C., Bau Hirsch, Y.M., Allan, J.S., Shaw, G.M., Sharp, P.M. and Mosaic Genome Structure of Simian Immunodeficiency African Green Monkeys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simian immunodeficiency virus PCR-amplified DNA extracted cocultured PBMCs derived from a wild female asymptomatic seaffrican green monkey captured in its natural habitat of Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U04005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    point of capture and throughout the study, she was housed in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 2.4%;
Similarity 100.0%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     individual cage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 10036)
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bp c
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                                                                                                                                                                                                                                                                                                                                                    of pol
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                                                                                                                                                                                                   1..10036
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/organism="simian immunodeficiency virus"
/specific_host="African green monkey"
                                                                                                       /strain="SIVagmSAB-1"
                                                                                                                                                     /clone="SAB-1/MJ8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sequenced_mol="RNA"
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                                                                                                                                                                                                                                                       Location/Qualifiers
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Pred. No. 7.65e-(
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 g
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and Hahn,B.H.
acy Virus from West
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/note="putative TAR 1"

/provira]

'note="sabaeus

subtype"

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ALPLRAKVIKLGDGQWGYQIYQPENKIIKVGKYAKIKKTAHTNELRMLAGIYQKIGKES
IVIWGQIPIMELPVERELWEOWWSDYKQVTWIPETENYSTPOLIRLWYKLVKDDIPGE
IVIYUDGAANRNSKEGKAGYLTDRGDQKVVALENTTNQKAELEAILLALRDSGSKVNI
ITDSQYAMGIIAGEPTESDNITVQQIIEELIKKEVYAWPAHKGVGGNEEIDKUS
QGIRQYLFLDRIEGEBDKYHAMMSMQOEFGLPALVAKEIVAACPKOQIKGESUVS
GGIRQYLFLDRIEGEBDKYHAMMSMOYEFGLPALVAKEIVAACPKOQIKGESUVS
GGIRQYLFLDRIEGEBDKYHAMMSMOYEFGLPALVAKEIVAACPKOQIKGESUVS
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/translation="MGASNSYLSGRKLDAFESVRLRPNGKKKYKLRHLVWASKELDRF
SLSANLLETKEGVVKILSVLLPLVPTGSENLIALFNLCCVLACIHAEIKVKDTEEAKA
KVKEBVPAEMTESATAISGQTKELQAKKKNEPTVTPSGGSRNYFIVSVNNOMVHQPL
SPRTLNAWVKVIEEKKFSAEVVPMFSALAEGAIPYDINOMLNAVGEHQGALQIVKDVI
NEEAAAWDLHHPPPQQPPAQGYLRDPGGSDLAGTTSTIQEQIEWTTRAQNAVNYGNIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="VIF protein"
/translation="MEKHWIVRPLWKVTGGQQERWTSLVKYHMHVSKQCVHWRYTPHT
/translation="MEKHWIVRPLWKVTGGQQERWTSLVKYHMHVSKQCVHWRYTPHT
KIRWMWYSYOEWVIPLKDGALIKVTNYWHLTPEKGWLETYATGIGYSKGEWFTELDPW
TADHIIHWSYFPCFTDRAVQQAIRGEKYLWCKHQVGHQPTGQPTGVGYQALRVYTNGL
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VQLGIPHPAGLQQREQITVLDIGDAYFSCPLDPDFQKYTAFTIPSVNNREPGIRYQYK
VLPQGWKGSPTIFQTTANKILQEFRQKNPDVDIYQYMDMLIASDRPKAEHLYNYQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQRTRARRSSNSPVKAVCCSGETAETAVAKPLATTEPLRGGLQLPQVSLWRRPMKTVY
IEGQKVTALLDTGADDSVIQGIELGDNWKPRIIGGIGGCINVKAYHNQEVKIEDKTCK
ATILVGETPVNIIGRNVLAQLGVTLNLTQREIEPIKVHLKPGQDGPRIRQWPLSKEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"put
1017..2681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITQLHTDNGT NFTSQQVAAICWWGKIEHTFGVPYNPQSQGVVESMNKQLKEIIGQIRD
DAERLETAVIMAVHIHNFKRKGGIGGYSAAERLINIIHTELETKTLQQKISKIQNFRV
/product="ENV protein"
/translation="MKLLTVLLWLSGCWSLVWLVQYVTVFYGIPVWKNSSVQAFCKTP
NTNLWASTNCIPDDEPEGTIAEVPIPNITEKFDAWKNRNPLVGQAESNIHLLFESTLK
                                                                                                                                                                                                                                               /product="REV_protein"
/translation="MSLGQEELLRRFRIIKFLYTTNPYPPGQGTARQRRRARQRWAKQ
RQQVIHLAERILETPYSQIDHLAQEFDQLYLDNLQQPPSLPPGHPTENQTANSSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="TAT protein"
/translation="MDQEQEARQVWEELQEELHRPLQACDNTCFCKVCCFHCILCFH
KKALGIRYVFRPRASKISHNQVSLHN"
join(6411..6474,8683..8918)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="VPX protein"
/translation="MASGGMLPPVGGDPPKDPPKNPREEIPGWLETWDLPREPEDEWL
RDMLODLNSEAQCHEPRALLFRLWWNIVEEPAIDHGQTRLEGWYKYCRILQKALFVHM
KGRCCKPKTHPAYGPGAGGPPPGLGGASGGAASAAPGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRVAPTSRRGSSOGSPQESQRRDTRMARNMGFAQRAVRRMAPRHVTGPQFRGPVPLPK
ESPFPSLVEYCGRTSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGRTAGEVD"
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/translation="FFRVWPLGQRETQEFPSDLHQTNSSPNGTGLQQAGGKLVCRQTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="N-terminal uncertain; NCBI gi: 466231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFVQQGARPRGPLGGRGRPLNPNIKCYNCGKPGHLARFCKAPRRQGCWKCGSPDHQMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="NCBI g1: 466233"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="NCBI gi: 466235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="NCBI g1: 466232"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. The authors group the outlying V169 gag sequence with their subtype E. The naming of this subtype was made independently of envelope subtype studies, and so gag sequences in this subtype are not necessarily related to envelope sequences classified as subtype E in the 1992 and 1993 compendiums.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Louwagie, J.J., McCutchan, F., Brennan, T., Peeters, M., Brennan, T., Sanders-Buell, E., Eddy, G., van der Groen, G., Fransen, K., Gershy-Damet, M., Deleys, R. and Burke, D. Phylogenetic analysis of gag genes from seventy international HTV-1 isolates provides evidence for multiple genotypes AIDS 7, 769-780 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1 (HIV-1), Rwandan isolate VI69. Human immunodeficiency virus type 1 Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
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1 (bases 1 to 1459)
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Similarity 100.0%;
16; Conservative
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QGEFFYCKMDWFLNYLNNKSVDPDHNNCAKNNTKPCWQRTYVPCHIRQVVNDWYTLSK
KTYAPPREGHLECNSTATALYVELNYNSKNRTNVTLSPQIESIWANELGDYKLVEIKP
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SFAMAGYRDVKKNYSTVWDDQEVVCEBGREKSNATHTVGCYMHCUTSVIKEACDKT
YWDTFSLRYCA,PAGYALLRCADTDYSGHKACRNVTVSACTRLINTTVSTGIGINGSYV
ANRTEIWQKNGNSNDSVIIRLNRYFNLTIRCRRPGNKTVLPVTIMAGLVFHSQKYNTR
                                                                                                                                                      SPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKDTINEEAAEWDRLHPVHAGP
NPPGQMREPRGSDIAGTTSTLQEQIQMMTSNPPIPVGDIYKRWIILGLNKIVRMYSPV
SILDIRQGPKEPFRDYVDRFFKTLRAEEATQEVKGWMTDTLLIQNANPDCKTILKAMG
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QKNLLAAVEQQQQMLKLTIWGYKNLNARYTALEKYLEDQARLNIWGCAFRQYCHTTYL
WKYNNTPDWENMTWQEWERQIEKYEANISRILEQAHEQEQKNLDSYQKLVSWSDFWSW
                                                               SAPPAESFGFREEITPSPKQEQKDEGLSPPLASLKSX"
                                                                                                                                                                                                                                            /translation="MGARASVLSGGKLDAWEKIRLRPGGRKKYKMKHLIWASRELERFALDPGLLETSEGCRKIIGQLQPSLQTGSEELRSLYNTVAVLYEVHQKVEVKDTKEALE
KLEEEQNKSQQKKQQVAADKGVSQNYPIVQNLQGQMVHQAISPRTLNAWVKVIEEKAF
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EQYPSAQG"
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/product "NEF protein"
/translation="MGGKSKOQRHSLWLWSKLRQAPVIQYDMLADPLLGQSSHIQE
ECAKSLROGLIRQGISSTEEGVKMKHQGRQPSWYDEDEEEVGFPVRPCLFLRANTYK
LAIDFGHFLKEKGGLEGIYYSERRKKILDLYALNEWGIVDGWQNYTDGPGTRYPKCFG
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                                                                                                                      PGATLEEMMTACQGVGGPGHKARVLAETMSQATNAAIMMQKSNFKGQRRTVKCFNCGK
/organism="Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                        /gene="gag
                                                                                                                                                                                                                                                                                                                                                                                           /product="gag protein"
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Pred. No. 7.65e-02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               These sequences were kindly provided prior to publication by Dr. Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory Rockville, Maryland. Twenty-one full length gp160 coding sequences from eight African countries (Djibouti, Gabon, Kenya, Senegal, Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with thirty-two previously published full-length gp160 env sequences. Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274, VI191, and VI525 have corresponding gag sequences published by Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993 compendum. This sequence clusters with C subtype env sequences. See also accession numbers L22939-L22957 and L23064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Louwagie, J.J., Janssens, W., Mascola, J.J., Fischer, C.L., van der Groen, G., McCutchan, F.F.E., Eddy, G. and Burke, D. Genetic diversity of the HIV-1 envelope glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1, DJ373 proviral DNA encoding env, tat, vpU, rev, a
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Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
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                                                                                                                                                                                     /note="rev protein, exon 2 (first expressed exon)"
/translation="MAGRSGDSDEALLQAVRITKILYQS"
/note="rev protein, exon 3 (AA at 2621)"
/translation="SPYPEPKGTRQAQRNRRRRWRARQRQIHSISERILSTCLGRPA
                                                                                                                                                                                                                                                                                               /note="tat protein, exon 3 (AA at 2620)"
/translation="PLSRTQGDPTGPEESKKKVESKTKADPLD"
join(226..>302,2619..>2838)
                                                                                                                                                                                                                                                                                                                                                                                   GISYGRKKRRQRRSAPSSSEDHONLISKO"
                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="blood"
/tissue_type="blood"
join(87..>302,2619..>2707)
join(87..>302,2619..>2707)
/note="tat protein, exon 2 (first expressed exon)"
/note="tat protein, exon 2 (first expressed exon)"
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                                                   /translation="MIDLLAKVDYRLAVAAFIIAFIIAIVVWTIAYIEYRKLLRQRK
IDRLIERIRERAEDSGNESDGDTDELSTMVDRGNLRLLDAVDV
                                                                                                       /note="vpu protein"
                                                                                                                                                                 EPVPFQLPPIERLNLDCSESGGTSGTEGVGN"
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277 c 365 q
/note="env polyprotein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequenced_mol="DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="lymphocyte"
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/cell_type="lymphocyte"
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                                                                                                                                                                                                                                                                                                                                                                                                                                Clone HAN2/3, from which most of the sequence shown was derived, is inactive perhaps as the result of mutations leading to frameshifts in the gp41 portion of the env ods. Clone 2/2 is infectious (in MT-2 cells) and its env sequence has been inserte in this entry: bases 7100-7608 (annotated below).
ú
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226 bp upstream from the beginning o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome.
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Similarity 100.0%;
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/translation="mGNKWSKGWPAVRERIRKTKPAAERVAAAAEGVGAASQDLDKY
GALTTSNTPANNADCAWLETQEEEEEVGFPVRPQVPLRPMTYKGAFDLSFFLKEKGG
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IFIMIVGGLIGLRIIFAVLSIVNRVRQGYSPLSFQTLIPNPRGFDRPRGIEEEGGEQ
DKGRSTRLVSGFLALAWDDLRSLFLFSYHRLRDLILIVARVVELLGQRGWETLKYLG
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LTRDGGTNSTDETFRPGGGDMRDWRSELYKYKVVEIKPLGLAPTKAKRRVVEREKR
AALAAVELGFLGAAGSTMGAASITLTVQARQLLSGIVQOQSNLLKALEVHQHKLQLT
VMGIKQLQTRVLAIERYLKDQQLLGIWGCSGKLICTTAVPWNSSWSNKSQEEIWDNM
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ENLTNNAKIIIVQLNQSVEINCTRPNNNTRQSIRIGPGQTFYATGDIIGDIRQAHCN
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wqeanptlfcasdakayetevhnvwathacvptdpspqelvmenvtenfnmwkngmv
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Pred. No. 7.01e-01;
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Matches 15; Conservative
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 CAAAAATTACAAAAT 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The small orfs include: orf 1, in size and position similar to vif but without statistically significant homology; orf 2 that is "tat" like; orfs 3 (denoted D in [1]) and 4 (denoted H in [1]) seen also in the Petaluma strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The PPR isolate is approximately 91% homologous to the previously characterized Petaluma isolate. The latter infected feline kidney cells and the G355-5 cell line but replicated less efficiently on feline PBL's. In contrast, PPR productively infects PBL's but not the other cell lines. The authors point out interesting differences in the LTRs and coding regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 9468)
Phillips,T.R., Talbott,R.L., Lamont,C., Muir,S., Lovelace,K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kindly provided in computer readable form by T. Phillips, Scripps Research Foundation, La Jolla CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunodeficiency virus
J. Virol. 64, 4605-4613 (1990)
full staff_review
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                                                          h 2.3%;
Similarity 100.0%;
15; Conservative
                                                                                                                         /note="orf 4 (orf H in [J. Virol. /codon_start=8950 3605 a 1366 c 2092 g 2405 t terminus of 5'LTR.
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5709..6915
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                                                          Score 15; DB 3; I
Pred. No. 7.01e-01;
0; Mismatches 0
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uery match 2.1%;
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Matches 14; Conservative
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                                                                                                                                 This sample is part of a set of sequences generated through the WH Global Programme on AIDS. The virus was derived from an asymptomatic individual, from Brazil, whose route of infection is thought to be due to homosexual contact. The blood sample was taken in 1992. This env sequence clusters with HIV-1 B subtype sequences. The full name of this sequence is HIV192BR017WHO.01_1gCR; it was presented in alignments in an abbreviated form in the April 94 Human Rettroviruses and AIDS compendium update as B2BR017W.01_1gCR.
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Simian
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                                                                                                                                                                                                                                                                                                                                                                                                             HIVU08687 273 bp ss-RNA
Human immunodeficiency virus
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Wain-Hobson,S.
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WHO Global Programme on AIDS.
                                                                                                                                                                                                                                                                                                                                                                                 C2V3 of env cds.
U08687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence kindly supplied in computer-readable Pasteur Institute. Clone la is infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetic organization of a chimpanzee lentivirus related
                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1 (HIV-1),
Brazil; derived from a primary isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respect to the vpU gene product.
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Similarity 100.0%;
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(bases 1 to 9811)
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                                                                      downstream from the beginning of env
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2353
                                                                                        /note="env polyprotein (AA at 1)"
41 c 45 g 58 t
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5913
6111
8503
6111
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6386
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       Score 14; DB 3; Le
Pred. No. 5.15e+00;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
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tat, exon 2 (first expressed exon)
tat, exon 3 (AA at 8420)
rev, exon 2 (first expressed exon)
rev, exon 3 (AA at 8421)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
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AA at 2074)
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017 from Brazil,
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STANDARD
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Best Local
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E COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242
                                                                                                 This transcript was derived from the Visna K1514 viral strain: 364 nucleotides truncated at the 3' end during cDNA synthesis were reconstructed with a fragment of the visna provirus lambda vis 109 clone before cloning.

The sequence before cloning.

The sequence consists of four exons. Comparison with the 9.4 kB full genomic sequence indicates that the four exons result from splicing at positions 303-304; 349-350 (coordinate 4888); and 501-502 (coordinate 6097) in the LTR, pol and env sequences. Transfent-expression assays performed in eucaryotic cells demonstrated that this cDNA clone has a trans-acting effect on transcription of the visna virus genes. The putative proteins vep and stm were produced in vitro; Vep appears to be a rev-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACAATTTGATAAT 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sample is part of a set of sequences generated through the WHO Global Programme on AIDS. The virus was derived from an asymptomatic individual, from Brazil, whose route of infection is thought to be due to homosexual contact. The blood sample was taken in 1992. This env sequence clusters with HIV-1 B subtype sequences. The full name of this sequence is HIV192BR017WHO.01diisCD; it was presented in alignments in an abbreviated form in the April 94 Human Retroviruses and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLVTR 1174 bp ss-RNA VRL Visna lentivirus, strain K1514 cDNA; partial LTR,
                                                                                                                                                                                                                                                                                                                                                                                                                        J Virol 62, 4813-4818 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mazarin, V., Gourdou, I., Querat, G., Sauze, N. and Vigne, R. Genetic structure and function of an early transcript of visna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and partial env regions (two regions). M25409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1 (HIV-1), sample 017 from Brazil; derived from a primary isolate.

1. (bases 1 to 345)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Visna lentivirus (isolate K1514) cDNA clone from visna provirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compendium update as B2BR017W.01di1sCD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WHO Global Programme on AIDS.
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Human immunodeficiency virus type 1, sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lambda-vis-109 clone.
l (bases 1 to 1174)
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Similarity 100.0%;
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                                                              to/span
863
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56 c 61 g 80 t
                    879
230
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                  Vep1 protein (alternate start at 405) env stm (short transmembrane ) protein 326 g 213 t
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Pred. No. 5.15e+00;
0; Mismatches 0;
                                                                                     description
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017 from Brazil,
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partial pol
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Query Match 2.1%; Best Local Similarity 100.0%;

Score Pred.

No ;

DB 3; I 5.15e+00;

Length 1174;

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FEATURES
CDS
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JOURNAL
STANDARD
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       CDS
                                                                                                                                                                                                                                                 SGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This isolate, also called HIV2-ALT by the authors, was taken from a healthy Ghanian woman. Tree analysis reveals that it likely arose prior to the branching of HIV2s and SIVs, i.e. the sooty mangabey and macague isolates. [1] calls attention to an extension of the gag-pol overlap region resulting in a dilated (by 20 residues) pol orf. The env cds begins at 6671; tat-exon1 at 6375 and rev-exon1 at 6601, with the possible donor splice site at 6665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV2D205 7817 bp ss-RNA UNA 31-OCT-1 Human immunodeficiency virus type 2 (HIV-2), isolate D205; gag, pol, vif, vpX, vpR, partial env.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kindly provided in computer readable form by H. Rubsamen-Waigmann, Georg Speyer Haus, Frankfurt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dietrich, U., Adamski, M., Kreutz, R., Rubsamen-Waigmann, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
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TNILDIKQGPKEPPQSYVDRFYKSLRAEDGTDPAVKNMMTQTLLJANANDCKLVLKGL
GNMPTLEEMTJAQOGIGGPGQKARLMAEALKEALTPAPIPEPAAVQQKAGKRGTVTQUD
CGKQGHTARQCRAPRRQGCWKCGKTGHIMSKCPERQAGFLGLGPWGKKPRNFPMTQVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKEVWTVNAIGKLYGVLNWAAQLFPGIKTRHICKLIRGKWILITEEVQWTELAEAELQE
WKIILEQEQEGSYYKERVPLEATVOKKLANOWTYK IHQGKVUKVGKYAKVKUTHTNG
VRLLAHVVOKIGKEALVIWGEIPVFHLEVERETWDQWWTDYWQVTWIPEWDFVSTPPL
IRLAYNLVKDEDLEGRETYYTDGSCGNERTSKEGKAGYVTDRGKDKYKVLEGTTNQQAELE
AFALALTDSEPQVNIIVDSQYVWGIIAAQPTETESPIVAKIIEBMIKKEAVYVWWVPA
HKGLGGNQEVDHLVSQGIRQVLFLEKIEPAQEEHEKYHGNVKBLVHKFGIPQLVAKQI
VNSCDKCQQKGEAIHGOYNADLGTWOMCTHLEGKIMIVAGGFIEAEVIPQEGTG
ROTALFILKAARWPIHLHTDNGANTTSPSVKMYAWWGIEOTFGVPYWPQSGGVVE
AMNHHLKNQIDBLRDQAVSIETVVLMATHCMNFKRRGGIGDMTPAERLVNMITTEQEI
OFFQARNLKFQNFQYYXREGRDQLWKGPGELLWKGEGAVIIKVGTEIKVVPRRKAKII
/translation="meeekdwivvptwripgrlerwhslikylkyrtgeloqvsyvph

HKVGWAWWTCSRIIFPLNKGAWLEVQGYWNLTPERGFLSSYAVRLTWYERNFYTDVTP

DVADQLLHGSVFSANEVRRAIRGEKILSYCNYPSAHEGOVPSLOFYLALRVVQEGK

NGSQGESATRKQRRRNSRRSIRLARKNNNRAQQGSGQPFAPRTYFPGLAEVLGILA"

5877...6212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ctranslation="MGARGSVLSGKKTDELEKVRLRPGGKKKYMLKHVVWAVNELDRF
GLAGRELLESKEGCGKILKVLAPLVPTGSSNLKSLENIVCVIFCLAEKVKDTEEAKK
IQARHLAADISEKMPATWARDTAPSGGNVEVOLLAGNVYHLPLSPRTLNAWKKLVEEKK
FGAEVVPGFQALSEGCTPYDINOMLNCVGEHQAAMQIIREIINEEAADMDQQHPSPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="KTGMLEMMKNRTHHVKMPRKTGGFFRVRTLGKEASQLPHDPSAS
GSDTICTPDEESRGHDTSGGDTICAPCRSSSGDAEKLHADGETTEREPERETLGGGDRG
FAAPQFSLMRRPVYKACIEGGQSVEVLLDTGVDDSIVAGIELGSNYTPKLYVGGIGGFU
TKEYKDVEIEVVGKRVEATIMTGDTPINIFGRNILNTLAMTLNFPVAKVEPVKVELKP
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MLIDERELNKYTQDFTEVNWVEPTROVAEKRRITVIDVGDAYESULDDNERQYTAFT
LPSYWNAEPGKRYIYKYLPOGWKGSOSIQYSWRKYLLDFFKANSDVIIQYMDDIL
ASDRSDLEHDRVVSQLKELLNDMGFSTPEEKFQKDPPFKWMGYELWPKKWKLQKIQLP
                                                                                                                                                                                                                                                                                                                 QGVTPSAPPMNPAEGMTPRGATPSAPPADPAVEMLKSYMQMGRQQRESRERPYKEVTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="gag polyprotein"
/codon_start=1
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Best Local Similarity 100.0%;
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K.Staskus, 20 DEC-1985.

K.Staskus, 20 DEC-1985.

[2] presents information about the original visua lentivirus sequence (11), which indicates that it is not an isolate from sequence (11), which indicates that it is not an isolate from stepenence in the previously thought, but is from LVI-1, one of several antigenic variants isolated from sheep after experimental infection with visua virus 1514. In [2], the genome of visua virus 1514 was cloned and sequenced. The sequence in [2] differed from the originally reported sequence by 12 nucleotides in the envelope and 3' LTR, whereas an independently derived clone of LVI-1 (Gdovin and Clements, manuscript in preparation) showed no differences in the sequence of env and 3' LTR with the same regions in [1]. Furthermore, virus neutralization studies [2] showed that the Haase virus stock [1] is antigenically identical to LVI-1 and that the 1514 virus stock reported in [2] is distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eature 6876..6878
/note-"env polyprotein in-frame stop codon
2705 a 1602 c 1930 g 1580 t
5'-terminus of 5'LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Braun, M.J., Clements, J.E. and Gonda, M.A.

The visna virus genome: evidence for a hypervariable site in the env gene and sequence homology among lentivirus envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Visna lentivirus (Icelandic strains 1514 [2] and LVI-1 [1]) extrachromosomal proviral DNA, (clones VL and VS [1]).

[ bases 1 to 9202)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Virol. 61, 4046-4054 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sonigo,P., Alizon,M., Staskus,K., Klatzmann,D., Cole,S., Danos,O., Retzel,E., Tiollais,P., Haase,A. and Wain-Hobson,S. Nucleotide sequence of the Visna lentivirus: Relationship to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proviral genome.
M10608 M18039
                                                                                                                                                                                                                                                                                                                                                         Sequence for [1] kindly provided in computer readable form by K.Staskus, 20-DEC-1985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins
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TalGnfiySrhGDTLaGaGELIKILQRalflhfraGCQHSRIGQSGGGNpLSTIppp"
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FQVWQRSWAYWREEQGMSISYTKYRYLLLMQKAMFVHYTKGCRCLQEGHGPGGWRSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6601..6664
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protein coding regions were inferred from the AIDS virus coding sequences and by computer analysis. Subgenomic mRNAs are probably produced. The S protein is thought to be the equivalent of the tat protein in HIV's. Two long adjacent ORF's (bases 5956-8907) appear, when taken together, to correspond to the env gene in other retroviruses. [1] proposes that the stop codon that interrupts what would otherwise be a longer ORF may be the result of having sequenced a defective viral genome. This stop codon is not present in [2] due to a substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at also the sequenced and substitution of a 'c' for the 't' in [1] at the sequenced and substitution of a 'c' for the 't' in [1] at the sequenced and substitution of a 'c' for the 't' in [1] at the sequenced and substitution of a 'c' for the 't' in [1] at the sequenced and substitution of a 'c' for the 't' in [1] at the sequenced and substitution of a 'c' for the 't' in [1] at the sequenced and substitution of a 'c' for the 't' in [1] at the sequenced and substitution of a 'c' for the 't' in [1] at the sequenced and substitution of a 'c' for the 'c' in [1] at the sequenced and substitution o
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gag polyprotein precursor p55 (putative) p16-gag protein (putative) p14-gag protein (putative) p15-gag protein (putative) p16-gag	855	h 2.1 Similarity 100.0 14; Conservativ	5766 5790 5766 5990 5990 5990 6308 6308 6803 6803 7458 7458 7755 7755 7863 7863 7877 7877 7877 7877 7889 8073 8161 8161 8965 8161 8965 8161	9106 920 9106 920 161 1920 9178 918 8161 816 102 10 550 55 1420 1420 1420 1420 1420 162 1628 162 1628 162 1639 290 2909 290 3018 323 3231 323 3231 323 4678 467	from to/spa 489 181 489 191 918 157 1578 181 1871 500 4965 565 5657 594 5956 890 1 1 920 1 16
Ni .		; Score 14; DB 3; Length 9202; ; Pred. No. 5.15e+00; 0; Mismatches 0; Indels 0; Gaps 0	t in [1]; c in [2] a in [1]; g in [2] g in [1]; t in [2] g in [1]; a in [2] a in [1]; c in [2] t in [1]; c in [2] g in [1]; a in [2] g in [2]; a in [2] g in [3]; a in [2] g in [4]; a in [5]; a in [6]; a i	weat 5' copy leat 3' copy lentivirus virion lentivirus virion r (Lys-trNA) binding site polyadenylation signal nal stop codon in env in [ li]; gcc in [2] li]; a in [2] li]; g in [2] li]; g in [2] li]; a in [2]	cription polyprotein precursor p55 (putative) gag protein (putative) gag protein (putative) gag protein (putative) gag protein precursor (NH2-terminus pritein protursor (NH2-terminus ertain; AA at 1871) rotein (putative) rotein (putative) polyprotein (internal stop codon in [ polyprotein (internal stop codon in a genomic mRNA LTR

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                                                                The JRCSF and JRFL env nucleotide sequences differ by at least 3%; further characterization of them is forthcoming (Peng,S. et al., Nature 1990, in press). Both manifest insertions in nef previously reported for HIVBRVA.

from to/span description.

from to/span description.
790 2304 gag polyprotein
< 2085 5108 polyprotein (NH2-terminus uncertain; AA at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kindly provided in computer-readable form by Irvin Chen, UCLA School of Medicine, Los Angeles. JRCSF and JRFL (see <HIVJRFL) were isolated from cerebral spinal fluid and brain tissue of the patient JR, who died with Kaposi's sarcoma and severe AIDS encephalopathy (Science 236, 819-822, 1987). Both clones are infectious, but JRFL productively infects macrophages while JRCSF does not. (Peripheral blood was not available from the patient).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV-1 proviral DNA from extracellular virus taken from cerebral spinal fluid (1986). Infectious clone.

1 (bases 1 to 9540)

Koyanagi, S., Chen, I.S. Y. et al.
Unpublished (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome.
M38429
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                                                                                                                                                                                                5053 5631 v

5842 6056 t.

8366 8456 t.

5981 6656 r.

6073 6318 v

6073 6318 v

6236 9434 r.

1 635 552 378 397 853

3455 398 398 398 398

400 459 459 57 t.TR.
                                                                                                                                                                                                                R repeat 5' copy
Spl binding site III
Spl binding site II
Spl binding site I
spl binding site I
2308 g 2116 t
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Pred. No. 5.15e+00
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ALIGNMENTS	X13075	(13095	98821	98820	98819	98817	67131	67129	67127	67130	98818	67128	52141	57915	57912	57914	57913	30461	93913	92868	92701	59078	74830	160695	71025	64902	49894	67726	180591	36982	59532	36987	21210	75600	
	Enterococcus faecalis	rococcus faecali	is c	is CTR1-1	is CTR1-3	Arabidopsis CTR1 geno	Constitutive triple r	Constitutive triple r	Constitutive triple r	Constitutive triple r	Arabidopsis CTR1-2 mu	Constitutive triple r	Streptococcus pneumon	Arabidopsis thaliana	S,	S	sis thalia	о С	H gene	CaRAM2 gene	ger	n	Staphylococcus aureus	Fragment pHS 53 homol	IA gene which	DRRG 206 genomic clon	Tapetal specific prom	esto	ce of P-2 gene	hinge-VL ins	ain Expresse	-end PC	janr	Staphylococcus aureus	
		1.23e+01	. 2	.23e+0	2	1.23e	1.23e+0	1.23e+0	1.23e+0	1.23e	1.23e+0	1.23e+0	1.23e+0	1.23e+0	٠	3e+0	.23e+0	1.23e+01	.23e+0	.23e+0	N	.23e+0	1.23e+01	.23e+0	.23e+0	N1	.23e+0	.23e+0	.23e+0		.23e+0	.23e+0	0	3.04e+00	

### ALIGNMENTS

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RESULT
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30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, F.
Rosen CA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V74703 standard; DNA; 2424 BP.
V74703;
V74703;
16-MAR-1999 (first entry)
Staphylococcus aureus contig SEQ ID #392.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-s.aureus vaccines Claim 1; Page 1287-1288; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 97-374922/35.
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/note= "these bases represent a line of missing text in
/note= "the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JLT 2
V53479 standard;
V53479;
therapy; ss.
Staphylococcus
EP-841394-A2.
                                                                                                                                    DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; cardiac infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food polsoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock and the Orange of the Company of the composition of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1774
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Sequence 2424 BP; 839 A; 302 C; 462 G; 759 T;
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Pred. No. 0.00e+00;
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Claim 1: Page 146; 390pp; English.

Chaim 1: Page 146; And 146; A
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24-SEP-1997.
307485.
24-SEP-1996; US-027032.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Black MT, Burnham MKR, Hodgson JE,
Lonetto MA, Nicholas RO, Pratt JM,
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DB; W77686.
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llarity 99.0%;
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D, Pratt JM,
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Pred. No. 0.00e+00;
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CC The invention relates to a UDP-N-acetylmuramate:L-alanine ligase CC (Murc polypeptide) encoded by the S. aureus Murc gene. Host cells CC (Murc polypeptide) encoded by the S. aureus Murc gene can be used for CC containing an expression system comprising the Murc gene can be used for the recombinant production of the polypeptide. And activity or CC polypeptide are used to treat conditions requiring increased activity or CC expression of the polypeptide. Antagonists, inhibitory nuclear acid or CC competitive polypeptide are useful for inhibiting the polypeptide e.g. CC bacterial (especially S. aureus) infections. They are also useful against CC The antibacterial agents are useful to treat in-dwelling devices for CC infection prevention or generally as wound treatments to prevent adhesion CC diagnosing or prognosing a (susceptibility to) disease, for raising CC antibodies; to identify modulators or specific receptors; in rational CC drug design and as an immunogen for vaccines. The Murc gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant Murc gene; CC immunitation and poly; to determine bacterial serotype; and for genetic composition or thromosomal mapping; to determine bacterial serotype; and for genetic composition of the polypeptide of 
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Sequence 660
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MurC gene; UDP-N-acetylmuramate:L-alanine ligas;
bacterial; infection; H. pylori; cancer; ulcer;
immunogen; drug; genetic immunisation; ds.
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V80065;
17-MAR-1999 (first entry)
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07-JAN-1999.
26-JUN-1998; 305064.
03-JUL-1997; US-052720.
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acactttctctagaacacaagcatttttaaatgaatttgcagaaagtttatgtaaagcag
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17-MAR-1999
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P-PSDB; W87771.
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Key Locati
CDS 22..13
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                                                                                                                               Sequence
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07-JAN-1999.
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                                                                                                                               1351 BP;
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98.8%;
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(MurC polypeptide)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis genome contig SEQ ID NO Enterococcus faecalis; contig; detection; Enterococcus faecalis; computer readable medium Enterococcus faecalis.

Enterococcus faecalis.

W0985055-A2.

12-NOV-1998.

04-MAY-1998; U08985.

14-NOV-1998; U08985.

16-MAY-1997; US-046609.

16-MAY-1997; US-046655.
Claim 1; Page 1314-1315; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and fouse in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
Barash SC, Dillon PJ, Kunsch
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X13223 standard;
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PS Disclosure; Page 13; 39pp; English.

CC The invention relates to a UDP-N-acetylmuramate:L-alanine ligase (Murc C Disclosure; Page 13; 39pp; English.

CC The invention relates to a UDP-N-acetylmuramate:L-alanine ligase (Murc C Disclosure; Page 13; 39pp; English.

CC The invention relates to a UDP-N-acetylmuramate:L-alanine ligase (Murc C Disclosure; Page 13; 39pp; English.

CC polypeptide) encoded by the S. aureus Murc gene can be used for the creation of the polypeptide. Appoints of the polypeptide or competitive polypeptide are useful for inhibiting the polypeptide or competitive polypeptide are useful for inhibiting the polypeptide e.g.

CC bacterial (especially S. aureus) infections. They are also useful against the infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The Murc polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising CC antibodies; to identify modulators or specific receptors; in rational drug design and as an immunogen for vaccines. The Murc gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant Murc gene; for chromosomal mapping; to determine bacterial serotype; and for genetic for chromosomal mapping; to determine bacterial serotype; and for the PCR immunisation. The present sequence represents a primer used for the PCR
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Sequence
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New isolated MurC polypeptide from Staphylococcus aureus and nucleic acid - useful in diagnosis, treatment and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1998; 305064.
03-JUL-1997; US-052720.
(SMIK ) SWITHKLINE BEECHAM
(SMIK ) SMITHKLINE BEECHAM
BURDHAM MKR, WALLIS NG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MurC polynucleotides amplifying primer.
MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polybacterial; infection; H. pylori; cancer; ulcer; gastritis; immunogen; drug; genetic immunisation; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Similarity 100.0%;
19; Conservative
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No. 1.63e-01;
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is; vaccine;
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Streptococcus Streptococcus

02-OCT-1998

(first entry)

pneumoniae SP0070 nucleotide. pneumoniae; antigen; vaccine;

vaccine;

infection;

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RESULT
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CC The present sequence encodes a protein from Streptococcus pneumoniae. The present sequence encoding the Streptococcus pneumoniae protein CC can be useful in vaccines for inducing protective antibodies against CC pneumonia, otilis media or meningitis. Probes based on the nucleic acid care used to detect Streptococcus infection (by usual hybridisation or CC amplification methods), also for isolating Streptococcus genes or their CC allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or CC monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive cc immunisation (optionally coupled to a toxin). Vaccines are administered, CC immunisation (optionally coupled to a toxin). Vaccines are administered, CC immunisation (optionally acoupled to a toxin). Vaccines are administered, CC immunisation (optionally coupled to a toxin). Vaccines are administered, CC immunisation (optionally acoupled to a toxin). Vaccines are administered, CC immunisation (optionally coupled to a toxin). Vaccines are administered, CC immunisation (optionally acoupled to a toxin). Vaccines are administered, CC immunisation (optionally acoupled to a toxin). Vaccines are administered, CC immunisation (optionally acoupled to a toxin). Vaccines are administered, CC immunisation (optionally acoupled to a toxin). Vaccines are administered, CC immunisation (optionally acoupled to a toxin). Vaccines are administered, CC immunisation (optionally acoupled to a toxin). Vaccines are administered, CC immunisation (optionally acoupled to a toxin).
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Best Local :
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Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e pneumonia, bacteremia, meningitis or endocarditis Claim 1; Page 151-152; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae polypeptive Polypeptide; ORF; open reading frame;
                                                                                                                                        Black MT, Hodgson JE, Knowles DJC,
Reid RH, Zarfos PN;
WPI; 98-322654/28
P-PSDB; W62754, W63755.
                                                                                                                                                                                                                                                                                 (SMIK )
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24-NOV-1997; U21976.
27-NOV-1996; US-031879
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Choi GH, Hromockyj A, Johnson LS, Kunsch CA;
WPI; 98-272224/24
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07-MAY-1998.
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31-OCT-1996; US-029960.
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Local Similarity 100.0%;
les 19; Conservative
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                                                                                                                                                                                                                                                                             SMITHKLINE BEECHAM CORP. SMITHKLINE BEECHAM PLC.
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DRF; open reading frame; infection; bacterial;

bacteremia; diagnosis; prophylaxis; ds.
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/note= "no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "polypeptide"
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                                                                                                                                                                                                                                                Lonetto MA, Nicholas
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                                В
                                                                                                                                                                                                                                                                                                                                                             The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (VS2134 to VS2524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences deploted in SEQ ID NO: 1 to 391. The nucleotide sequences deploted in SEQ ID NO: 1 to 391 (VS2134 to VS5524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S. pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mNAN, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the sequences to amplification primers derived from the conjunter-based system for importance, or extragence of the modulation and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for importance, or extragence of the modulation.
                                                                                                                     Query Match
Best Local
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae genome fragment SEQ ID NO:61.
Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleu empyema, endocarditis or infection of the cerebrospinal fluid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of a Streptococcal The polypeptide can potentially be used
                                                                                                                                                                                                          fragments of the S. pneumoniae genome. Products from the invention can be used in diagnosis kits and assays, and p compositions and vaccines for S. pneumoniae. Sequence 11884 BP; 3440 A; 2668 C; 2183 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                            S. pneumoniae genome of commercial importance, or expression modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 524-530; 1409pp; English.
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855 tgaaacgacgtttaacacc
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Similarity 100.0%;
19; Conservation
                                                                                                                        h 2.9%;
Similarity 100.0%;
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                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA; 11864
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Pred. No. 7.17e-01;
                                                                                                                        Pred.
                                                                                                                                                  Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                           Mismatches
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                                                                                                                        No. 7.17e-01;
                                                                                                                                                  DB 47;
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                                                                                                                                                  Length 11864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ი</u>
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pharmaceutical
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                                                                                        Gaps
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RESULT ACCORDED TO THE SULT OF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PT antis, aureus vaccines
PS Claim 1; Page 1907; 3271pp; English.
CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S.aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S.aureus infection. The
CC saureus in a sample. S.aureus is implicated in numerous human diseases,
CC sincluding cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences
CC industrial rangments) are useful as primers or probes for isolating
CC chomologues of any of the S.aureus DNA sequences
CC communitor resadable medium.
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Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                 Methanococcus jannaschii large circular extrachromosomal element.
Methanococcus jannaschii; methanogenic archaeon; circular chromosome;
genome; autotrophic; extrachromosomal element; identification; ds.
Methanococcus jannaschii.
Methanococcus jannaschii.
Methanococcus jannaschii.
Mo9807830-A2.
26-FEB-1998.
22-RUG-1997; U14900.
22-RUG-1996; US-024428.
(GENO-) INST GENOMIC RES.
(UNII) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Bult CJ, Smith HO, Venter JC, White OR, Woese CR;
MPI: 98-169145/15.
The present sequence represents the large circular extrachromosomal element sequence of the Methanococcus jannaschii circular chromosome. The present invention describes M. jannaschii open reading frames from the
                                                                                                                                                         Complete genome sequence of methano-genic jannaschii - useful in identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JAN-1997; 100117.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(НИМА-) HUMAN GENOME SCI INC.
                                                                                                  Claim 13; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V21210 standard; DNA; 58407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus contig SEQ ID #1289.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyalid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V75600;
16-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0-NOV-1998 (first entry)
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                                                                                                  585-600;
                                                                                           614pp;
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Pred. No. 3.04e+00;
0; Mismatches C
                                                                                              English.
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                                                                                                                                                         archaeon,
M. jannaso
                                                                                                                                                      jannaschii
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F 16-JUL-1990; US-552751.

R 16-JUL-1990; US-552751.

R (TERE) TECH RES CENT FINLAND.

PI Alfthan K, Knowles JKC, Laukkanen ML, Sizmann D, Takkinen K, Teeri TT DR WPI; 92-134225/17.

PT Prod. of single chain fusion protein, pref. antibody - comprises PT transforming host cells, e.g. E. coli with expression constructs PT composed of proteins or domains, linked by spacer peptide(s) PS Example; Page '28; 56pp; English.

CC The sequence is that of the PCR primer VLl, which is used in the CC modification, for in-frame fusions with the hinge coding region, CC of the 5'-end of Ox VL CDNA.

SO Sequence 67 BP; 16 A; 22 C; 11 G; 18 T;
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RESULT

JD Q

AC Q

DT 10

DT 10

DE H

KW GG

KW L1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 1
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Best Local
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19-AUG-1993.
12-FEB-1993;
12-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
FI9103434-A.
                                                                                                                                                                                                 Human brain Expressed Sequence Tag EST00527.
Gene transcription product; genetic markers; tagging; in transcription; mapping; locations; chromosomes; chromosomes
                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                          Q59532 standard;
Q59532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          scAb: recombinant;
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Q36987 standard;
                                                                                                                              WO9316178-A.
                                                                                                                                                                                                                                                                                                                                16-MAR-1994 (first entry)
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17-JAN-1992.
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0N-1993 (first entry)
0X VL 5'-end PCR primer.
Per peptide; secretable; single chain; fusion protein; antibody;
Per peptide; secretable; single chain reaction; ss.
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Similarity 100.08;
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Similarity 100.0%;
18; Conservative
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    U01294.
US-837195.
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Q36982 standard; cDNA; 870
Q36982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue type, and for prepn. of antisense sequences, probes and constructs. EST00527 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also Q59041-Q61440. Sequence 474 BP; 155 A; 88 C; 75 G; 153 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 93-272882/34.

Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging of most human genes

Example 4; Page 190; 500pp; English.
                                                                                                   Example; Fig 4; 56pp; English.

The sequence is that of an Ox VH-CBHI hinge-VL insert which was used as part of a method for cloning secretable, biologically active single chain antibodies (scabs) and other secretable fusion proteins having at least 2 distinct functional proteins or domains. Sequence 870 BP; 213 A; 239 C; 222 G; 196 T;
                                                                                                                                                                                                                                                                                                                                                                               16-JUL-1991; 913434.
16-JUL-1990; US-552751.
(TERE-) TECH RES CENT FINLAND.
Alfthan K, Knowles JKC, Laukkanen ML,
MPI: 92-134225/17.
                                                                                                                                                                                                                                                                   Prod. of single chain fusion protein, pref. antibody - comprises transforming host cells, e.g. E. coli with expression constructs composed of proteins or domains, linked by spacer peptide(s)
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/note= "Ox VH"
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                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                          lepidoptera and diptera insects (Claim 1; Fig 2(1) and Fig 2(3); 66pp; English.

Claim 1; Fig 2(1) and Fig 2(3); 66pp; English.

A gene for Bacillus thuringiensis (B.t) P-2 toxin having the DNA sequence specified in Fig 2 (N80591), or any portion or deriv. of it, is claimed. Also claimed is the protein encoded by the gene, having the corresponding specified AA sequence in P80548. In isolating the P-2 gene, the P-2 protein was purified from a donor strain of B.t var. kurstaki and the partial AA sequence of the P-2 protein was determined. P-2 gene-specific oligo probe (N80590) was synthesised based on the AA sequence. The P-2 toxin encoded by the cloned gene has insecticidal activity against lepidoptera and diptera insects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N80591 standard: DNA: 1370
N80591;
12-JAN-1991 (first entry)
                                                                                                                                                                                                                                                                                            N.B. The DNA/protein sequence in N80591/P80548 is as given in specification and is missing bases 901-1800 and the corresp. Sequence 1370 BP; 486 A; 185 C; 236 G; 463 T;
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P-PSDB; P80548.
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07-APR-1988;
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16-APR-1987; US-039542.
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2.6 1608 1 US-07-621 Sequence 2, Applicatio 8.93e-01 2.6 1890 5 5312912-3 Patent No. 5312912. 8.99e-01 2.6 5873 4 PCT-US93-0 Sequence 4, Applicatio 8.93e-01 2.6 5890 1 US-07-928 Sequence 4, Applicatio 8.93e-01 2.6 5890 1 US-07-928 Sequence 6, Applicatio 8.93e-01 2.6 5890 4 PCT-US93-0 Sequence 6, Applicatio 8.93e-01 2.6 5890 1 US-07-928- Sequence 3, Applicatio 8.93e-01 2.6 5890 1 US-07-928- Sequence 5, Applicatio 8.93e-01 2.6 5890 1 US-07-928- Sequence 5, Applicatio 8.93e-01 2.6 5890 1 US-08-261- Sequence 5, Applicatio 8.93e-01 2.6 5890 1 US-08-261- Sequence 5, Applicatio 8.93e-01 2.6 5892 1 US-08-261- Sequence 4, Applicatio 8.93e-01 2.6 5812 1 US-08-261- Sequence 3, Applicatio 8.93e-01 2.6 5812 1 US-08-261- Sequence 3, Applicatio 8.93e-01 2.6 5812 1 US-08-03- Sequence 3, Applicatio 8.93e-01 2.6 5812 1 US-08-03- Sequence 7, Applicatio 8.93e-01 2.6 5812 1 US-08-261- Sequence 5, Applicatio 8.93e-01 2.6 5812 1 US-08-03- Sequence 5, Applicatio 8.93e-01 2.6 5812 1 US-08-261- Sequence 6, Applicatio 8.93e-01 2.6	by analysis of the total score distribut SUMMARIES Length DB ID Description	n 6.913; Variance 2.668; scale 2.591  The number of results predicted by chance to the result be analysis of the total score of the result be by analysis of the total score distribute.	Minimum Match 0% Listing first 45 summaries n-issued 1:5A_COMB 2:5B_COMB 3:5C_COMB 4:PCT9_COMB 5:backfiles1	TABLE jmetric	C 96.61 (1-660) 660 1 A	ב ה אל מ	**************************************

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US-08-307-	- 1	5268270-1	US-08-323-	US-08-323-	PCT-US94-0	US-08-234-	US-08-514-	US-08-514-	PCT-US96-0	US-07-991-	PCT-US95-1	5175383-1	us-08-982-	US-08-565-	- 1	US-08-362-	US-08-920-	4	US-08-920-	PCT-US93-0	-960-80-SD	US-07-919-	US-08-727-	S	
Sequence	Sequence	Patent No	Sequence	Sequence					Sequence	Sequence	Sequence	Patent No.	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence		Sequence		Sequence	
1, Applicatio	•	. 52682	<ol><li>Applicatio</li></ol>	<ol><li>Applicatio</li></ol>		Applicat	7, Applicatio	ъ	282,	4,	59, Applicati	). 5175383.	<ol> <li>Applicatio</li> </ol>	<ol> <li>Applicatio</li> </ol>			<pre>11, Applicati</pre>			<ol><li>Applicatio</li></ol>				<ol> <li>Applicatio</li> </ol>	
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#### ALIGNMENTS

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CORRESPONDENCE ADDRESS:
ADDRESSEN: Dennis R. Hoerner, Jr. Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/621,670
FILING DATE: 19901203
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: HOERNEY Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38,21(10523)A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEBRY: 1608 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
STRONDED STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/07621670
Sequence 2, Application US/07621670
Patent No. 5254801
GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
TITLE OF INVENTION: Heterologous Dominant Conditional Lethal
TITLE OF INVENTION: Genes and Use Thereof
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-621-670-2 STANDARD; DNA; UNC; 1608 BP.
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Best Local S
Matches 1
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Best Local Similarity 100.0%;
Matches 17; Conservative
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Patent No. 5312912
APPLICANT: HADWIGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DANIEL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOR GENETICALLY ENGINEERING DISEASE RESISTANCE INDUCIBLE TRAITS IN PLANTS
                                                                                                                                                                                                                                                                                                                               Sequence 4, Application PC/TUS9307347
Sequence 4, Application PC/TUS9307347
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1487 AATGAAGATTCTATTAA 1503
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                                                                                                                                                                                                                                                                                                                                                                                         PCT-US93-07347-4 STANDARD; DNA; UNC; 5873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496
                                                                                                                                                                                                                                                                                                                                                                                                                                       524
       ATTORNEY AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 13-JUN-1989
                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                         APPLICANT: Kieber Joseph J.
TITLE OF INVENTION: CONSTITUT
TITLE OF INVENTION: MUTATIONS
MUMBER OF SEQUENCES: 6
                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PROCEDURES AND REGULATORY DNA SEQUENCES
                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGAAGATTCTATTAA 540
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                                                                                       APPLICATION NUMBER: PFILING DATE: 19930805
                                                                                                                                                                                                                 STREET: One Liberty
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1890
                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                          ADDRESSEE: Woodco
                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                          STATE:
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Similarity 100.0%;
17; Conservative
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                                                                                                                                                                                                                                                                                                 Constitutive Triple Response Gene
                                .e E.
32,279
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Pred. No. 8.93e-01;
0; Mismatches (
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Pred. No. 8.93e-01
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                                   UPN-1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                          Version
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Matches 1
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                                                                                    MOLECULE TYPE: DNA (genomic) SEQUENCE 5873 BP; 1664 A; 1052 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application Sequence 4, Application Patent No. 5367065 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) SEQUENCE 5873 BP; 1664 A; 1052 C;
                    2560 GCTGTTGATGTGTATGT 2576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-928-464-4 STANDARD; DNA; UNC; 5873 BP
                                                                                                                                                                TELEPHONE: 215-568-3100 INFORMATION FOR SEQ ID NO: 4:
 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 GCTGTTGATGTGTATGT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.0%;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATI
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and ADDRESSEE: No. 5367065ris
                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ecker, Joseph J.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitut:
TITLE OF INVENTION: Mutations
                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 5873 base pairs
                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 5873 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: lir
 GCTGTTGATGTGTATGT
                                                                                                                              TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 19920 CLASSIFICATION: 80
                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: No. 536:
STREET: One Libert;
CITY: Philadelphia
                                                                                                            TOPOLOGY:
                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                 REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                          2.6%;
Similarity 100.0%;
17; Conservative
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                                                                                                                                                                                                                                                                                                                                                      U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ecker, Joseph R.
Kieber, Joseph J.
ENTION: Constitutive Triple Response Gene and
                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                       19920810
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 75
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US/07928464
                                                                                                                                                                                                                                                                                      Release #1.0,
                                                                                                                                                                                                                                                                  US/07/928,464
                                                                                                                                                                                                         32,279
                                           Pred.
                                                               Score 17;
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                                            Mismatches
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                                                    No. 8.93e-01;
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                                                                                       1238
                                                                                       G; 1919 T; 0 OTHER
                                                                                                                                                                                                                                                                                       Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G; 1919 T; 0 OTHER
                                                                 DB 1;
                                                                Length 5873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5873;
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                                           Gaps
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RESULT ID U

US-07-928-464-3

STANDARD; DNA; UNC; 5890

ВP

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COUNTRY: U.S.A.
ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/928,464
FILING DATE: 19920810
CLASSIFICATION: 800
ATTOCHERY AGENT INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/07928464 Sequence 3, Application US/07928464 Patent No. 5367065 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION UNMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 3:
                  LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                              FEATURE:
NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
ADDRESSEE: No. 5367065ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 5890 base pairs
TYPE: NUCLEIC ACID
                                                                                  FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                 FEATURE
                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: One Liberty
CITY: Philadelphia
STATE: PA
                                            intron
2039..2173
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1720..1936
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354..1001
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1478..1574
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1002..1176
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                   exon
2174..2379
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1937..2038
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1575..1719
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Onerv Match	CC NAME/KEY: CC LOCATION: SQ SEQUENCE 5890	j .	g n	aj h	rj h	g ·		<b>н</b> д 1	'aj	ᄪ	CC NAME/KEY: CC LOCATION: CC FEATURE:	FE	CC FEATURE:	77		NAME/K LOCATI FEATURE:	CC NAME/KEY: CC LOCATION: CC FEATURE:	ਸ ਸ				CC LOCATION:
2 6%: Score 17: DB 1: Length 5890:	intron : 50575890 BP; 1666 A; 1055 C; 1240 G; 1929 T; O OTHER.	exon 49605056	intron 4883.4959	exon 47884882	intron 46744787	exon	: intron :- 4439.4541	exon 43704438	intron: 41374369	exon 4038 .4136	3944.4037		** .	intron	exon 3669.3769	intron 3589.3668	exon 35203588	intron 32443519	exon 32033243	intron 3013.3202	exon 27373012	23802736

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GCTGTTGATGTGTATGT 75 GCTGTTGATGTGTATGT 2593

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2577 59

Query Match 2.6%; Best Local Similarity 100.0%; Matches 17; Conservative

Score 17; DB 1; L Pred. No. 8.93e-01; 0; Mismatches 0

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Length 5890;

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RESULT
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                                                                                                                                                                                              XXXXXX
                                                                                                                                                                                                      PCT-US93-07347-3 STANDARD; DNA; UNC; 5890 BP
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 5890 BP; 1667 A; 1055 C; 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application PC/TUS9307347 Sequence 6, Application PC/TUS9307347 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                      2.6%;
Local Similarity 100.0%;
les 17; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 215-568-3100 INFORMATION FOR SEQ ID NO: 6:
                                                                                   APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: UP TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kieber, Joseph
TITLE OF INVENTION: Const
TITLE OF INVENTION: Mutat
                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 5890 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                               STREET: One Libert
CITY: Philadelphia
STATE: PA
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CITY: Philadelphia
                                                             ADDRESSEE: Woodco
            COUNTRY: (
                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19103
                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                    One Liberty Place - 46th Floor
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                     U.S.A.
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                                                                                                                                        Ecker, Joseph R
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                                                                         Woodcock, Washburn, Kurtz, Mackiewicz and
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Pred. No. 8
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                                                                                                                                                                                                                                                                                                                 DB 4;
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NAME:
REGISTRATION NUMBER: UPN-
REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TTTEPHONE: 215-568-3100
TTT NO: 3:
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SEQUENCE CHARACTERISTICS:
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NAME/KEY:
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APPLICATION NUMBER: PC
FILING DATE: 19930805
CLASSIFICATION:
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NAME/KEY:
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FEATURE:
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          NAME/KEY:
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TYPE: n
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                          LOCATION:
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                                         LOCATION:
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1177..1477
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1002..1176
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3203..3243
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2039..2173
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1937..2038
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354..1001
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1720..1936
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1..353
          intron
3589..3668
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3244..3519
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2380...
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2174..2379
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1575..1719
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1478..1574
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3013..3202
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2737..3012
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LOCATION: FEATURE:

FEATURE:

intron 3770..3858

NAME/KEY: LOCATION: NAME/KEY:

exon 3859..3943

FEATURE

NAME/KEY:

exon 4038..4136

NAME/KEY: LOCATION:

intron 3944..4037

LOCATION: FEATURE:

NAME/KEY:

exon 3669..3769

LOCATION: FEATURE: FEATURE:

NAME/KEY: LOCATION:

intron 4137..4369

NAME/KEY:

exon 4370..4438

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NAME/KEY: intron
LOCATION: 5057..5890
SEQUENCE 5890 BP; 1666 A; 1055 C; 1240 G; 1929 T; 0 OTHER
                                                                                                                                                                                         Sequence 6, Application US/07928464 Sequence 6, Application US/07928464 Patent No. 5367065
                                                                                                   GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz
ADDRESSEE: No. 5367065rls
                                                     One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                            STANDARD; DNA; UNC; 5890
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Best Local Similarity 100.0%;
Matches 17; Conservative
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5890 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: 11near
MOLECULE TYPE: DNA (genomic)
SEQUENCE 5890 BP; 1667 A; 1055 C; 1240 G; 1928 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/07928464 Sequence 5, Application US/07928464 Patent No. 5367065 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2577 GCTGTTGATGTGTATGT
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                                       TELEPHONE: 215-568-31 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 GCTGTTGATGTGTATGT 75
                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
FORMATION FOR SEQ ID NO: 5:
           SEQUENCE CHARACTERISTICS:
LENGTH: 5890 base pairs
                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPI
                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ecker, Joseph F
APPLICANT: Kieber, Joseph
TITLE OF INVENTION: Consti
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NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPI
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                                                                                                                                  APPLICATION NUMBER: FILING DATE: 199208 CLASSIFICATION: 800
                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Woodcock, Washburn, Kurtz, ADDRESSEE: No. 5367065ris
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NUCLEIC ACID
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Constitutive Triple Response
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Pred. No. 8.93e-01;
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STREET: One Liberty CITY: Philadelphia

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2577 GCTGTTGATGTGTATGT 2593

59 GCTGTTGATGTGTATGT 75

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Query Match Best Local S Matches

FEATURE: NAME/KEY:

LOCATION: NAME/KEY:

intron 4883..4959

FEATURE

FEATURE:

LOCATION: NAME/KEY: LOCATION: NAME/KEY:

intron 4674..4787

exon 4542..4673

NAME/KEY: LOCATION:

exon 4788..4882

FEATURE:

FEATURE: FEATURE:
NAME/KEY:

LOCATION:

intron 4439..4541

LOCATION: FEATURE:

exon 4960..5056

2.6%; Local Similarity 100.0%; les 17; Conservation

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Best Local Similarity 100.0%;
Matches 17; Conservative
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Best Local Similarity 100.0%;
Matches 17; Conservative
Sequence 4, Application US/08003311B Sequence 4, Application US/08003311B
                             XXXXXX
                                     US-08-003-311B-4 STANDARD; DNA; UNC; 6295 BP
                                                                                   2577 GCTGTTGATGTGTATGT 2593
                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 5890 BP; 1666 A; 1054 C; 1240 G; 1930 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application PC/TUS9307347 Sequence 5, Application PC/TUS9307347 GENERAL INFORMATION:
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 5890 BP: 1666 A; 1054 C;
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                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: UPN-1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5890 base pairs
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                                                                                                                                                                                                                                                                                                                                           ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
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                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 199308
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CITY: Philadelphia
STATE: PA
                                                                           GCTGTTGATGTGTATGT 75
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Pred. No. 8.93e-01;
0; Mismatches 0
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Pred. No. 8.93e-01;
                                                                                                              Mismatches
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Query Match
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Sequence 4, Application US/08261432
Patent No. 5602322
                                                                                                                                                                                                                                                                                                                                               XXXXXX
                                                                                                                                                                                                                                                                                                                                                               US-08-261-432-4 STANDARD; DNA; UNC; 6295 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2982 GCTGTTGATGTGTATGT 2998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
SEQUENCE 6295 BP; 1815 A; 1104 C; 1295 G; 2081 T; 0 OTHER.
                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6295 base pair
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07,928,464
FILING DATE: August 10, 1992
ATTORNEY/AGENT INFORMATION:
NAME: LOTI Y. Beardell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-110
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Local Similarity 100.0%;
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/003,311B
FILING DATE: January 12, 1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                   STREET: One --
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CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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COUNTRY: U.S.A.
ZIP: 19103
                                                                                           ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: No. 5602322ris
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                                                                         One Liberty Place - 46th Floor
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Best Local :
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Sequence 3, Application US/08261432
Patent No. 5602322
                                                                                                                                                                                                                                                                                                                                                                                               US-08-261-432-3 STANDARD; DNA; UNC; 6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 6295 BP; 1815 A; 1104 C; 1295 G; 2081 T; 0 OTHER
                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.6%;
Local Similarity 100.0%;
hes 17; Conservation
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                            NERAL INFORMATION:

ECKET, Joseph R.

APPLICANT: Kieber, Joseph J.

TITLE OF INVENTION: Constitutive |

TITLE OF INVENTION: and Mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: li
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APPLICATION NUMBER: 08/01
FILING DATE: January 12,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: WOrdPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGTTGATGTGTATGT 75
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                                                                                                                                                                                                         STREET: One Liberty CITY: Philadelphia
                                                                                                                                                                                                                               ADDRESSEE: Woodcock Washbu ADDRESSEE: No. 5602322ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lori Y. Beardell REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
NAME: Lori Y. Beardel REGISTRATION NUMBER:
                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                   U.S.A.
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                                                                                                                                                                                                                                           Woodcock Washburn Kurtz Mackiewicz
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cy 12, 1993
                                                                                         US/08/261,432
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34,293
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Pred. No. 8.93e-01;
0; Mismatches (
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Best Local S
Matches 1
Query Match 2.6%;
Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08261432 Sequence 5, Application US/08261432 Patent No. 5602322
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SEQUENCE 6312 BP; 1817 A; 1107 C
                                                                    SEQUENCE
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US-08-261-432-5 STANDARD; DNA; UNC; 6312 BP
                                                                                                                                                                                                TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
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Local Similarity 100.0%;
hes 17; Conservative
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                                                                    MOLECULE TYPE:
QUENCE 6312 BP;
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LOTI Y. Beardell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ecker, Joseph J.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
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TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/261,432 FILING DATE: June 17, 1994
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                                                                                                           TOPOLOGY:
                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP:
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                                                                                                                                                          LENGTH: 6312 base pairs TYPE: nucleic acid
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                                                                                                         linear
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SYSTEM: PC-DOS/MS-DOS
                                                               DNA (genomic)
1817 A; 1106 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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Pred. No. 8.
  Score 17;
Pred. No.
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                                                                 1297 G; 2092 T; 0 OTHER
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  DB 1; I
8.93e-01;
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8.93e-01;
                     Length 6312
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Search completed: Sat Nov 27 15:06:19 1999 Job time : 73 secs.
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and CC CITY: Philadelphia
CC CITY: Philadelphia
CC CITY: Philadelphia
CC COMPUTER: Philadelphia
CC COMPUTER: PA
CC COMPUTER: ISBM PC COMPATIBLE
CC COMPUTER: IBM PC COMPATIBLE
CC OPERATION SYSTEM: PC-DOS/MS-DOS
COMPUTER WOOTHER: DATA:
CC OPERATION NUMBER: US/08/003,311B
CLASSIFICATION NUMBER: 07/928,464
FILING DATE: January 12, 1993
CLASSIFICATION NUMBER: 07/928,464
FILING DATE: August 10, 1992
ATTORNEY/ACENT INFORMATION:
CREETERNOE/DOXET NUMBER: UPN-1108
CRECTION NUMBER: 34,293
CRECTISTRATION NUMBER: 34,293
CRECTISTRATION NUMBER: 34,293
CRECTISTRATION NUMBER: UPN-1108
CRECTISTRATION NUMBER: UPN-1108
CRECTIC SECUNDATION: 100-1108
CRECTISTRATION NUMBER: UPN-1108
CRECTION NUMBER: 10, 1992
CRECTISTRATION NUMBER: UPN-1108
CRECTISTRAT
                                                                                                                                                                    Query Match 2.6%;
Best Local Similarity 100.0%;
Matches 17; Conservative
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US-08-003-311B-3 STANDARD; DNA; UNC; 6312 BP.
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TITLE OF INVENTION: Constitutive '
TITLE OF INVENTION: and Mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGTTGATGTGTATGT 3015
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CANT: Ecker, Joseph R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                          Score 17; DB 1; Length 6312; Pred. No. 8.93e-01;
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# VERSION KEYWORDS SOURCE ORGANISM RESULT LOCUS DEFINITION ACCESSION g989634 H49793.1 H49793 218 bp mRNA EST 22-JAN-1999 Y921bb6.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:274139 5', mRNA sequence. H49793 GI:989634

NID

REFERENCE AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 218)
1 (bases 2 to 218)
1 (bases 3 to 218)
1 (bases 3 to 218)
1 (bases 3 to 218)
1 (bases 1 Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced

TITLE JOURNAL COMMENT

gi:785128.

Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Tel: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1080
High quality sequence stops: 102
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1080 Std Error: 0.00

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REFERENCE
AUTHORS
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Best Local Similarity 100.0%;
Matches 21; Conservative
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                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1079
High quality sequence stops: 276 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1079
Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                           Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 387)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holmen,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,S., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T91899 387 bp mRNA EST ye02a01.rl Soares fetal liver spleen lNFLS image:116520 5', mRNA sequence.
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Unpublished (1995)
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/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
46 c 48 g 79 t 2 others
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/clone="IMAGE:274139"
                                                                                  Location/Qualifiers
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No. 2.62e-08
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 AAGGTACTGCTGTTGATGTG
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Minobe, Y. and Sasaki, T
Rice cDNA from root
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RICR2171A Rice root Oryza sativa cDNA clone R, mRNA sequence
                                                             h 3.0%;
Similarity 100.0%;
20; Conservative
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                                                                                                                                                                                                                                                                                                            tsasaki@abr.affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified pT?T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

//db_xref="CDB:472137"
                                                                                                                                                                                                           /strain="Nipponbare, sub_species Japonica"
/note="Prepared from seedling root "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="20 week-post conception fetus"
/lab_host="DH108 (ampicillin resistant)"
81 c 100 g 134 t 1 others
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/clone="IMAGE:116520"
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 70
                                                             Score 20; DB 8; L
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0; Mismatches 0
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Pred. No. 2.62e-08;
0; Mismatches n
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Local Similarity 100.0%;
hes 19; Conservative
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discoideum cDNA clone
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SWMFCA2133SK Brugia malayi microfilaria cDNA (SAW94LS-BmMf) Brugia
malayi cDNA clone SWMFCA2133 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
                                     Eukaryota; Dictyosteliida; Dictyostelium 1 (bases 1 to 264)
                                                                            Dictyostelium discoideum
                                                                                                 Dictyostelium discoideum.
                                                                                                                                    C84769.1 GI:2864916
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Molecular Parasitology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae; Brugia.
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Developmental cDNA in Dictyostelium discoideum (229)
                       Mizuno, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12, 1996 this sequence version replaced gi:1406902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note-"Vector: lambda Unizap XR; Site_1: Ecor I; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from microfilariae of Brugia malayi isolated from jirds and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 3.5 x 10E5 independent recombinants and average insert size was 900 base pairs. The library was constructed by Lori Saunders. The library is available from Dr. S.A. Williams, email genome esmith.edu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome@smith.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib-"Brugia malayi microfilaria cDNA
(SAW94LS-BmMf)"
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/strain="TRS Labs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="SWMFCA2133"
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HS_3020_B1_A12_T7 CIT Approved Human Genomic Sperm Library sapiens genomic clone Plate=3020 Col=23 Row=B, genomic surv
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On Apr 14, 1993 this sequence version replaced gi:693199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E. Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
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Class: BAC ends
                                                                                                                                                                                                                                                                                          Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
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1 (bases 1 to 399)
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                                                                                                                                  /organism="Homo sapiens"
/note="Organ: sperm; Vector:
E-Coli DH10B"
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/strain="AX4"
/db_xref="taxon:44689"
/clone="SSF674"
                                                   /sex="male"
70 c
                                                                                  /clone_lib="CIT Approved Human Genomic Sperm Library D"
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/clone="Plate=3020 Col=23 Row=B"
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/dev_stage="slug"
34 c 17 g 78 t 2 others
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Ld
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 497)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

Washu-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A1256065 497 bp mRNA EST 12-NOV-1998 ui94f07.xl Sugano mouse liver mlia Mus musculus CDNA clone IMAGE:1890085 3' similar to gb:M22382 MITCCHONDRIAL MATRIX PROTEIN Pl PRECURSOR (HUMAN); gb:X53584 Mouse mRNA for HSP60 protein
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On Jan 17, 1998 th
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AI256065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
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19; Conservative
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                                                               140
                                                                                                                                                 /dev_stage="adult"
/lab_host="DH10B"
120 c 98 g
                                                                                                                            /clone_lib="Sugano
                                                                                                                                              /clone="IMAGE:1890085"
                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                /sex="female"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 TACAAGATTTAATTGATAA 501
Unpublished (1997)
Other_GSSs: RPCI-11-180011.TJ
Other_GSSs: RPCI-11-180011.TJ
Contact: Shaying Zhao, William Nierm
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, J
Tel: 301 838 0200
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1 (bases 1 to 614)
Suzuki, K., Shimizu, H. and Urushiihara, H.
Sexual cDNA in D. discoideum(970724)
Unpublished (1997)
Un Sep 12, 1996 this sequence version replaced gi:1318551
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C25739.1
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                                                                                                                                                                                                                                                                                                                                                   AQ415275 618 bp DNA GSS 22 RPCI-11-180011.TV RPCI-11 Homo sapiens genomic clone RPCI-11-180011, genomic survey sequence.
                                                                                                                                       Zhao,S., Adams,M.D., Nies
Venter,J.C.
Use of BAC End Sequences
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 618)
                                                                                                                        Map Building
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                                                                                                                                                                                                                                                                                                    AQ415275.1
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Location/Qualifiers
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3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Hideko Urushihara
Institute of Biological Sciences
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/map="x27.3-28"
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/strain="KAX3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="FC-AX23"
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                                                                                                                                                                           Nierman, W., Malek, J.,
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Pred. No. 5.23e-05;
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Best Local Similarity 100.0%;
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616 TACAAGATTTAATTGATAA 634
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                                                                                                                                                                                                                                                                                                 Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305,
Email: d402huesakura.cc.tsukuba.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C89676 674 bp mRNA C89676 Dictyostelium discoideum SS discoideum cDNA clone SSA606, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                           Developmental cDNA in Dictyostelium discoideum
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2152830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum Eukaryota; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C89676
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 674)
Yoshino, R., Morio, T. and Tanaka, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: hbe@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dictyostelium discoideum.
                                                                    h 2.9%;
Similarity 100.0%;
19; Conservative
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/note="Vector: pBACe3.6; Site_1:
RPCI11 Human Male BAC Library"
/db_xref="GDB:7569082"
                                                                                                                                                                                                            /organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SSA606"
                                                                                                                                                   /clone_lib="Dictyostellum discoideum
/dev_stage="slug"
/dev_stage="slug"
90 c 97 g 218 t
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98 c 80 g 201 t
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/clone="RPCI-11-180011"
/clone_lib="RPCI-11"
/sex="Male"
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                                                                    Score 19; DB 20; L
Pred. No. 5.23e-05;
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Best Local Similarity 100.0%;
Matches 19; Conservative
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CONTact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MI
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21;
Class: BAC ends.
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1 (bases 1 to 679)

Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map
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g2977185
B94848:1 GI:2977185
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CIT-HSP-2163E2.TF CIT-HSP H
                                                                     Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                AU009689 72 bp mRNA
AU009689 Schizosaccharomyces po
Schizosaccharomyces pombe cDNA
                                     Schizosaccharomyces.

1 (bases 1 to 72)
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AU009689.1
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                    Morimyo, M. and Mita, K.
                                                                                                                      fission yeast.
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Identification of expressed sequence
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/sex="Male"
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/clone="2163E2"
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/note="Vector: pBeloBAC11;
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169 c 138 g
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Pred. No. 5.23e-05;
0; Mismatches 0;
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Homo sapiens genomic clone 2163E2,
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pombe late log phase cDNA
NA clone spc05248, mRNA see
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Local Similarity 100.0%;
hes 18; Conservative
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National Institute of Radiological Sciences
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Genome Institute of Radiological Sciences
National Institute of Radiological Sciences
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On Jan 14, 1998 this sequence
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Eukaryota: Fungi; Ascomycota: Archiascomycetes:
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On Jan 17, 1998 this sequence version replaced gi:1900413.
                                                                                                                                                                                                                                    Email: morimyo@nirs.go.jp.
Location/Qualifiers
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l: morimyo@nirs.go.jp.
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                                               /note="Vector: M13mp19; The cDNA library of /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA schizosaccharomyces from 5, to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
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/strain="972"
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l: morimyo@nirs.go.jp.
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Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
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On Jan 19, 1998 this sequence version replaced gi:2286292.
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Schlzosaccharomyces pombe was prepared by cloning cDNA
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Result	SUMMARIES  Query Query Match Length DB ID Description Pred. No.
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adation" se" 1"			ovatus		R. Whitehead, National ch, ARS, USDA, 1815 N.		Bacteroides ovatus	roidaceae; Bacteroides.			BCT 12-00 e (asdI) gene, complete		Homo sapiens clone DJO Caenorhabditis elegans	sophila melanogast an Chromosome 11p1	uman DNA sequence **	aenorhabdit albicans c	Gallus gallus mRNA for	Lae	= "	- S	sapiens chro		Arabidopsis thaliana g	omo sapie	aenorhabditis	.pombe chromo:	elegans cosmid CO2	HS H
					Center for University						OCT-1994 Se cås.		2.42e+02 2.42e+02 2.42e+02	.42e+0	.42e+0	2.42e+0	2.42e+0 2.42e+0	2.42e+0	.42e+0	5.42e+0	5.42e+0	5.420+0	5.420+0	.42e+0	.42e+0	.42e	.42e+	.42e+ .42e+

/translation="mrryanllavlalstnlalhaqtnelviqtkklgaeiqptmygl ffeDinyaadgglyaelvknrsfefpqhlmgmktygkvslmndgpfernphyvrlsdp ghahkhtgldnegffgigvkkgeeyrfsvmarlpqgstketlrielvdtqsmgerqal

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Human Xp22 cosmid U27H1,
U69570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-SEP-1996) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Feb 7, 1997 this sequence version replaced gi:1552535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 39489) Lu, J. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
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Similarity 100.0%;
16; Conservative
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GLRKDLAQALADIHPGVERFPGGGIVEGTDLETRYDMKKSVGPVENRPLRENRWGYTF
THREFDDY QSYGLGFYEYFLLSEEMGAAPLPILNGGLSCQYQNUNDPKAHVAYCDLDN
YIQDALDLIEFANGNVNTTWGKVRADMGHPAPFNLKFIGIGREQWGKEYPERLEPFIK
AIRKAHPEIKIVGSSGPNSEGKDFDYLMPEMKRLKVDLVDEHHYPRESWFLAGGAYYD
NYDRKGPKVPAGEYAGHGKGKKKNHYHAALLEAAFMTGLERNADIVHAATYAPLFAHV
EGWQMRPDMINFDNLNSYRTTSYYVQOLYAQNKGTNYLPLTMKKKNTGAEGQNGLFA
SAVYDKRNELIVKVANTSATIQPISLMFEGLKKQDVLSNGRCIKLRSLDLDKDNTLE
OPFGIVPQETPYSIEGHNFTTELEFTTFAYYKFTKK
OPFGIVPQETPYSIEGHNFTTELEFTTFAYYKFTK
OPFGIVPQETPYSIEGHNFTTELEFTTFAYYKFTK
OPFGIVPQETPYTTELFTTELFTTY
                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="Alu" 2147. .2419
                           /rpt_family="Alu"
7504. .7578
                                                                                                                                                                                                /note="similar to ESTs with GenBank Accession Numbers
w27937 and N29255"
                                                                                                                                                                                                                                                                                         complement(4928. .5080)
/rpt_family="L1"
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/rpt_family="Alu"
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350. .798
                                                                                                                                         /note="Region: 39g10"
/db_xref="dbEST:W27937"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
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rpt_family="MIR"
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Pred. No. 2.28e+00;
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     1 (bases 1 to 41351)
1 (bases 1 to 41351)
Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,R., Sulston,J., Thierry-Miey,J., Thomas,K., Vaudin,M.,
                                                                                                                                                                                                   Caenorhabditis elegans strain=Bristol N2.
Caenorhabditis elegans
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
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Similarity 100.0%;
15; Conservative
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17958. .18376
/note="similar to ESTs with GenBank Accession Numbers W29126, N47571, W27937 and N20542"
/note="Region: yy91f09.s1"
complement(20857. .21139)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="MLTIb" 7669 c 7510 ~
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/rpt_family="Alu"
36873..37150
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/note-"Region: 39910"
complement(14647. .14754)
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/rpt_family="MLT1f"
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complement/second
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/rpt_family="MERIA"
                                                                                                                                                                                                                                                                                                                       GI:1065935
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Waterston, R., Watson, A., Weinstock, L.,
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Pred. No. 1.14e+01;
0; Mismatches 0;
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2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 41351) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of C. elegans cosmid F42C5 Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Du, z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368 (6466), 32-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 41351)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ing sequences below are predicted from computer analysis, using program Genefinder(P. Green and L. Hillier, ms in preparation)
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SKHQIFRIYTAFCWNYTEKGVFHLFDNMEHKPCVCPLTDMDKCNISTCLECLKSNWLYKCSFC
GEAFFEVGLGIVREFNEDVNILELVGLYKRNCYDFLEEWWRCEPSHLGFPCLSCSYSE
ELEICYFCEFLDKHRALKTKFRIENSIQMRQNLSLEFNYSGLNDFFIRWQCSDCKKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(979. .1116,1265. .1333,1382. .1501,
1545. .1778,1973. .2164))
/gene="F42C5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(2977. .3636,3722. .3835,3885. .3997, 4245. .4323,4369. .5030,5213. .5405,5480. .5670,5778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2977. .6924)
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VFKIKLLDVSKVMTDVKVNYQDYLRNTLDEHSNSNKSDVLKEIDTLIYNKEKLNEVLI
TAKKLLGKCQKFTTSDSFKVINDSLTELMRFKFEDDILIELKTIIKKNGSAEQSFLTK
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polyadenylated RNA-binding protein NAB3 (SP:P38996)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDETIDKYNEMVNELPGLQLKSVEPIHQAAIQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F42C5
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                                                                                                                                                                                                                                                                                                                                                                            'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F42C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Caenorhabditis elegans"

ob_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Genetics,
St. Louis, MO 63110, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,y. .2164)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
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19671. .23147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAIMTACYIMLVRHYRTKYKMRRAQTTTTLAKPGKEPRIMSEVKKSIWRIAVFHFVC
WAPFWGFTMLPNYIYQIDQFLHGDNEEESGGESIFLVYCRLVSNCLPYINAAGNWVLY
ALLNYDVRKHIYNQFKKKRKFTLKFNPVNTSSNC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(7399. .8928)
/gene="F42C5.5"
                                                                                                                                                                    complement(join(27841. .27950,27997. .28302,28353. .28452,
                                                                                                                                                                                                                                                                 ICARGDESYVAYTETYCQVANDDVTCYAFRPM'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(24822. .26102)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MHSGLCCIYDLHFSLCLSLPSSPEETQTEGSIGTTTVVKIESDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(23283. .23477,23525. 24683. .24752))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(23283. .24752)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYHGTWIFGSAACYIIRSIEIFAKLFSVVLLTVMSLERYIIVCTRLRHIYRAWMSLVP
LAVGTIFGVLVPTIIHYFYLQHFSVPFDPDVTWVCLPLMSNEVFNLFAQYTFVVGFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLVGTPGNLWIIYKLFRAKLWSGASVQLTVSQRSRIYIFALACSDMFLLLTLPATASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAA81482.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="PID:g1065940"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oin(19671. .19844,21175. .21253,21319. .21427,21912. .22163,
2382. .22873,22922. .22974,23026. .23147)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .25703,26059. .26102))
"F42C5.7"
                                                                                                                                                                                                                                  (27841. .28656)
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REFERENCE
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                            JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC006755 199917 bp DNA HTG 23-FEB-1999 Caenorhabditis elegans clone Y40C5, WORKING DRAFT SEQUENCE, 1
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                                                                                                                                                                                                                                                     2 (bases 1 to 199917)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1.
Caenorhabditis elegans.
                                                                                                                                                                                    University School of Medicine,
                                                                                                                                                                                                          Submitted (23-FEB-1999) Genome
                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                        The sequence of Caehorhabditis
                                                                                                                                                                                                                                                                                                                                                     Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.9%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                   NOTE: This is a 'working draft' sequence. It currently consists of I contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                 63108,
                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 199917)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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NETYAQRPRASETLKFYRCSISWFFFSWWAYLGSKICCVIPPWTDVNLTIPGIRDAPPA
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LVRTRGGNEKYRALRLDSGNFSWASEQTTRKTRIVDTMYNATNNELVRIKTLVKGAII
SVDAAPFRQWYEAHYALPLARKKNAKLSEEDNAILNKKRSHHTMKKYTERQKTAAVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(29490. .29582,29645. 30136. .30396,30445. .30934,31019. .
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/db_xref="PID:g1065942"
/db_xref="GI:1065942"
                                                                                                                                                                   USA
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join(28209. .28440,29481.
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/note="coded for by C.
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U59225
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U59225.1
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-MAY-1996) Moredun 408 Gilmerton Road, Edinburgh, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lainson,F.A., Thomson,N., Rowe,H.A., Langford,P.R., Aitchison Donachie,W. and Kroll,J.S.
Occurrence of [copper, zinc]-cofactored superoxide dismutase Pasteurella haemolytica and its serotype distribution FEMS_Microbiol. Lett. 142 (1), 11-17 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasteurella haemolytica serotype A2 [Cu,Zn]-superoxide (sodC) gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lainson, F.A.
Direct Submission
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Pasteurella haemolytica
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Similarity 100.0%;
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Similarity 100.0%;
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                            Conservative
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                                                                                                     /db_xref="GI:1389831"
/translation="AKEKGGKLTAGLAAGGHWNDNKAPHHGFPWSDDAHLGDLPALTV
LHDGTSTNPVLAPRLKKLDEIKGRSLMIHEGGDNHSDHPAPL"
69 c 54 g 58 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Caenorhabditis
/db_xref="taxon:6239"
/clone="Y40C5"
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1. .199917
                                                                                                                                                                                                                                                                                                                                                /serotype="A2"
/specific_host="sheep"
/db_xref="taxon:746"
                                                                                                                                                               /evidence=experimental
/product="[Cu,Zn]-superoxide dismutase"
/prottein_id="AAB38771.1"
/db_xref="PID:91389831"
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Scotland, UK, EH17 7JH
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                       G47706 436 bp DNA STS 23-MAR-1999 Z25840_1 Zebrafish AB Danio rerio STS genomic clone Z25840 5'
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Similarity 100.0%;
14; Conserveting
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                                                                                                                                      zebrafish
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                                                                                                    Danio rerio
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/product="[Cu,Zn]-superoxide dismutase"
/protein_id="Ana88772.1"
/db_xref="pID:g1389833"
/db_xref="GI:1389833"
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/function="detoxification
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/specific_host="sheep"
/db_xref="taxon:746"
/clone="pNT2"
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Ziniti, J., Jackson, D.G. and Fishman, M.C.
A Zebrafish microsatellite map
Unpublished (1999)
                                 Schistosoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://zebrafish.mgh.harvard.edu
Primer A: TTGGAAATGTAGCGTGGTGA
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Email: fishman@mgh.cvrc.harvard.edu
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Massachusetts General Hospital
Mail code 1494100A, 149 13th Street,
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Similarity 100.0%;
14; Conservative
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/note="Vector: ml3MP19 with added BstXI site; V-type:
/note="Vector: ml3MP19 with added BstXI site; V-type:
Phage; Genomic DNA from a single adult Zebrafish of AB
strain was digested with AluI, Cac8I, HaeIII, NlaVI, or
RsaI. Fragments in the range of 250-500 bp were gel
RsaI. Fragments in the range of 250-500 bp were gel
RsaI. Fragments were
                                                                                                                                                                                                                                                                                                                                                                                                                                                       purified and a BstX1 linker was added. The fragments wer cloned into a modified Mi3mpl9 vector and transformed into E. Coli DH5alpha. Microsatelllite sequences were screened with labeled d(CA)15 and d(GT)15 oligonucleotide
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/clone="225840"
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De María,A.C. and Gomes,S.L.

Characterization of the sks1 multidrug

Dictyostelium discoideum
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Dictyostelium discoideum
Eukaryotae; mitochondrial eukaryotes;
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 Вe
                       Unpublished
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Retrotransposable elements in the Schistosoma japonicum genome (in) Tada, I., Kojima, S. and Tsuji, M. (Eds.);

PROCEEDINGS OF THE 9TH INTERNATIONAL CONGRESS OF PARASITOLOGY
                                                                                                                                                                                                                                                                U96916
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AF073334.1 GI:3702849
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Schistosoma japonicum
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 Maria, A.C. and Gomes, S.L.
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RFKAFVVNGISAIHSHTKMNQWRYMPSKQNVANYVPRG"
1 250 c 362 g 443 t
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/protein_id="AAC62956.1"
/db_xref="PID:93702850"
/db_xref="GI:3702850"
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/dev_stage="egg"
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                                                                                                                                                                                                                                                                                                                                    Submitted (15-NOV-1996) to the DDBJ/EMBL/GenBank databases. Sachiyo Yoshioka, Tsukita Cell Axis Project ERATO JST, Kyoto Research Park; 17 Chudouji Minamimachi, Shimokyo-ku, Kyoto, Kyoto 600, Japan (E-mail:syoshi@cell.tsukita.jst.go.jp, Tel:+81-75-315-7913, Fax:+81-75-315-6420)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_lib:library of H. No
Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (strain:PR745) cDNA clone_lib:library of H. Nojima clone:SY1604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-APR-1997) Departamento de Bioquimica, Sao Paulo, Av. Prof. Lineu Prestes, 748, sala 1207,
                                                                                                                                                                                                                           DNA Res. 4 (6), 363-369 (1997) 98162722
                                                                                                                                                                                                                                                                              Yoshioka, S., Kato, K., Nakai, K., Identification of open reading
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1 (bases 1 to 1724)
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PKRHLISDUHTLMANNUYRVLTVMLDTYF"
a 166 c 177 g 603 t
                                                                                 /organism="Schizosaccharomyces pombe"
/strain="PR745"
/db_xref="taxon:4896"
/clone="Sy1604"
/clone=1b="library of H. Nojima"
                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MMRSLMSLLGREGLGEKTDATPLPDTAETHISSLALLKMLQH
ARAGVPLEVMGLMLGELIDEYTIRVIDVFAMPOSGTSVSVALIDPVFQTKMLDMLKQT
GRDELVIGWHISHPGFGCWLSSVDVNTPONSFEDLOSRAVAVVVDPLOSVRGKVVIDAF
RTIKTSPTAEPRQITSNLGHLQDPSIQALIHGSIRNYYSIAINYRKNELEQKMLLNLH
/protein_id="BAA13911.1"
/db_xref="PID:d1014608"
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/protein_id="AAB57823.1"
/db_xref="ptb:92104757"
/db_xref="GI:2104757"
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/db_xref="taxon:44689"
/db_xref="taxon:44689"
join(<260. .392,490. .749,863. .1198,1315. .
join(260. .392,490. .749,863. .1198,1315. .1
                                  /codon_start=
                                                    'note="unnamed protein product"
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haromycetales; Schizosaccharomycetaceae;
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Best Local Similarity 100.0%;
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Best Local Similarity 100.0%;
Matches 14; Conservative
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ATU48698 2316 bp mRNA PLN 22-MAR-1996
Arabidopsis thaliana putative receptor serine/threonine kinase PR5K
(PR5K) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1964)
Mizuki,N., Sarapata,D.E., Garcia-Sanz,J.A. and Kasahara,M.
The mouse male germ cell-specific gene Tpx-1: Molecular st
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha;
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SFEESPSLEKIKIPDDCNVPYLRRNIDLAGAEESVEQALITVGTLLTMMYRTPATKKI
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GSWKRGTNISYNYHVLKDWCLESGVPEAYLQLEELLQTSKILQFVKDDPNYVARVRDF
                                                                                                                                                                                                                                                                                                                                                                                                     /sub_species="domesticus"
/db_xref="taxon:10090"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="PID:g1749708"
/db_xref="GI:1749708"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="BALB/cJ"
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                                                                                                                                                                                                                                                                                                                            'gene="TPX-1"
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romosome 17"
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Pred. No. 5.42e+01;
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Pred. No. 5.42e+01;
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Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
                                         Y07910.1 GI:1546880
nad2 gene; NADH dehydrogenase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-FEB-1996) Michael A. Lawton, AgBiotech Center, Rutgers University, Foran Hall, Cook College, New Brunswick,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawton, M.A., Wang, X.Q. and Zafian, P. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang, X., Zafian, P., Choudhary, M. and Lawton, M. The PRK receptor protein kinase from Arabidopsis thaliana structurally related to a family of plant defense proteins proc. Natl. Acad. Sci. U.S.A. 93 (6), 2598-2602 (1996)
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Similarity 100.0%;
14; Conservative
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nidus mitochondrial nad2 gene.
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NSITEEEEKFAKKLVLVALWCIQMNPSDRPPMLKVTEMLEGNLEALQVPPNPLLFSPE
ETVPDYLEDSDJTSTEFNPSHFERGTLLASEDVLQHGSRSS"
443 c 527 g 657 t
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IVHFDIKPQNILMDENLCPKISDFGLAKLCKNKESIISMLHMRGTFGYIAPEMFSKNF
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/db_xref="GI:1235680"
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/protein_id="AAC49208.1"
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/strain="Columbia"
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Malek, O. and Knoop, V.
Trans-splicing group II introns in plant mitochondria: the complete set of cis-arranged homologs in ferns, fern allies, and a hornwort RNA 4 (12), 1599-1609 (1998)
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/gene="nad2"
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Bacillus subtilis
Bacillus subtilis
Eubacteria; Firmicutes; Low G+C gram-positive
Bacillaceae; Bacillus.
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hsmBI gene; hsrBI gene; modification methyltransferase; restriction
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BACHSMR 2892 bp DNA
BACILus subtilis ISB8 modification methyltransferase (hsmB1) gene, complete cds, restriction endonuclease (hsrBI) gene, complete cds. L01541:S52585
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/db_xref="pip_igl43054"
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KAGIETVNLYSAFVALTVDLMSDGGETVFIIPRSFCNGPFREFRQHLLNKTSIKHMH
LFESSDKAFKDDEVLGENVISKLEKGTVFIERSFCNGPFSFSVEENREMPGEGTV
PLFYPNHFVGTSLEYPKMMKKPNAIIRNEKVEKWLYPNGHYVVVKRENSKEEKRRIVA
GVLTPESVHDPVVGFENGLNVLHYNKGGISKEVAYGLAYLNSTPVDKYERIFNGHTQ
GVLTPESVHDPVVGFENGLNVLHYNKGGISKEVAYGLAYLNSTPVDKYERIFNGHTQ
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1714. .2664
/gene="hsrBI"
/codon_start=1
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662 c 638 g
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/note="C to U RNA editing"
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CURL, http://www.sanger.ac.uk/yeast/home.html)
Protein coding regions (CDS) have been predicted with the help of
Protein coding regions (CDS) have been predicted with the help of
Computer analysis using the Genefinder program in PomBase (an ACEDB
database) with additional predictions for the branch-acceptor sites
supplied by the program Sp3splice. CAUTION: It is possible that for
any individual CDS we may have underestinated or overestimated the
number of introns/exons or we may not have chosen the correct
splice donor/acceptor sites. CDS are numbered using the following
system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10
(cosmid name), .01 (first CDS), c (complementary strand).
The more significant matches with motifs in the PROSITE database
are also included but some of these may be fortuitous. The length
in codons is given for each CDS.
IMPORTANT: This sequence MAY NOT be the entire insert of the
sequenced clone. It may be shorter because we only sequence
overlapping sections once, or longer, because we arrange for a
small overlap between neighbouring submissions. Cosmid c22H10 is
overlapped at the 5' end by cosmid c17G8 and at the 5' end by
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S.pombe ch
269730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-FEB-1996) Schizosaccharomyces pombe chromosome I sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: barreligesanger.ac.uk
3 (bases 19711 to 21680)
3 (bases 1971 to 21680)
4 Carishichuk, and McIntosh, J.R.
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Eukaryota; Fungi; Ascomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the World Wide Web.
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Barrell, B.G., Rajandream, M.A. and Walsh, S.V.
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1 (bases 1 to 27227)
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Similarity 100.0%;
14; Conservation
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TWSEABSPLIGITPMMEFCRINVGKEEABNSRETERTMAGPTAGTALVNDKRPTR
PVNSPRAVYQLEAETLLEIKO'NTEEWSELLARYLSNROTLVERYAKERQNNILPOGI
AEGKEIYITPGEHSELIKAIIEEFAPRYVPGGRLIYAGDTGEKMGYFDEELLROLGVV
IDSHGKMPDVVIYFPEKKWLLLIESVTSHGPVDHKRHEELAKLFNGSTAGIVYVTAFP
NRSLMARYLNNISWETEWVADAPSHLIHENGVRFLGPYE"
419 c 602 g 839 t
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product="restriction endonuclease"
protein_id="AAAA18170.1"
/db_xref="piD:9143055"
/db_xref="GI:143055"
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J. No. 5.42e+01;
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                                                                                                                   /note="SPAC22H10.03c, RanBP7/importin-beta/Cselp superfamily, len: 993, some similarity to sw:YGZ1_YEAST, RanBP7/importin-beta/Cselp superfamily - yeast (23.4% identity in 1049 as overlap); contains PS00215 witochondrial energy transfer proteins signature" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                          complement(3001. .6242)
/gene="SPAC22H10.03c"
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/note="splice branch and ctaactttattggtttag"
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/translation="MGLSTSNTHILNSPQQLQYKMAFYYKNNLGYQNIPYGYQLNDFR
ASFEKARTFDMEDDLEFCPSLSDEELVSIYQSTGLSPTSSSPSLSPMTPNLYPNVLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MVQLDDALQDAYKKVEREESLILGAKAMVASTKNPEVKRRLESNIAVSENNIKYLRERIDALKVESGSERESQSDKDSSKKYSDSAKSTNSDDHLLSYNRSAEDLFNSEKPLSPEKISTMLQHLQMRLSIEQQCVSG"
                                                                                                                                                                                                                                                                                        complement(join(3001..3120,3160..3212,3270..34 3483..3601,3649..3818,3859..6080,6137..6242))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SPAC22H10.02"
/note="splice branch and
ctaactgitgaactag"
/protein_id-"CAA93604.1"
/db_xref="PID:e1359017"
/db_xref="PID:g4007778"
                                                                           superfamily
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="pck1"
/note="SPAC22H10.01c, partial pck1 gene, len: > 137,
conflict with SW:PCK1_SCHPO P36582 protein kinase C-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Schizosaccharomyces pombe"
/strain="972h-"
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/gene="SPAC22H10.02"
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                                                                                            /product="similar to RanBP7-importin-beta-Cselp
                                                                                                                                                                                                                                                                    /gene-"SPAC22H10.03c"
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chromosome="I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-"overlap with cosmid c17G8'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="SWISS-PROT:P36582"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    splice donor sequence, gtaggt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         splice donor sequence, gtaagc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown, len: 158"
                                                                                                                                                                                                                                                                                                                                                                                                                acceptor sequence
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misc_feature
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/gene="SPAC22H10.04"
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/note="SPAC22H10.04, len: 307, similar to PIR:S42558
phosphoprotein phosphatase (58.0% identity in 307 aa
overlap); PS00125 Serime/threonine specific protein
                                                                                                                                                                                                                                                                                                                                            complement(6081. .6099)
/gene="SPAC2H10.030"
/note="splice branch and acceptor sequence,
ctaactatctttacgaag"
complement(6131. .6136)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"splice donor sequence, gtaagt"
complement(5917. .5943)
/gene-"SPAC22H10.03c"
/note-"PS00215 Mitochondrial energy transfer proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(3264...3269)
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/note="splice donor sequence, gtacga"
complement(3441...3454)
/gene="SPAC22H10.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="splice branch and acceptor sequence, ctaacatttttag"
complement(3154 . 3159)
/gene="SPAC22H10.03c"
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SSAVKLDCAKAAELGNSVIPLLENLVATNASDPYICGIIEDTEDIIHAANNYESMCE
ITLPELLQVLNQEDPINVAVIGATILSCLIRAGPSPLPNGFVGYVLPPVKITQIHSG
TELLQLSQEILKGLLEKDTPQLLETEISGSSGFQYILFILHQLLDKESDDSACFLVGF
TLLELADHASQNVDLQSILLSCIKRLAIAEQPRFIGSIIYVFAKLIVKDSLGMMHFLT
SSLLABQGLFAFEVLATVWCDNFVYESNFKNISIICIAMKIYSFDSPLLDSVQVKGE
LISHSNRIITRSQSKLHPEEYSYVSVGEKILRLLSEEFVSLSKDAIVEEVSDDGADDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3853. .3858)
/gene="SPAC22H10.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="splice donor sequence, gtatgt"
complement(3819. .3834)
/gene="SPAC22H10.03c"
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complement(3643. .3648)
/gene="SPAC22H10.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ttaaccaaaactag"
complement(3477. .3482)
/gene="SPAC22H10.03c"
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complement(3213. .3230)
/gene="SPAC22H10.03c"
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/gene-"SPAC22H10.03c"
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LTPYVTFVELVWNIIRKLDPYIREVVFSDGLDDSAFGDKYELFXLVELLLFYGVAL
GSKFVQNLFYSNTVPVPBPLPFCIPLLVQYTQLPKHQIEVYESDVSEYIAMEFSMDFAS
DTVRGAAISVLSAFEEHTTLPIQQSLREMSATYILNNEINWIYQEALLYACCSVDAAS
DTVRGAAISVLSAFEEHTTLPIQQSLREMSATYILNNEINWIYQEALLYACCSVDAAS
                                                          phosphatases signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctgacttttatttag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="splice branch and acceptor sequence, ttaacgaattgtccaaag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="AVESKIIKLLEQVQSADENSRIQAELGLRDLEKYHDFAAKITDI
ASSGASVPLRQGSLIYLQRYTYHHWSPLEDFADGODIEDENVEKHVRETLLHLLVSLD
NETLIKAANAYAVSLIANVDYDEWEFUVPAUHLLQSSMENSLINASLUVLDELVDESL
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'product="putative phosphoprotein phosphatase"
                                                                                                                                                                                                                                                                                     'note≖"splice donor sequence, gtatgt"
'212. .8313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="splice branch and acceptor sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="splice branch and acceptor sequence
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CDS gene

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/db_xref="SWISS-PROT:Q10298"
                                                                /protein_id="CAA93605.1"
/db_xref="PID:e223751"
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Note: remainder of annotations omitted

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밁
                                                       Query Match 73.7%;
Best Local Similarity 100.0%;
                                              Matches
                     8409 CATCGTTCATTAAT 8422
18 CATCGTTCATTAAT 5
                                            14;
                                            Conservative
                                                        Score 14; DB 27;
Pred. No. 5.42e+01;
                                              0;
                                              Mismatches
                                       0; Indels 0;
                                                                  Length 27227;
                                            Gaps
                                              0
```

Search completed: Sat Nov 27 15:08:51 1999 Job time: 135 secs.

çp

Statistics: Mean 6.299; Variance 1.047; scale 6.018	Statis
Pase: HIV-NA8 1:H_PRI 2:H_UNA 3:H_VIR	Database:
Post-processing: Minimum Match 0% Listing first 45 summaries	Post-p
thed: 1052 seqs, 1486975 bases x 2	Searched:
ch STD: Dbase 0; Query 0	Nmatch
Scoring table: TABLE jmetric Gap 60	Scorin
Title: >US-09-103-287-5  Description: (1-19) from US09103287.seq  Perfect Score: 19  N.A. Sequence: 1 CTTCATTAATGAACGATGC 19  Comp: GAAGTAATTACTTGCTACG	Title: Descrip Perfect N.A. Se
	Tabula
on: Sat Nov 27 15:14:34 1999; MasPar time 0.62 Seconds	Run on:
ch_nn n.a n.a. database search, using Smith-Waterman algorithm	MPsrch_nn
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	,
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

000	0 0 0	n	a	00000	₽ 6
17 18 19 20	14 15 16	10 11 12	876	443410	Result No.
100	100	11111	====	12 12 12 12	Score
52. 52. 52. 6	522. 52. 666	57.9 57.9 57.9 52.6	57.9 57.9 57.9	63.222	% Query Match
9625 9636 9672 9811	1113 1696 3534 9625	1773 9170 9623 781	672 781 1217	991	% Query Match Length
	Νωωω	ա ա ա ա	<u>μ</u> ωω	<b></b>	DB
SIVAGM3 HIV2ISYR HIV2ST SIVCPZ	SIVGRI3E SIVAGMT17 SIMSP2 SIVAGM3	SIVAGMT49 SIVAGMTYO SIVAGM677 HIV260415K	SIV2010G HIV27924A1 HUMB2M1	SIV2010G HIV27924A1 SIVAGMT49 SIVAGMTYO SIVAGM677	ID
Simian immunodeficien Human immunodeficienc Human immunodeficienc Simian immunodeficien	Simian immunodeficien Simian immunodeficien Simian spumavirus, pa Simian immunodeficien	Simian immunodeficien Simian (African green Simian immunodeficien Human immunodeficienc	Simian immunodeficien Human immunodeficienc Human beta-2-microglo	Simian immunodeficien Human immunodeficienc Simian immunodeficien Simian (African green Simian immunodeficien	Description
1.82e+00 1.82e+00 1.82e+00 1.82e+00	1.82e+00 1.82e+00 1.82e+00 1.82e+00	1.33e-01 1.33e-01 1.33e-01 1.82e+00	1.33e-01 1.33e-01 1.33e-01	7.33e-03 7.33e-03 7.33e-03 7.33e-03 7.33e-03	Pred. No.

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45	44	43	42	41	40	39	3 8	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24	23	22	17
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47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	52.6	52.6	0.0
10359	9892	9794	9229	9229	4549	3328	3328	3292	3292	2854	2854	2707	2707	2649	2346	2346	1696	1471	781	345	345	11443	10359	ACTT
N	w	w	ω	w	ω	w	ω	ω	ω	w	w	ω	ω	ω	w	ω	ω	ω	ω	w	ω	w	N	Ç
HIV2BEN	SIVSTM	SIVAGM155	HIVMAL	HIVMAL	HSPUENV	HIVDJ264A	HIVDJ264A	HIVDJ263A	HIVDJ263A	HIVUG0317	HIVUG0317	HIVU08795	HIVUG0314	HIVU08794	HIVTH0065	HIVU08810	SIVAGMT17	HIVLBV23	HIV260415K	HIVU08828	HIVU08828	HIV2CAM2	HIV2BEN	STACER
Human immunodeficienc	Simian (stump-tailed	Simian immunodeficien	Human immunodeficienc	Human immunodeficienc	Human spumaretrovirus	Human immunodeficienc	Simian immunodeficien	Human immunodeficienc	STILL TIME TIME TO THE TOTAL															
1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.79e+01	1.82e+00	1.82e+00	1.026+00

## ALIGNMENTS

CDS	FEATURES source	,		JOURNAL STANDARD COMMENT	TITLE	REFERENCE	ACCESSION SOURCE	RESULT 1
/CLORE "GAGADZOLO" /Strain "SIVbab2010" /organism "Simian immunodeficiency virus" /specific_host = "Papio cynocephalus - hamadryas" <1>672 /gene = "gag" /codon_start = 1 /product = "gag protein" /translation = "VATVRQCCHLVKKEKSAAETSSGRQKNDRSTATSSGQSQNFPAQ	transmission of Siv in the Wild. Location/Qualifiers 1.672	over a 672 bp region of gag and a 906 bp region of env for animal 2010 (only the env region was analyzed for isolates ver266 and ver385). Jin et al. note that the viral strain derived from the yellow baboon (animal 2010) clusters with SIV strains of the vervet subtype, including ver266 and ver385, and believe that this is the first evidence for simian-to-simian cross-species	study with strong SIV(agm) seroreactivity. They lived in a national park where yellow baboons and African green monkeys share the same habitat. In this study, molecular characterization was performed for virus derived from one of the SIVagm seroreactive yellow baboons (animal 2010) and from two vervet African green monkeys (animals ver266 and ver385). With this aim in mind, incultured leukovete NAW ass EGP-amphified closed and sequenced	U. Virol. (In press, 1994) full staff_review Two wild yellow baboons from Tanzania were identified in a previous		+	yellow baboon sample SIVbab2010.  U10899 Simian immunodeficiency virus from PCR-amplified DNA extracted from uncultured leukocytes derived from an asymptomatic pregnant female yellow baboon from Tanzania.	

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ACCESSION
SOURCE
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STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.2%;
Best Local Similarity 100.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to now, HIV-2 sequences have been derived almost solely from cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA) from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the patient 7024 was a between the countries of the patient 7024 was a between was a solation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patient 7924 was a heterosexual 48-year old teacher from Guinea Bissau, who was living in the Washington, D.C. area. Originally he lived in an urban area in West Africa before traveling extensively and coming to the United States. After seeking medical care for a STD, patient 7924 was identified as HIV-2 positive. Subsequent Western blot analysis of peripheral blood cells showed HIV dual reactivity. Virus isolation was successfully performed at the University of Alabama at Birmingham. Sample 7924A clusters with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               full staff_review
This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retroviridae; Lentivirinae.

1 (bases 1 to 781)
Gao.F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV27924A1 781 bp ds-DNA VRL 23-AUG-1994 Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag seque sample 7924A, clone 1, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetic diversity of human immunodeficiency virus type 2: Evidence for five distinct sequence subtypes with differences in virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 2 Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a 48 year ord necessions who showed HIV dual seroreactivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a 48 year old heterosexual male originally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L33081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        approximately 304 bp downstream from the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the subtype A HIV-2 viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Virol. 68, 7433-7447 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQGNTWVHVPLSPRTLNAWVKAVEEKKFGAEIVPMFQALSEGCTPYDINQMLNVLGDH
QGALQIVKEIINEEAAQWDIQHPPPAGPLPAGQLRDPRGSDVAGTTSTVQEQLEWIYT
ANPRVDVGAIYRRWIILGLQKCVKMYNPVSILDIKQGPKEPFKDYVDRFYRTIRAEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     532145
/translation="aneldreglaeslleskegcQrIIsVLDPLVPTgsenlkslfnT
VCVVWCIHAEEKVKDTEEAKKIVQRHLVAETGTAEKMPNTSRPTAPPSGKGGNYPVQS
IGGNYTHVPLSPRTLNAWVKLVEEKKEGAEVVPGFQALSEGCTPYDINQMLNCVGDHQ
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                                                                                                     /codon_start=
                                                                                                                                /note-"NCBI gi: 532146"
                                                                                                                                                               /gene="gag"
                                                                                                                                                                                                                                                                 /tissue_type="PBMC"
                                                                                                                                                                                                                                                                                                   /sequenced_mol="DNA"
                                                                                                                                                                                                                                                                                                                                 /proviral
                                                                                                                                                                                                                                                                                                                                                                /organism="Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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Pred. No. 7.33e-03;
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COMMENT

This sequence was obtained from a lambda clone derived African green monkey imported from Kenya.

from

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ACCESSION
SOURCE
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    JOURNAL
STANDARD
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Best Local Similarity 100.0%;
Matches 12; Conservative
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STANDARD
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L19253
Simian immunodeficiency virus proviral DNA, isolate TAN-49 from Ugandan tantalus monkey (Cecopithecus tantalus).
Simian immunodeficiency virus
Simian immunodeficiency virus
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
Retroviridae; Lentivirinae.
1 (bases 1 to 1773)

DannifforG. Goldstein, S., Ogen-Odoi, A.,
Miki,K., Kitamura,T. and Hayami,M. Sequence of simian immunodeficiency virus monkey, a new member of HIV/SIV group Nature 333, 457-461 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               594 \cdot a 375 \cdot c 480 \cdot g 324 \cdot t 193 \cdot nt upstream from the gag cds start.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hirsch, V.M., McGann, C., Dapolito, G., Goldstein, S., Ogen-Odoi, A. Biryawaho, B., Lakwo, T. and Johnson, P.R.
Identification of a new subgroup of SIVagm in tantalus monkeys Virology (1993) In press full staff review
Kindly submitted prior to publication by Dr. Vanessa Hirsch, Immunodeficiency Viruses Section, NIAID/NIH, Twinbrook II, Rockville MD 20852. SIVagm-tan strains cluster with other previously characterized agm strains taken from vervets and grivets. See related tantalus isolate sequences 17, 27, 40, and 9 (accession numbers 119250-L19252, L19254).
                                                                                                       Simian (African green monkey) immunodeficiency virus, extra-
chromosomal closed-circular DNA, TYO-1 clone lambda-SAH12.
1 (bases 1 to 9170)
Fukasawa,M., Miura,T., Hasegawa,A., Morikawa,S., Tsujimoto,H.,
                                                                                                                                                                                                                                  SIVAGMTYO 917
Simian (African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279.a 157 c 195 g 150 t 111 bp downstream from the start of gag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIVAGMT49 1773 bp ds-DNA VRL 09-JUN-1993 Simian immunodeficiency virus, isolate TAN-49, complete gag cds.
                                                                                                                                                                                                              TYO-1, complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sequenced_mol="DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAMQIIREIINEVAADMDVAHFIFGFLFAGQLREFRGSDIAGTTSTVEEQIQWMFRAQ NPVFVGNIYRRWIQIGLQKCVRMYNFTNILDVKQGFKESFQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="gag"
1..1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Simian :/cell_line="CEMss" /haplotype="na"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 195..1773
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                                                                                                                                                                                                                                                        9170 bp ss-RNA
                                                                                                                                                                                                                                       green monkey) immunodeficiency virus, isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12; DB 3; 1
Pred. No. 7.33e-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunodeficiency virus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1] finds that SIVAGMTYO is approximately equally distantly related to the HIV-1's and the HIV-2/SIV (macaque) group; over a "conserved" stretch of the pol protein, TYO is only 87% similar to AGM385 and 82% similar to AGM266, the latter two differing by 20%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIVAGMTYO appears to lack a vpR coding region. [1] suggests that this may account for SIVAGMTYO's lack of pathogenicity. The env
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences
                                                              8547..>9170
/note="3' LTR"
9054..9170
                                                                                                                                                                                                      /note="1
8077..80
                    /note="R repeat 3'
9151..9156
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="15764..7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"
5703..5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="R repeat 5'
220..237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="rev protein, exon 5764..7983
/note="mRNA polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                 /note="tat, rev, nef subgenomic mRNA intron
5770..8367
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                                                                                                                                                                 3201..8890
                                                                                                                                                                                   /note="
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/codon_start=5236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="vif protein"
/codon_start=4755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=5546
join(5703..5763,7984..8177)
/note="rev protein"
/codon_start=5703
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                                                                                                                                          'note="nef protein"
                                                                                                                                                                                                                                                                 note-
                                                                                                                                                                                                                                                                                                    'note="env polyprotein (in-frame stop codon at 8077)"
'codon_start=5770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oin(5546..5763,7984..8068)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=432
                                                                                                                       codon_start=8201
                                                                                                                                                                                                                                                                                                                                                pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1634
                                                                                                                                                                                                    .e="rev protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "tat protein, exon 2 (first expressed exon)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tat intron 2"
                                                                                                                                                                                 in-frame stop
                                                                                                                                                                                                                                                                                                                                                                                                                            ev intron 2"
                                                                                                                                                                                                                                                             at protein, exon 3 (AA at 7985)"
                                                                                                                                                                                                                         exon 3 (AA at 7986)"
                                                                                                                                                                                   'n
                                                                                                                                                                                 env cds"
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Best Local Similarity 100.0%;
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full staff_entry
full staff_entry
form by Phillip Johnson, NIAID/Georgetown University.
The typical stop codon "tag" in rev (position 8574) is "cag"
making rev in SIvgri-1 (lambdaII) longer than rev in most
other sequences. The gri-1 sequence is the most divergent
primate lentivirus reported to date.
primate lentivirus reported to date.
primate lentivirus form (2011) filers
join(5993.6195,8370..8750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i (bases 1 to 9623)
Fomsgaard, A., Hirsch, V.M., Allan, J.S. and Johnson, P.R.
A highly divergent proviral DNA clone of SIV from a distinct
species of African green monkey.
Virology 182, 397-402 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simian immunodeficiency virus from an African grivet (green monkey), gri-1, lambda clone II (biologically active clone); proviral DNA, also denoted 677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cap site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simian immunodeficiency viruses from unusual genetic diversity
J. Virol. 64, 1086-1092 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson, P.R., Fomsgaard, A., Allan, J., Gravell, M., London, W.T., Olmstead, R.A. and Hirsch, V.M.
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2 (bases 1 to 2
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                                   /codon_start=5683
5993..6195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note—"The normal stop codon 'tag' in rev (position 8574) is 'cag' making rev in SIVgri-1 longer than rev in most other sequences. The gri-1 sequence is the most divergent primate lentivirus reported to date."
                                                                                                                                                                                                                                                                                                    /note="primer (Lys-tRNA) binding site"
897..2438
                                                                                                                                                                                                                                                                                                                                            /rpt_type=R repeat 5' copy
690..707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(6135..6195,8371..8750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="rev"
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                                                                               'gene="vpx"
                                                                                                                                                                                                                     gene-"pol"
                                                                                                                                                                                                                                                                               'gene="gag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=6135
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683..6039
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141..5314
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No. 7.33e-03;
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                                                                                                                                                             Two wild yellow baboons from Tanzania were identified in a previous study with strong SIV(agm) seroreactivity. They lived in a national park where yellow baboons and African green monkeys share the same habitat. In this study, molecular characterization was performed for virus derived from one of the SIVagm seroreactive yellow baboons (animal 2010) and from two vervet African green monkeys (animals ver266 and ver385). With this aim in mind, uncultured leukocyte DNA was PCR-amplified, cloned and sequenced over a 672 bp region of gag and a 906 bp region of env for animal 2010 (only the env region was analyzed for isolates ver266 and ver385). Jin et al. note that the viral strain derived from the yellow baboon (animal 2010) clusters with SIV strains of the vervet subtype, including ver266 and ver385, and believe that this is the first evidence for simian-to-simian cross-species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desrosiers,R.C., Shaw,G.M., Sharp,P.M. and Hahn,B.H. Infection of a yellow baboon with SIV from African gree evidence for cross-species transmission in the wild J. Virol. (In press, 1994) full staff_review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simian immunodeficiency virus (SIVbab) partial gag sequence, yellow baboon sample SIVbab2010.
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Simian immunodeficiency virus
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Similarity 100.0%;
12; Conservative
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          /Clone="gaguacco"
/Strain="SIVBab2010"
/organism="Simian immunodeficiency virus"
/organism="Simian immunodeficiency virus"
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8937..9623
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8600..9271
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/gene="gag"
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                                                                                                                                                Location/Qualifiers
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s of 5' LTR.
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                                                                                                                                                                                                                                                                                                                                                          recombinant clones were manufacture. The recombinant clones were manufacture. The recombinant clones were manufacture. The recombinant clones were mastered to a heterosexual 48-year old teacher from Guinea Patient 7924 was living in the Washington, D.C. area. Originally he lived in an urban area in West Africa before traveling extensively and coming to the United States. After seeking medical care for a STD, patient 7924 was identified as HIV-2 positive. Subsequent Western blot analysis of peripheral blood cells showed HIV dual reactivity. Virus isolation was successfully performed at the reactivity. The hamma at Birmingham. Sample 7924A clusters with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to now, HIV-2 sequences have been derived almost solely from cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA) from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetic diversity of human immunodeficiency virus type 2: Evidence for five distinct sequence subtypes with differences in virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gao, F., Yue, L., Robertson, D.L., Hill, S.C., Hui, H., Biggar, R.J., Neequaye, A.E., Whelan, T.M., Ho, D.D., Shaw, G.M., Sharp, P.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          who showed HIV dual seroreactivity. Human immunodeficiency virus type 2
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                                                                                                                                                                                                                                                                                                                              the subtype A HIV-2 viruses.
NCBI gi: 532145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viridae: ss-RNA enveloped viruses; Positive strand RNA virus; Retroviridae; Lentivirinae.
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Similarity 100.0%;
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QGALQIVKEIINEEAAQWDIQHPPPAGPLPAGQLRDPRGSDVAGTTSTVQEQLEWIYT
/gene="gag"
/note="NCBI gi: 532146"
/codon_start=2
                                                                                                                                                 /sequenced_mol="DNA"
/tissue_type="PBMC"
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/translation="VATVRQCCHLVKKEKSAAETSSGRQKNDRSTATSSGQSQNFPAQ
                                                                                               /partial
                                                                                                                                                                                                                                                 /organism="Human immunodeficiency
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Pred. No. 1.33e-01
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STANDARD
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Matches 11; Conservative
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                   ORGANISM
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Human beta-2-microglobulin gene, exon 1.
M17986
1 of 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

1 (bases 1 to 1217)

Guessow,D., Rein,R., Ginjaar,I., Hochstenbach,F., Seemann,G. Kottman,A. and Ploegh,H.L.

The human beta-2-microglobulin gene: Primary structure and definition of the transcriptional unit

J. Immunol. 139, 3132-3138 (1987)
Ugandan tantalus monkey (Cecopithecus tantalus).
Simian immunodeficiency virus
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus
                                                  SIVAGMT49 1773 bp ds-DNA VRL 09-JUN-1993 Simian immunodeficiency virus, isolate TAN-49, complete gag cds L19253 Simian immunodeficiency virus proviral DNA, isolate TAN-49 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Draft entry and computer-readable sequence by E.J.Baas, 03-DEC-1987.
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Similarity 100.0%;
ll; Conservative
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4 a 325 c 322 g 29
upstream of EcoRl site.
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846..>1217
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943..949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="microglobulin
883..942
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AAMQIIREIINEVAADWDVAHPIPGPLPAGQLREPRGSDIAGTTSTVEEQIQWMFRAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <883..949
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="beta-2-microglobulin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="beta-2-microglobulin precursor"
/gene="B2M"
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0; Mismatches C
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Pred. No. 1.33e-01; 
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       mature peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signal peptide"
                                                                                                                                                                                                                                                                             Length 1217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of simian immunodeficiency virus monkey, a new member of HIV/SIV group Nature 333, 457-461 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hirsch,V.M., McGann,C., Dapolito,G., Goldstein,S., Ogen-Odoi,A
Biryawaho,B., Lakwo,T. and Johnson,P.R.
Identification of a new subgroup of SIVagm in tantalus monkeys
Virology (1993) In press
full staff_review
                                                                                                                                                                                                                                                                                                                SIVAGMIYO appears to lack a vpR coding region. [1] suggests that this may account for SIVAGMIYO'S lack of pathogenicity. Proceeds contains an in-frame stop codon at positions 8077-8079, similar to the in-frame stop codons found in the SIV macaque and HIV-2 ROD35 envelope coding regions, except that SIVAGMIYO'S stop codon is found 96bp downstream from the 3' splice junction of tat and rev, which is the location of the stop codon in the other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIVAGMTYO 9170 bp ss-rNA VRL 01-MAR-1989 Simian (African green monkey) immunodeficiency virus, isolate TYO-1, complete genome.
                                                                                                                                                                              [1] finds that SIVAGMTYO is approximately equally distantly related to the HIV-1's and the HIV-2/SIV (macaque) group; over a "conserved" stretch of the pol protein, TYO is only 87% similar to AGM385 and 82% similar to AGM266, the latter two differing by 20%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was obtained from a lambda clone derived African green monkey imported from Kenya.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosomal closed-circular DNA, TYO-1 clone 1 (bases 1 to 9170) Fukasawa, M., Miura, T., Hasegawa, A., Morikawa, Miki, K., Kitamura, T. and Hayami, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similan (African green monkey) immunodeficiency virus, extra-
chromosomal closed-circular DNA, TYO-1 clone lambda-SAH12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X07805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kindly submitted prior to publication by Dr. Vanessa Hirsch. Immunodeficiency Viruses Section, NIAID/NIH, Twinbrook II, Rockville MD 20852. SIVagm-tan strains cluster with other previously characterized agm strains taken from vervets and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Retroviridae; Lentivirinae.
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                                            /note="pol polyprotein
1634)"
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                                                                                       /note="5' LTR" <1634..4819
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375 c 480 q
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1..1773
/codon_start=1634
join(5546..5763,7984..8068)
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/cell_line="CEMss"
                                                                                                                                                    Location/Qualifiers
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                                                                    (NH2-terminus uncertain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1773;
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London, W.T.,

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REFERENCE
AUTHORS
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LOCUS
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                                                                     SOURCE
                                                                                     ACCESSION
                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                           Query Match 57.9%;
Best Local Similarity 100.0%;
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Cap site o
                                                                                  SIVAGM677 9623 bp ss-DNA VRL 02-APR-1991
Simian immunodeficiency virus from African Green Monkey;
gri-1 lambdaII or 677 Clone (from a grivet); complete genome.
M66437 M29973
                                Simian immunodeficiency virus from an African monkey), gri-1, lambda clone II (biologically proviral DNA, also denoted 677.
Fomsgaard, A., Hirsch, V.M., Allan, J.S. and Johnson, P.R
                     (bases
                                                                                                                                                                                                                                                                                                                                               of genomic RNA.
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1720 c 2263 g 2015 t
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/note="in-:
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5703..5763
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join(5703..5763,7984..8177)
/note="rev protesin"
/codon_start=5703
                                                                                                                                                                                                                                                                                                                                                                                                                   'note="R repeat 3' copy"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="tat protein, exon 3 (AA at 7985)"
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/codon_start=4755
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/codon_start=432
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|32..1991
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                   1 to 9623
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Pred. No. 1.33e-01;
0; Mismatches 0
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ORIGIN 5' t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kindly submitted prior to publication and in a computer readable form by Phillip Johnson, NIAID/Georgetown University. The typical stop codon "tag" in rev (position 8574) is "cag" making rev in SIVgri-1 (lambdaII) longer than rev in most other sequences. The gri-1 sequence is the most divergent primate lentivirus reported to date.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson, P.R., Fomsgaard, A., Allan, J., Gravell, M., Olmstead, R.A. and Hirsch, V.M.
Simian immunodeficiency viruses from African green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A highly divergent proviral DNA clone of SIV from a distinct species of African green monkey. Virology 182, 397-402 (1991) full-staff_entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unusual genetic diversity

J. Virol. 64, 1086-1092 (1990)
3243 a 1807 c 2470 g 5' terminus of 5' LTR.
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                3243 a
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                                                              /gene="rev"
8600.9271
/gene="nef"
/codon_start=8600
.gene="3"
.gene="3"
.note="3"
/note="3"
                              /rpt_type=R repeat 3' copy
.9506..9511
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690..707
                                                                                                                                                                                                                                                             8368.
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/gene="rev"
6202..8766
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                                                                                                                                                                                                                                                                                                                                                             /gene="tat"
5135..6195
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                                                                                                                                                                                       'number=3
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|368..8750
                                                                                                                                                                                                                                         number=3
                                                                                                                                                                                                                                                                                           'gene≖"env"
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                                                                                                                                                                                                                                                        codon_start=6202
368..8449
                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=5683
993..6195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="primer (Lys-tRNA) binding site"
97..2438
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                                                                                                                                                                                                                                                                                                                                                                                                 number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="vpx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="vif"
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Query Match 52.6%;
Best Local Similarity 100.0%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells was used for virus isolation.

Patient 60415K was a heterosexual 34 year old asymptomatic man from urban Senegal, who was living in the Washington, D.C. area. He traveled extensively before coming to the United States where he was identified as HIV-2 positive after seeking medical care for a STD. He was married to an American IV drug user. Virus isolation was successfully performed at the University of Alabama at Birmingham. Virus 60415K clusters with the subtype A HIV-2 viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRL 23-AUG-1994
Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag sequence,
sample 60415K, clone 8, partial cds.
L33076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full staff_review
This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up to now, HIV-2 sequences have been derived almost solely from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetic diversity of human immunodeficier for five distinct sequence subtypes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 2 Viridae; ss-RNA enveloped viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retroviridae; Lentivirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 2 PCR-amplified DNA recovered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI gi: 532131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.9%;
Similarity 100.0%;
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                                                                                                               downstream from the start of gag
                                                                                                                                                            NPVPVGNIYRRWIQIGLQKCVRMYNPTNILDIKQGPKEPFQS"
                                                                                                                                                                                     VCVAWCIHAEEKVKDTEGAKQIVQRHLVAETGTAEKMPSTSRPTAPPSGEGGNFPVQH
VGGNYTHIPLSPRTLNAWVKLVEEKKFGAEVVPGFQALSEGCTPYDINQMLNCVGDHQ
AAMQIIREIINEEAAEWDVQHPIPGFLPAGQLREPRGSDIAGTTSTVDEQIQMMFRPQ
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                                                                                                                                                                                                                                                            translation="ANELDRFGLAESLLESKEGCQRILTVLDPLVPTGSENLKSLFNT/
                                                                                                                                                                                                                                                                                /codon_start=
                                                                                                                                                                                                                                                                                                         /note-"NCBI gi: 532132"
                                                                                                                                                                                                                                                                                                                                                              /partial
                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="PBMC"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /sequenced_mol="DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ∕organism="Human immunodeficiency virus type 2"
                                                                                                                                                                                                                                                                                                                                     'gene="gag"
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               Score 10;
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0; Misma
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Pred. No. 1.33e-01;
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            1.82e+00;
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                                                            Length 781;
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                                            Simian immunodeficiency virus proviral DNA, isolate TAN-9 from Ugandan tantalus monkey (Cecopithecus tantalus). Simian immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was obtained as part of a study designed to determine the breadth of genetic variation of SIV infecting African green monkeys. With this aim in mind, Jin et al. PCR-amplified, cloned and sequenced the LTR and partial envelope region from 12 isolates (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1, tan-10, and tan-49). These isolates were derived from different African green monkey species inhabiting various geographical regions. Most of the vervet and grivet viruses and all of the sabaeus and tantalus viruses were derived from feral
                                                                                                                                                      SIVAGMT17 1696 bp ds-DNA
Simian immunodeficiency virus,
                                                                                                                                   L19250
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Hirsch,V.M., Allan,J.S., Shaw,G.M.,
Mosaic Genome Structure of Simian In
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Viridae; ss-RNA enveloped viruses; Positive strand RNA virus; Retroviridae; Lentivirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              approximately 727 bp downstream
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Similarity 100.0%;
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188 c 271 g 259 t
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IRQVVNDWYTLTKKTYAPPREGHLECNSTVTALYVEINYNNKSGPINVTLSSQVRSIW
AYELGDYKLVEITPIGFAPTDVRRYTGPSREKRVPFVLGFLGFLGAAGTAMGAAATAL
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GRVFHSQXYNTKLKQAWCHSQGNWLGAWKEVREKIKEEKNLTEVKIENIHLRRQWGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="envelope protein"
/translation="TLRVRYCAPAGYALLKCNDKDYNGFAPKCKNVSVVHCTRLINTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="simian immunodeficiency virus"
/specific_host="African green monkey"
/note="grivet subtype"
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                                                                                                                                                      isolate TAN-17, complete gag cds.
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., Sharp,P.M. and Hahn,B.H.
Immunodeficiency Virus from West
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1113;
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        JAMSP2 3534 bp ss-RNA VRL 09-
Simian spumavirus, partial pol cds, complete env cds.
M33561
2 of 2
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/codon_start=524
648 c 674 g 104
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/cell_line="CEMss"
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                                                                                                              Score 10; DB 3; Length 3534; Pred. No. 1.82e+00; 0; Mismatches 0; Indels
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intection prevention or generally as wound treatments to prevent adhesion	The antibacterial agents are useful to treat in-dwelling devices for	Helicobacter pylori infections and related cancers, ulcers and gastritis.	bacterial (especially S. aureus) infections. They are also useful against	competitive polypeptide are useful for inhibiting the polypeptide e.g.	expression of the polypeptide. Antagonists, inhibitory nucleic acid or	polypeptide are used to treat conditions requiring increased activity or	recombinant production of the polypeptide. Agonists or the MurC	an expression system comprising the MurC gene can be used for the	polypeptide) encoded by the S. aureus MurC gene. Host cells containing	The invention relates to a UDP-N-acetylmuramate:L-alanine ligase (MurC	Disclosure; Page 13; 39pp; English.		nucleic acid - useful in diagnosis, treatment and prevention of	New isolated MurC polypeptide from Staphylococcus aureus and related	WPI; 99-062655/06.	Burnham MKR, Wallis NG;	) SMITHKLINE	(SMIK ) SMITHKLINE BEECHAM CORP.	03-JUL-1997; US-052720.	26-JUN-1998; 305064.	07-JAN-1999.	EP-889123-A2.	Staphylococcus aureus.	Synthetic.	immunogen; drug; genetic immunisation; PCR primer; ss.	bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine;	<pre>MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide;</pre>	MurC polynucleotides amplifying primer.	17-MAR-1999 (first entry)	V99651;	V99651 standard; DNA; 19 BP.

Result No.

Score

Query Match

Length

DB

f

Description

Pred. No

Statistics:

Mean 4.607;

Variance 2.283; scale 2.018

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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119 119 113 113 113

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V99651 V53479 V80065 V99650 T83852 N70260 T72632 Q55627 N504111

Murc polynucleotides DNA encoding a Staphy Partial nucleotide se UDP-N-acetylmuramate DNA encoding a Staphy Sequence encoding the Mangifera indica ACC Human GM-CSF gene. Secretion enhancing s

2.76e-03 2.76e-03 2.76e-03 2.76e-03 2.76e-03 5.81e+00 2.43e+01 2.43e+01 2.43e+01 2.43e+01

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Matches 1
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Matches 1
                                                                                                                                                                                                                This sequence encodes a Staphylococcus aureus protein of unknown function, and represents a DNA Sequence of the invention.

The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, respiratory, cardiac, gastrointestinal, central nervous, eye, kidney,
                                                                                                                                           respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection. Sequence 619 BP; 208 A; 117 C; 79 G; 215 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; cardiac infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of bacteria to matrix proteins. The MurC polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to identify modelators or specific receptors; in rational drug design and as an immunogen for vaccines. The MurC gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant MurC gene; for chromosomal mapping; to determine bacterial serotype; and for genetic
                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid sequences from Staphylococcus aureus WCHU29 - useful in vaccines and for treatment of bacterial infections of e.g. respiratory tract and central nervous system Claim 1; Page 146; 390pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Black MT, Burnham MKR,
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24-SEP-1997; 307485.
                 137 cttcattaatgaacgatgc 155
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                                                                       100.0%;
Similarity 100.0%;
19; Conservation
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Pred. No.
0; Misma
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Pred.
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...matches 0;
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Reichard RW,
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. 2.76e-03;
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RESULT ID V

V80065 standard; DNA; 660

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CC The invention relates to a UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoded by the S. aureus MurC gene. Host cells containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Appoints or the MurC polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. competitive polypeptide are useful for inhibitory nucleic acid or competitive polypeptide are useful for inhibitory nucleic acid or competitive polypeptide are useful for inhibitory nucleic acid or competitive polypeptide are useful for they are also useful against Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The MurC polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising antibacterial muncles of determine haterial services are useful in antisense/ribozyme therapeutics; to detect mutant MurC gene; for corporation of actoring to determine haterial services.
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Best Local
EP-889123-A2.
07-JAN-1999.
26-JUN-1998; 305064.
03-JUL-1997; US-052720
                                                                                                                                                                                                                                                                                                                             UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoding DNA.
MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide;
bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine;
immunogen; drug; genetic immunisation; ds.
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bacterial; infection; H. pylori; cancer; ulce
immunogen; drug; genetic immunisation; ds.
Staphylococcus aurene
                                                                                                                                                                                                                                                                                                       Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunisation. The present sequence represents a partial nucleotide sequence (MurC:ORF) of the MurC gene.
Sequence 660 BP; 233 A; 83 C; 120 G; 224 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated MurC
nucleic acid - use
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03-JUL-1997;
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07-JAN-1999.
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Similarity 100.0%;
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US-052720.
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useful in diagnosis, treatment and prevention
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                                                                                                                     "UDP-N-acetylmuramate:L-alanine ligase
  (MurC polypeptide)"
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Pred. No. 2.76e-03;
0; Mismatches 0
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gastritis; vaccine;
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Query Match
Best Local Similarity
Matches 14; Conser

Conservative

73.7%; 93.3%;

Score 14; Pred. No. 0; Misma

DB 43; 5.81e+00;

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Mismatches

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131 A; 101 C;

150

e.g. Staphylococcal food

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194 poisoning,

and conditions relating

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP. Black MT, Burnham MK, Hodgson JE, Pratt JM, Reichard RW, Rosenberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The MurC polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to identify modulators or specific receptors; in rational
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9730070-A1.
21-AUG-1997.
19-FEB-1997; U02318.
20-FEB-1996; US-011888.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Pages 3-4; 39pp; English
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Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              design and as an immunogen for vaccines. The MurC gene sequences are ul in antisense/ribozyme therapeutics; to detect mutant MurC gene; chromosomal mapping; to determine bacterial serotype; and for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCATCGTTCATTAATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shock syndrome; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aureus
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 A;
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Pred. No. 2.76e-03;
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260 G;

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Length 1351; Indels

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sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source control of bacterial gene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect

protect

The present sequence encodes a Staphylococcus aureus protein of unknown function. The present sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA

Claim 9; Page 711; 989pp;

aureus infection to isolate antimicrobial Novel polypeptide(s) from

compounds,

ĭ,

English.

Staphylococcus aureus strain WCUH29 compounds, and in vaccines against S.

used

P-PSDB; W27890

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RESULT
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Best Local
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T72632;
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Sequence encoding the 46 amino acid product of the sacQ gene of amylol1quefaciens called 'enhancing DNA sequence (EDS) Apro'.
Gram-positive bacteria; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N70260
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Key
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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 87-179522/26.
Enhancing expression of genes in bacterial transformation with enhancing DNA sequence
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25-OCT-1985; US-791350.
20-OCT-1986; US-921343.
(BIOT-) BIOTECHNICA INT INC.
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01-JUL-1987.
27-MAR-1997.
20-SEP-1996; AU0591
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87-179522/26.
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Similarity 100.08;
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                                                                                                                                                                                                                                                        /product= miacc/
/note= "Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        /EC_number= 4.4.1.14
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                                                                                                                                                                              "Sequence represents 75% of the coding sequence and does not contain the star
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Pred. No. 2.43e+01;
0; Mismatches (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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CC This sequence represents the novel gene, miacc2, which is a member cof the mango ACC synthase multigene family. ACC synthase an enzyme CC involved in the pathway for ethylene biosynthesis and the rate of CC endogenous expression of ACC synthase is considered to limit CC endogenous expression of ACC synthase is considered to limit CC often deleterious to crops, especially if some form of mechanical CC wounding has occurred and diminishes their post harvest quality and CC storage life. Novel ACC synthase genes expressed in transgenic plants CC using either sense or antisense expression system may be used to control the regulation of plant development, in particular fruit ripening, CC reducing senescence and thus improving storage life.

Sequence 1113 BP; 320 A; 212 C; 264 G; 317 T;
                                                                                                                                                                                              Query Match
Best Local S
Matches 1
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Best Local :
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                                                                                                                                                                                                                                                                                    Application of optimised gene expression for scientific, industrial and therapeutic purposes Disclosure; Fig 13; 110py; French.

Alterations were made to the TATA box sequence of the human and mouse GM-CSF genes (see Q55627 and Q55628, respectively) and the effects of the various alterations on gene expression were measured. Results indicated that resonances of the LFF type are most strongly affected by changes in the TATA box; it was further shown that
N50411 standard; DNA; 1707 BP
N50411;
20-JAN-1992 (first entry)
Secretion enhancing sequence.
Protease; Bacillus; ss.
                                                                                                                                                                                                                                                               LFF resonances control expression. Sequence 1138 BP; 274 A; 306 C;
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 94-028256/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Perez
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Botella JR;
WPI: 97-202875/18.
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20-SEP-1995;
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22-JUN-1992; FR-007571.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PERE/) PEREZ J.
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1 CTTCATTAATGAA 13
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                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 68.4%;
Local Similarity 100.0%;
                                                                                                                                gttcattaatgaa 189
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|GTTCATTAATGAA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GM-CSF gene
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                                                                                                                                                                                             h 68.4%;
Similarity 100.0%;
13; Conservative
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AU-005559.
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Pred. No. :
0; Mismai
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Mismatches - 0;
                                                                                                                                                                                                              2.43e+01;
                                                                                                                                                                                                                              DB 9;
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                                                                                                                                                                                                                                                               292
                                                                                                                                                                                                                           Length 1138;
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Best Local S
Matches 1
                                                                                  16-APR-1998.
03-OCT-1997; CA0729.
04-OCT-1996; US-027530.
(CONN-) CONNAUGHT LAB LTD.
(VIRO-) VIRGCENETICS CORP.
Alexander J, Bonnet MC, Cornet B, C,
Gajewczyk DM, Klein MH, Paoletti E,
WPI: 98-240821/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human GM-CSF encoding DNA.

Recombinant poxvirus; biological response granulocyte macrophage colony stimulating tumour; interleukin; cytokine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V29700
V29700;
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(AGEN ) AGENCY OF IND SCI TECH.

(NIIT ) MIN INT TRADE & IND.

WPI; 85-118649/20.

DNA base sequence - with improved protein-secretory power.

Claim I; Page 425-426; 8pp; Japanese.

The sequence enhances associated protein expression, and may act as a useful marker for recombinant plasmid expression.

Sequence 1707 BP; 505 A; 342 C; 398 G; 462 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
Recombinant poxvirus encoding biological response modifier for the treatment or prevention of tumours Disclosure; Fig 9A-F; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus amyloliquefaciens. 760058076-A.
                                                                    P-PSDB; W60031
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12-SEP-1983;
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Similarity 100.0%;
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/*tag= i
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/number= 3
1769..2577
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821..913
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Pred.
0; M
                                                                                                        E, Ta
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No. 2.43e+01;
                                                                                                          ox B, Diaz
Tartaglia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modifier; IL-12; GM-CSF;
factor; prevention;
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Sequence 3043 BP; 668 A; 824 C; 878 G; 673 T;
                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus contig SEQ ID *2/0.
Staphylococcus aureus contig SEQ ID *2/0.
Computer readable medium; vaccine; S.aureus infection; immunodetection; Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; clin infection; surgical wound infection; scalded skin syndrome;
                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating melanoma, pancreatic, breadisclosure; Page 80-82; 107pp; English. Cytokine genes, e.g the GM-CSF gene, and Cytokine genes, e.g. the GM-CSF gene, and Cytokine genes, and Cytokine genes
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14-AUG-1992; GB-017270.
27-EB-1993; GB-004024.
(IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1994
GM-CSF gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This DNA encodes the human granulocyte macrophage colony stimulating factor (GM-CSF). A murine GM-CSF which is similar to the human GM-CSF is
                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V74587;
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W09404196-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                        toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V74587 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 construct encoding cytokine for expression treating melanoma, pancreatic, breast, colo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gttcattaatgaa 462
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Similarity 100.0%;
13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 aureus
                              /note- "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" 3061..3120
                                                                                                                                                                                                                                                                                                  1261..1320
                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Pred. No. 2.43e+01;
0; Mismatches 0;
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Pred. No. 2.43e+01;
0; Mismatches 0;
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for tumor
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PS Claim 1; Page 1092-1094; 3271pp; English.

PS Claim 1; Page 1092-1094; 3271pp; English.

CC of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access comemory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so condition the sequences allows putative functions to be assigned so condition the condition of regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are clikely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The cc polypeptides can also be used in a kit for the immunodetection of cc including cellulitis, eyelid infections, food poisoning, osteomyelitis, cc including cellulitis, eyelid infections, food poisoning, osteomyelitis, cc skin and surgical wound infections, scalded skin syndrome, toxic shock csyndrome, etc. Organisms transformed with the DNA sequences can be used cf or recombinant production of the polypeptides. The new DNA sequences can be used computer readable medium.

CC computer readable medium.

CC computer readable medium.

CC computer readable medium.
                                                                                                                                                                                                                                                                                                                                  Enterococcus faecalis genome contig SEQ ID NO:72.
Enterococcus faecalis; contig; detection; Enterocov
vaccine; attenuation; computer readable medium; ds
Enterococcus faecalis.
w09850555-A2.
12 NOV-1998.
13 NOV-1998; U8985.
14 NOV-1997; US-046609.
16 NAY-1997; US-046655.
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Best Local
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                                                                  Claim 1; Page 526-538; 2084pp; English.
A computer readable medium has been developed which has reco
982 nucleotide sequences isolated from the Enterococcus faec
X12938 to X13919 represent these nucleotide sequences which
                                                                                                                                                                                         New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and fouse in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP-786519-A2.
30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861
                                            nuleotide sequences, also known as contigs. The computer based
                                                                                                                                                                                                                                                                                            Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                             identify
                                                                                                                                                                                                                                                                    sh SC, Dillon PJ, Kunsch CA; 99-045171/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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Similarity 100.0%;
13; Conservati
                                                                                                                                                                                                                                                                                                                HUMAN GENOME SCI INC
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Choi GH, Dillon PJ,
       importance.
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    fragments of the Enterococcus
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  products
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Pred. No. 2.43e+01;
0; Mismatches C
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                                                                                                                                                                haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilm (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a ROREt gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can similarly be used for hypophosphatemia.

Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T;
                                                                                  Query Match 68.4%;
Best Local Similarity 100.0%;
Matches 13; Conservative
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Best Local Similarity 100.0%;
Matches 13; Conservative
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09-APR-1997; U17658.
07-MAY-1997; US-852495.
01-CCT-1996; US-724394.
(PRCG-) PROGENTIOR INC.
Feder JN, Kronmal GS, Laue
Tsuchihashi Z, Wolff RK;
WPI, 98-240014/21.
                                        74200 ttcattaatgaag 74212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 8; 209pp; English.

The present invention describes hereditary haemochromatosis gene products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an individual unaffected by hereditary haemochromatosis (HH). Also described is a method to determine the presence or absence of the common hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hereditary haemochromatosis subregion from an unaffected individual. Bovine butyrophilin; BT; human hereditary haemochromatosis; HFB; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
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V57926 standard; DNA; 235033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sodium transport gene; ss.
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                                                                             Score 13; DB 51; Lenverge No. 2.43e+01; Pred. No. 2.47hes 0;
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Pred. No. 2.43e+01;
0; Mismatches 0
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of hereditary disorders in iron
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PS Claim 1; Fig 9; 209pp; English.

PS Claim 1; Fig 9; 209pp; English.

CThe present invention describes hereditary haemochromatosis gene. The present sequence products from the human haemochromatosis subregion from an hereditary comethod to determine the presence or absence of the common hereditary haemochromatosis (HFB) gene mutation in an individual comprising:

CC method to determine the presence or absence of a haplotype encrype where come the presence or absence of a haplotype genotype where come products for use in the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present comproducts for use in the diagnosis and treatment of HFE. The present comproducts for use in the diagnosis which are homologues of the milk comproducts of a grady products of the sed to develop products for the sed to develop products for the study, diagnosis and creatment of HPE. The present comproducts of the milk comproducts of the sed to develop products for the study, diagnosis and creatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can comproduct sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T;
                                                                                                      Query Match
Best Local :
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74151 ttcattaatgaag 74163
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| 13 TTCATTAATGAAG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feder JN, Kronmal
Tsuchihashi Z, Wol
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30-SEP-1997; U17658.
07-MAY-1997; US-852495.
01-OCT-1996; US-724394.
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V57903;
21-DEC-1998 (first entry)
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Hereditary haemochromatosis gene
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Feder JN, Kronmal GS, Lauer
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                                                                          68.4%;
Similarity 100.0%;
13; Conservation
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                                                                                                        Pred.
                                                                                                                          Score 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e products - used to develop products of hereditary disorders in iron
                                                                                Mismatches
                                                                                                        No. 2.43e+01;
                                                                                                                            DB 50;
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                                                                                                                          Length 237326;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Nov 27 15:14:58 1999; MasPar time 4.56 Seconds 360.285 Million cell updates/sec

Title: Tabular output not generated.

Description:
Perfect Score:
N.A. Sequence:
Comp: >US-09-103-287-5 (1-19) from US09103287.seq 19 1 CTTCATTAATGAACGATGC 19 GAAGTAATTACTTGCTACG

Scoring table: TABLE jmetric

Gap 60

Nmatch STD:

Searched: 165359 seqs, 43243793 bases x 2

Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-issued 1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1

Statistics: Mean 4.354; Variance 1.867; scale 2.332

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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11111	112	112 112	12 12 12	12 12 12	Score
57.9 57.9 57.9 57.9	57.9	63. 63. 22.	56666	5555	Query Match
1299 1391 1391 1391 1521	11613	3344 4129 7616	730 730 1340 1521	730 730 730 730	Query Match Length 63.2 287
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US-08-463- PCT-US95-0 US-08-261- US-08-984-	US-08-484- US-08-374-	US-08-984- US-08-426- US-08-370- PCT-US94-0	US-08-332- US-08-332- US-07-971- US-08-753-	08-08	ID 
Sequence 1, Applicatio	,00,	sequence 1, Applicatio Sequence 1, Applicatio Sequence 12, Applicati Sequence 54, Applicati	1, 55,	49, Appl 55, Appl 55, Appl 55, Appl	Description Sequence 1, Application
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Sequence 7,	Sequence 16	Patent No.	ω	Sequence 2,	Sequence 1,	Sequence 1,	Sequence 18	Sequence 1,	Sequence 31	Sequence 31,			Sequence 5,	Sequence 1,	Sequence 1,	Sequence 5,		Sequence 1,	Sequence 1,	45	Sequence 1,	7,	Sequence 1,
<ol><li>Applicatio</li></ol>	16, Applicati	5180808.	Applicatio	Applicatio	Applicatio	Applicatio		Applicatio			`		Applicatio	Applicatio		Applicatio			Applicatio	, Applicati	Applicatio	Applicatio	Applicatio
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### ALIGNMENTS

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TOPOLOGY: linear	STRANDEDNESS: single	TYPE: nucleic acid	LENGTH: 287 base pairs	SEQUENCE CHARACTERISTICS:	INFORMATION FOR SEQ ID NO: 1:	TELEFAX: (212) 596-9090	TELEPHONE: (212) 596-9000	TELECOMMUNICATION INFORMATION:	REFERENCE/DOCKET NUMBER: DCB-1	REGISTRATION NUMBER: 27,794	NAME: Haley Jr., James F.	ATTORNEY/AGENT INFORMATION:	CLASSIFICATION: 435	FILING DATE: 06-APR-1995	APPLICATION NUMBER: US/08/418.071		SOFTWARE: Word Perfect 5.0	OPERATING SYSTEM: PC-DOS/MS-DOS	COMPUTER: IBM PC Compatible	MEDIUM TYPE: Floppy disk	COMPUTER READABLE FORM:			STATE: New York		STREET: 1251 Avenue of the Americas	ADDRESSEE: Fish & Neave	CORRESPONDENCE ADDRESS:	NUMBER OF SEQUENCES: 18	OF INVENTION:		Z			APPLICANT: Wu, Rey-Yuh	GENERAL INFORMATION:	5846705	<ol> <li>Application</li> </ol>	Sequence 1, Application US/08418071		XXXXXX	US-08-418-071-1 STANDARD; DNA; UNC; 287 BP.	

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  Matches
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                                       NAME/KEY: CDS
LOCATION: 2...
SEQUENCE 730 BP; 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5639634
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Banana SEQUENCE 287 BP; 98 A;
                                                                                                                                                  TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 TCATTAATGAAG 247
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DESCRIPTION:
HYPOTHETICAL:
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                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 730 base pairs
TYPE: nucleic acid
                                                                                                                                                                     TELEFAX: (312) 984-9740
                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1. CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/332,643
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                         FEATURE:
                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: CADHERIN
                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Fire STREET: Street Cliry: Chicago
                                                                                                                                                                                                     NAME: NO. 5639634and, Greta E. REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
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Similarity 100.0%;
12; Conservative
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Similarity 100.08;
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48 C; 76 G; 65 T; 0 OTHER.
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        Score 12;
Pred. No.
                                         C; 164 G;
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                                          180 T; 0 OTHER
          DB 1; L
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                                                       Query Match 63.2%;
Best Local Similarity 100.0%;
                                                                                           NAME/KEY: 'CDS
LOCATION: 2..730
SEQUENCE 730 BP; 209 A; 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 55, Application Sequence 55, Application Patent No. 5597725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-188-228-55
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 07/8/4/
APPLICATION NUMBER: US 07/8/4/
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E
NAME: No. 5597725and, Greta E
NAME: No. 5597725and, Greta E
              386 TTCATTAATGAA 397
                                                                                                                                                                                                            TELEFAX: (312) 474-04
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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 2 TTCATTAATGAA 13
                                                                                                                              MOLECULE TYPE: FEATURE:
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 730 base pairs
                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCATTAATGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
                                                                                                                                                     TOPOLOGY: .
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                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                    (312) 474-6300
(312) 474-0448
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                                                                                                                                                     linear
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                                                                                                                                         CDNA
                                                                                                                                                                single
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US/08188228
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                                            Score 12; DB 1;
Pred. No. 1.15e+01
0; Mismatches
                                                                                            C; 164 G; 180 T; 0 OTHER
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US-08-332-638-55

STANDARD; DNA; UNC;

730

Sequence 55, Application US/08332638

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Query Match
Best Local
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LOCATION: 2..730
SEQUENCE 730 BP; 209 A; 177 C; 164 G; 180 T; 0 OTHER.
                                                                                                                         Sequence 55, Application US/08188228 Sequence 55, Application US/08188228 Patent No. 5597725
                                                                                                                                                                                    XXXXXX
                                                                                                                                                                                                US-08-188-228-55 STANDARD; DNA; UNC; 730 BP
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                                                                                                                                                                                                                                                                                   386 TTCATTAATGAA 397
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Local Similarity 100.0%;
hes 12; Conservative
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/872,643
                                                                                                                                                                                                                                                         2 TTCATTAATGAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: NO. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                       NUMBER OF SEQUENCES: 6: CORRESPONDENCE ADDRESS:
                                                                                  APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND
                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 730 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/332,638 FILING DATE: 01-NOV-1994
             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
COMPUTER: IB
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Chicago
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INVENTION: CADHERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08332638
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Pred. No. 1.15e+01;
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Best Local S
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LOCATION: 2..730
SEQUENCE 730 BP; 209 A; 177
                                                                                                                                                                                                                                                                                 Sequence 49, Application US/08332643
Sequence 49, Application US/08332643
                                                                                                                                                                                                                                                                                                                             XXXXXX
                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                        US-08-332-643-49 STANDARD; DNA; UNC; 730
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                386 TTCATTAATGAA 397
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                                                                                                                                                                                                                                                                                                                                                                                                  13 TTCATTAATGAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 63.2%;
Local Similarity 100.0%;
les 12; Conservative
                                                                                   ADDREST STREET: STREET: STREET STREET Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/8:
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597723and, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                              NUMBER OF SECUENCES:
                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                         APPLICANT: Suzuki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/188,228 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .730 base pairs
                                                                                                                                                    Two First National Plaza, 20 South Clar!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                          Marshall, O'Toole, Gerstein, Murray & Bicknell
                                                                                                                                                                  Bicknel
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                                                                                                                                                                                                                                         Shintaro
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C; 164 G;

180 T; 0 OTHER

31340

Score 12; DB 1; Pred. No. 1.15e+01

Length 730; 0; Indels

Mismatches

0

Gaps

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BP

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Matches

RESULT

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Query Match
Best Local S
Matches 1
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FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: NO. 5639634and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30795

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750

TELEPAX: (312) 984-9740

TELEPAX: (252) 984-9740

TELEPAX: 25-3856

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

FUNCTH: 730 base pairs
                                                                                                                                                                                                                                                                                                                                                                              Sequence 55, Application US/08332638
Sequence 55, Application US/08332638
Patent No. 5646520
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 2..730
SEQUENCE 730 BP; 209 A; 177
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Local Similarity 100.0%;
hes 12; Conservative
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                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
           ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646/50and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/872,643
                                                                                                                                                                                                                                                   STREET: Chicago
CITY: Chicago
CTATE: Illinois
TISA
                                                                                                                                                                                                                                                                                                                               APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERII
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                        APPLICATION NUMBER: US 0 FILING DATE: 17 APR 1992 APPLICATION NUMBER: US/0
                                                                                                                                      APPLICATION NUMBER: FILING DATE: 01-NOV
                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCATTAATGAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 730 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                            60606
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                                                                                                                                      01-NOV-1994
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                                                                                                                                                     US/08/332,638
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Pred. No. 1.15e+01;
0; Mismatches 0
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                                      FEATURE:
                                               MOLECULE TYPE: DNA (genomic)
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LOCATION: 2..730
SEQUENCE 730 BP; 209 A; 177
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INFORMATION FOR SEQ ID NO:
                                                                                                                                           SEQUENCE CHARACTERISTICS
                                               FEATURE:
                                                            MOLECULE TYPE: CDNA
                                                                             TYPE: nucleic acid STRANDEDNESS: sing TOPOLOGY: linear
                               NAME/KEY: CDS
                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                         TELEPHONE: (312) 474-6300
                                                                                                                            LENGTH:
                                                                                                                          730 base pairs
                                                                                                                                                                                          (312) 474-0448
                                                                                             single
 C; 164 G; 180 T; 0 OTHER
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386 TTCATTAATGAA 397 Match 63.2%; Local Similarity 100.0%; 12; Conservative Score 12; DB 1; Pred. No. 1.15e+01 0; Mismatches Length 730 0; Indels 0 Gaps 0

13 TTCATTAATGAA 2

US-07-971-558-1 STANDARD; DNA; UNC; 1340 BP

Sequence 1, Application US/07971558 Sequence 1, Application US/07971558 Patent No. 5441736 GENERAL INFORMATION:
APPLICANT: GERLACH, GERALD F.
APPLICANT: WILLSON, PHILIP J.
APPLICANT: WILLSON, PHILIP J.
APPLICANT: ROSSI-CAMPOS, AMALIA
APPLICANT: POSTIER, ANDREW A.
APPLICANT: POSTIER, ANDREW A.
TITLE OF INVENTION: MEMBRANE LIPOPROTEIN A AND USES THEREOF STREET: DOUGLE CITY: PALO ALTO CALIFORNIA "INITED ST NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESSEE: ROBERTA L. ROBINS STREET: 635 BRYANT STREET

ZIP: 94301 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19921105
CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L. COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 COUNTRY: UNITED STATES OF AMERICA 94301 US/07/971,558

TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999 TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear LENGTH: 1340 base pairs <u>..</u>

NAME/KEY: CDS LOCATION: 158..1252 SEQUENCE 1340 BP; 502 A; 183 C; 265 G; 390 T; 0 OTHER

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Best Loc
Matches
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Best Local Similarity 100.0%;
Matches 12; Conservative
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                 Sequence 1, Application US/08984246
Sequence 1, Application US/08984246
Patent No. 5869307
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE 1521 BP; 357 A; 396 C; 429 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08753233 Sequence 1, Application US/08753233 Patent No. 5728568
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                                                                                                  US-08-984-246-1 STANDARD; DNA; UNC; 1521 BP
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                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5728568
GENERAL INFORMATION:
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8 AATGAACGATGC 19
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NAME: BIOWN, SCOTT A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sullivan, Franc
APPLICANT: Kriz, Ron
APPLICANT: Kumar, Ravindra
                                                                                                                  10
                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                            h 63.2%;
Similarity 100.0%;
12; Conservative
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                                                                                                                                                                                                                                                                                                                                    1521 base pairs
       Sullivan, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                            double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/753,233
                                                                                                                                                                                                            Score 12; DB 2; Leg
Pred. No. 1.15e+01;
0; Mismatches 0;
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Pred. No. 1.15e+01;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: G152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 49-8224
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
                                                                                                                                                                                                                                                   Sequence 1, Application US/08426236
Sequence 1, Application US/08426236
Patent No. 5629188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA SEQUENCE 1521 BP; 357 A; 396 C; 429 G; 339 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                      US-08-426-236-1 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                            XXXXX
                                                                                                                                                                                                                                                                                                                                                                                                         363 TCATTAATGAAG 374
                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 63.2%;
Local Similarity 100.0%;
ZIP: 02173
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                               12 TCATTAATGAAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                        NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
                                                                                                                                                                                           APPLICANT: Shiba, Kiyotaka
APPLICANT: Schimmel, Paul R.
APPLICANT: Ripmaster, Tracy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/984,246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kriz, Ron
APPLICANT: Kumar, Ravindra
TITLE OF INVENTION: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                   TITLE OF INVENTION: Human Alanyl-tRNA Synthetase Proteins. TITLE OF INVENTION: Nucleic Acids and Tester Strains Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                            STREET: Two Mil:
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brown, Scott
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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                                                                                     Massachusetts
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87 CambridgePark Drive
                                                                                                              Two Militia Drive
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Pred. No. 1.15e+01
0; Mismatches
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                                                                                                                            Smith & Reynolds, P.C
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Query Match 63.2%;
Best Local Similarity 100.0%;
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US-08-370-319C-12 STANDARD; DNA; UNC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 111..3014
SEQUENCE 3344 BP; 827 A; 823 C; 966 G; 728 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 TCATTAATGAAG 1
                                                        APPLICATION NUMBER: 08/272,351 FILING DATE: 8-JULY-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                           APPLICANT: Traversari, Catia: W lfel, Thomas; Coulie, Pierre; APPLICANT: Boon-Falleur, Thierry; De Plaen, Etienne TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
           ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 585609
                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  TITLE OF
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NAME: Brook, David E.
REGISTRATION NUMBER: 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA to mRNA
                                                                                                                     APPLICATION NUMBER: US/08/370,319C FILING DATE: 10-JANUARY-1995
                                                                                                                                                       OPERATING SYSTEM: PC-
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                            STATE:
NAME: Hanson, No. 5 REGISTRATION NUMBER:
                                             APPLICATION NUMBER:
                                                                                                                                                                                 COMPUTER:
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STRANDEDNESS: doub
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New York City
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2, Application US/08370319C
5856091
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Pred. No.
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No. 1.15e+01
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2713 GTTCATTAATGA 2724
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SEQUENCE CHARACTERISTICS:
14 GTTCATTAATGA 3
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                                                                                                                                                                               FEATURE:
                                                                                                                              OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                   LENGTH:
                                                                     63.28;
Similarity 100.08;
                                                          Conservative
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Pred. No. 1.
0; Mismatcl
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Sequence 54, Application PC/TUS9401149 Sequence 54, Application PC/TUS9401149 PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 387
APPLICATION NUMBER: 28-JUL-1989 PCT-US94-01149-54 STANDARD; DNA; UNC; 7616 BP GENERAL INFORMATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 1.
FILING DATE: 05-NOV-1993
PRIOR APPLICATION DATA: SOFTWARE: PatentIn Relu CURRENT APPLICATION DATA: APPLICATION NUMBER: PC FILING DATE: 18-FEB-1992 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER: APPLICATION NUMBER: US 013,415 FILING DATE: 01-FEB-1993 PRIOR APPLICATION DATA: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk TITLE OF INVENTION: Vaccinal Polypeptides NUMBER OF SEQUENCES: 72 CORRESPONDENCE ADDRESS: APPLICANT: Shatzman, Allan APPLICANT: Scott, Miller APPLICANT: Dillon, Susan B APPLICANT: Kane, James APPLICATION NUMBER: US 108,914 FILING DATE: 18-AUG-1993 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS CLASSIFICATION: FILING DATE CITY: King of Prussia STREET: ADDRESSEE: SmithKline Beecham Corporation - Corporate ADDRESSEE: Patents 19406-2799 Pennsylvania U.S. USA PatentIn Release #1.0, Version Mailcode UW2220 -James US 387,200 US 751,896 US 149,150 US 837,773 PCT/US94/01149 709 Swedeland

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INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 7616 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
COMPANDEDNESS: double
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LOCATION: 1879..2790
SEQUENCE 7616 BP; 1913 A; 1926 C; 1936 G; 1841 T; 0 OTHER.
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Sequence 10,
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                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
APPLICATION NUMBER: US 08/019,940
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5443
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Local Similarity 100.08;
nes 12; Conservation
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APPLICANT: Fu, Ying-Hui
APPLICANT: Friedman, David L.
APPLICANT: Pizzuti, Antonio
APPLICANT: Fenwick, Faymond G.
APPLICANT: Fenwick, Raymond G.
TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
NUMBER OF SEQUENCES: 13
CORRESPONNERS: TALLIFICE.
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 30-AUG-1984
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 77010-3095
                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: dou TOPOLOGY: unknown
                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                       CITY: Houston
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                                                                                                                                                                                                                            Texas
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Application US/08484044
                                                                                                                                                                                                                                                  : Fulbright & Jaworski, L.L.P
1301 McKinney, Suite 5100
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Pred. No. 1.15e+01;
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                                                                                                                                             Version #1
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Matches 1:
    Query Match 57.9%;
Best Local Similarity 100.0%;
Matches 11; Conservative
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                                                                                      ANTI-SENSE; I
SEQUENCE 872 BP;
                                                   STRANCE
TOPOLOGY:
MOLECULE TYPE: DNA (SECONDETICAL: YES
NOTI-SENSE; NO
NOTI-SENSE
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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NAME: Price, D.Douglas
REGISTRATION UNMBER: 24,514
REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,983A
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dayan, Alain APPLICANT: Bertrand, Richard
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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TELEFAX: 202 393-5350
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ZIP: 20004
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CITY: Washington D.C.
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DEDNESS: double
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# ALIGNMENTS

FEATURES Source	RESULT 1 LOCUS DEFINITION ACCESSION NID VERSION VERSION SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT
Contact: Kyeong Tae Pih Department of Plant Molecular Biology Gyeongsang National Univ., Plant Molecular Biology and Biotechnology Research Center Tinju, Kyoungnam 660-701, Korea Tel: 82-591-751-5193 Fax: 82-591-759-9363 Email: ihhwang@nongae.gsnu.ac.kr Seg primer: T3 Seg primer: T3 Location/Qualifiers 1. 306 /organism="Arabidopsis thaliana" /strain="Columbia" /note="Subtracted cDNA library from salt(NaCl)-treated	AA389827  OS195 NaCl-treated Arabidopsis subtraction library Arabidopsis thaliana cDNA 5' similar to ERECTA homologue, mRNA sequence. AA389827  92042813  EST  EST  AA389827.1 GI:2042813  EST  thale cress. Arabidopsis thaliana ELWARYOta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatcophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.  1 (bases 1 to 306) Pih,K.T., Park,J.M., Jang,H.J., Kang,S.G., Piao,H.L. and Hwang,I. EST of salt inducible mRNA in Arabidopsis thaliana Unpublished (1997) On Sep 12, 1996 this sequence version replaced gi:1395018.

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1 (bases 1 to 316)
Pih.K.T., Park, J.M., Jang, H.J., Kang, S.G., Piao, H.L. and Hwang, I. EST of salt inducible mRNA in Arabidopsis thaliana Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1394226.
                AA389812 355 bp mRNA EST 23-APR-1997 0S172 NaC1-treated Arabidopsis subtraction library Arabidopsis thaliana cDNA 5', mRNA sequence.

AA389812
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Department of Plant Molecular Biology
Gyeongsang National Univ., Plant Molec
Biotechnology Research Center
Jinju, Kyoungnam 660-701, Korea
Tel: 82-591-751-5193
Fax: 82-591-759-9363
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/db_xref="taxon:3702"
/clone_lib="NaCl-treated Arabidopsis subtraction library"
/dev_stage="7 day-old"
/dev_stage="7 day-old"
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  Sequence
Plate: 32
                                                      401 Queen Anne Avenue North, Seattle, WA 98109, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                   Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                              Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Furlong, J., Shaker, R., Schmidt, S., Traicoff, R. and Hood, L.E. Construction of a Characterized Clone Resource for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ231915 367 bp DNA GSS 25-SEP-19
HS_3243_B1_A11_MR CIT Approved Human Genomic Sperm Library sapiens genomic clone Plate=3243 Col=21 Row=B, genomic surv
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Department of Plant Molecular Biology
Gyeongsang National Univ., Plant Molecular Biology
Biotechnology Research Center
Jinju, Kyoungnam 660-701, Korea
Tel: 82-591-751-5193
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Pih,K.T., Park,J.M., Jang,H.J., Kang,S.G., Piao,H.L. and Hwang,I.
EST of salt inducible mRNA in Arabidopsis thaliana
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1394805.
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 367)
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Similarity 100.0%;
14; Conservative
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jwallace@u.washington.edu
ce Tagged Connector
3243 row: B column: 21
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/db_xref="taxon:3702"
/clone_lib="NaCl-treated Arabidopsis subtraction library"
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80 c
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/strain="Columbia"
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High qu
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Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; Violales; Salicaceae; Populus.
1 (bases 1 to 397)
Ctaking Toman C ( Variagon 1 Unitabor M Bobdon)
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AI164965
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Royal Institute of Technology (KTH)
Teknikringen 34, S-100 44 STOCKHOLM,
Tel: +46 8 790 8287
Fax: +46 8 24 54 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Sterky F
Department of Biotechnology
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Similarity 100.0%;
14; Conservation
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n quality sequence stop: 397.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 fredrik@biochem.kth.se
                                                             /Organism="Populus tremula x Populus tremuloides" / note="Vector: pBluescript SK; Site_1: Sali; Site_2: Noti. Cambial region tissues, including developing xylem, the meristematic cambial zone and the developing and mature phloem, was harvested from 1.5 m actively growing trees. CDNA was prepared and cloned into lambda gt22a. DNA was isolated and subcloned into pBluescript SK using Sali and Noti restriction enzymes."
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E-Coli DH10B"
/clone_lib-"Hybrid aspen plasmid library"
/tissue_type="Cambial region"
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/clone_lib="CIT Approved Human Genomic
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Best Local Similarity 100.0%;
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Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
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Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
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A069p23u Hybrid aspen plasmid library Populus tremula
tremulcides cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Biotechnology
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Similarity 100.0%;
14; Conservative
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/note="vector: pBluescript SK; Site_1: SalI; Site_2: NotI;
Cambial region tissues, including developing xylem, the
meristematic cambial zone and the developing and mature
phloem, was harvested from 1.5 m actively growing trees.
cDNA was prepared and cloned into lambda gt22a. DNA was
isolated and subcloned into pBluescript SK using SalI and
NotI restriction enzymes."
/db_xref="taxon:47664"
/map="824A05; 12; 12924.13-12924.31"
/clone_lib="Hybrid aspen plasmid library"
/tissue_type="Cambial region"
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80 c 113 g
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/lab_host="E.coli"
75 c 116 g 62 t 1 other
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Pred. No.
    Score 14; DB 23; L
Pred. No. 9.42e-03;
0; Mismatches 0;
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                                                           Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC, Hood
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle,
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: Jwallace@u.washington.edu
                                                                                                                                                   EST
                                                                                                                                                                                                                                 R65414 406
13918 Lambda-PRL2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ132767 406 bp DNA GSS 22-SEP-1998
HS_3064_B2_H01_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3064 Col=2 Row=P, genomic survey
            1 (bases 1 to 406)
Newman, T., deBruijn, F.J.,
McIntosh, L., Ohlrogge, J.,
                                                                                                                                thale cress.
                                                                                                                                                                 R65414.1
                                                                                                                                                                                                                   sequence.
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Similarity 100.0%;
14; Conservative
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                                                                                                                                                                   GI:937881
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E-Coli DH10B"
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/clone_lib="CIT Approved Human Genomic
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Arabidopsis thaliana
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Pred. No. 9.42e-03;
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             Green, P., Keegstra, K., Ken
Raikhel, N., Somerville, S.,
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On Apr 14,
                                                                                                     Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Beni
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
On Oct 17, 1997 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 416)
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Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Tel: 517-353-0854
Fax: 517-353-9168
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MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
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cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution
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primer: T7 dye primer.
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/db_xref="taxon:3702"
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Best Local Similarity 100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mz92a02.yl Soares mouse lymph node NbMLN IMAGE:720842 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 531)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,G., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
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Seq primer: -40m13 f
High quality sequence
                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the sequence of the contact of the co
                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
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AI464854.1 GI:4318884
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www-bio.llnl.gov/bbrp/image/image.html
                                  correct orientation)
Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer: -40m13 fwd. ET from Amersham
h quality sequence stop: 413.
    Location/Qualifiers
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314 286 1810
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to vector length is 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "/db_xref="taxon:9606"
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polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
118 c 91
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/clone="IMAGE:1638997"
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Pred. No. 9.42e-03;
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Mus musculus cDNA clone
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g1700787
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Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 550)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -40RP from Gibco
High quality sequence stop:
Location/Qualifiers
                                                                                                                          FMax: 314 400 1010
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                    WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996) On Sep 12, 1996 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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Similarity 100.0%;
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                                                                                                 primer: -28M13 rev2 from Amersham
                                                                              quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
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/organism="Mus musculus"
/strain="C57BL/6J"
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91 c 105 g
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/clone="IMAGE:720842"
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/strain="C57BL/6J"
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Pred. No. 9.42e-03;
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Best Local Similarity 100.0%;
Matches 14; Conservative
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B95213 165 bp DNA GSS 25-JUN-199 CIT-HSP-2172J8.TF CIT-HSP Homo sapiens genomic clone 2172J8,
                                                                                                                                                                                                                                                                                                                                                                         Submitted (28-SEP-1998) Molecular Biology, Sidney Kimmel Cancer Center, 10835 Altman Row, San Diego, CA 92121, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l (bases 1 to 1154)
Wong,R.M.Y. and McClelland,M.
End Sequences of Salmonella typhimurium LT2 Lambda DASHII Clones,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium. Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF094894 1154 bp DNA GSS Salmonella typhimurium clone 506-T7, Li-Cor
                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1154)
Wong, R.M.Y. and McClelland, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF094894.1 GI:4322736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    survey sequence.
                                                                                                                                                                        73.7%;
Similarity 100.0%;
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                                                                                                                                                        Conservative
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/dev_stage="4 weeks"
/lab_host="DH10B"
a 98 c 127 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

/db_xref="taxon:1090"
/clone="IMAGE:596874"
                                                                                                                                                                                                                                                                                          /organism="Salmonella typhimurium"
/strain="LT2"
/db_xref="taxon:602"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="end sequence from lambda clone"
/clone="506-T7, Li-Cor"
322 c 299 g 253 t
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Pred.
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Pred. No. 9.42e-03;
0; Mismatches 0;
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                                                                                                                                                     e 14; DB 41; Le
. No. 9.42e-03;
Mismatches 0;
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B95213.1
                                                                Tumor Gene Index
Unpublished (1997)
On Apr 14, 1993 this sequence version
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 176)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA national Cancer Institute)
                                                                                                                                                                                                                                                                                                                      AA262179 ' 176 bp n
zs25b04.s1 NCI_CGAP_GCB1
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Clones are available from
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
B95213
               Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                           EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21;
Class: BAC ends.
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 165)
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Similarity 100.0%;
13; Conservative
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/clone="2172J8"
/clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Sperm"
28 c 35 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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                                                                                                                                                                                                                                                          GI:1898516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13;
Pred. No.
0; Misma
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2.66e-01;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA210523 217 bp mRNA EST 19-FEB-1997 mu30d06.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:640907 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1370 Std Error: 0.00 Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 150.
                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                           Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 217)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g1807761
AA210523.1 GI:1807761
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                                                       MGI:392899
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Similarity 100.0%;
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primer: -28m13 rev2 ET from Amersham
h quality sequence stop: 137.
    Location/Qualifiers
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/tissue_type="germinal center B cell"
/lab_host="DH10B"
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                  148 TCGTTCATTAATG 160
16 TCGTTCATTAATG 4
                                                        h 68.4%;
Similarity 100.0%;
13; Conservative
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                                                                                                                              /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
a 25 c 37 g
                                                                                                                                                                                                                                                                                                                    and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two
                                                                                                                                                                                                                                                 rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                           (Pharmacia), digested with Not I and cloned into the Not I
                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                          /sex="male"
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                                                                                                                                                                                                                                     /db_xref="taxon:10090"
                                                        Score 13; DB 9; I
Pred. No. 2.66e-01;
0; Mismatches C
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Search completed: Sat Nov 27 15:13:06 1999 Job time : 236 secs.

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	Query  Match Length DB ID Description Pred. No.	Result No. Score
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	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.	Pred. No. score gre and is de
	Mean 6.028; Variance 3.018; scale 1.997	Statistics:
	17.gb_bal 18.gb_ba2 19.gb_htg1 20.gb_htg2 21.gb_in1	
	embl58 1:em_ba1 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2 7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph 13:em_pl 14:em_ro 15:em_sts 16:em_vi Genbanklil	Database:
	Minimum Match 0% Listing first 45 summaries	Post-processing:
	646147 seqs, 1385953633 bases x 2	Searched:
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	1 GTTACAAATATTAAAGAAG 19 CAATGTTTATAATTTCTTC	N.A. Sequence: Comp:
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	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	Relea Copyr
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## ALIGNMENTS

			CDS	90:0	gene		source	FEATURES			JOURNAL	TITLE	AUTHORS	REFERENCE	JOURNAL		TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	NID .	ACCESSION	DEFINITION	RESULT 1
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AF034076 HUMMCCPA04 ATT18B16 I05615 AB019232 HS248E1 AC006145 HS171N11 AC002449 HS28BM22 G14874 AF010534

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Cloning and characterization of the novel gene for mast cell
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EVVAVFQPHTFSRTQAFLNEFAESISKADRVFLCEIFGSIRENTGALTIQDLIDKIEG
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                                         DNA chromosome 4, BAC
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Bevan, M., Benes, V., Rechmann, S., Borkova, D., Ansorge, W.,
Bancroft, I., Mewes, H.W., Mayer, K. and Schueller, C.
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  6638. .6731,6805. .6913,7005. .7053,7174. .7190,7281. .7307,
  7733. .7790,7870. .8681,8733. .11411))
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/gene="T18B16.10"
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/gene="T18B16.10"
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                                                                                                                                                                                                                                                                                                                                                                                                  /note="similarty to hypothetical protein YIL106w, Saccharomyces cerevisiae, PIR2:S48466; Contains ATP/GTP-binding site motif A (P-loop), pos.38-46; contains EST gb:H77164, T04732"
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/gene="T18B16.10"
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ILDMSKTSLPELADTIADVVNLNKLLLRNCSLIEELPSIEKETHLEVEDVSGGTKLKN
INGSFGEMSYLHEVNLSETNLSELPDKISELSNLKELIIRKCSKLKTLPLLEKLTNL
INGSFGEMSYLHEVNLSETNLSELPDKISELSNLKELIIRKCSKLKTLPLLEKLTNL
IFDVSGCTELEFIEGSFENLSCLHKVNLSETNLGELPNKISELSNLKELILRNCSKLK
ALPNLEKLTHLVIFDVSGCTNLDKIEESFESMSYLCESILCSSKRIVLADSSCIERDQ
MSQIKECLTSKSEGSSFSNVGEKTREKLLYHGNRYRVLDPEVPLNIDIVDIKRSTDLK
TEYLAKAETVSLAENGSKSVSSLFDELQMSVKGCWEERCKNMDVLFESDEQLEKEKS
SSPSLQTIMISNIPLLTSLYSSKGGFIFKNLKKLSVDCCPSIKWLFPEIPDNLEILRV
KFCDKLERLFEVKAGELSKLRKHLLDLPVLSVLGANFPNLEKCTIEKCPKLKAREDE
                                                                     complement(6914. .7004)
/gene="T18B16.20"
/number=5
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DDFFKNMTQLQSLNLSGLAIKSSPSTIEKLSMLRCFILRHCSELQDLPNFIVETRKLE
VIDIHGARKLESYFDRVKDWKDYKGKNKNFAQLQLLEHLDFSETKIIRLPIFHLKDST
/gene="T18B16.20"
                                                                                                                                                                                    complement(6805.
/gene="T18B16.20"
                                                                                                                                                                                                                                                                  complement(6732.
/gene="T18B16.20"
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/gene="T18B16.20"
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/gene="T18B16.20"
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/gene="T18B16.20"
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GTLTEFCTPENCSTMTAGPKYEYRWADGVQIKKPIEVSAPKYVEYLMDWIETQLDDET
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GGDKRKGLGKIILIDDMIQTIQSKKKNITTIIASGNRLRREVHGKFFEKPEMQDLEVV
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NPVLQLSYELLKPDETVKRPVIACFWHILDFYKYSGCAYYRDLIVHWMLEGYFDPVKS
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Note: remainder of annotations omitted.

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Best Local :
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105615
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yasukazu Nakamura, Kazusa DNA Research Institute, Laborator Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, Fax:+81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
1. (bases 1 to 80818)
                          HS248E1 84107 bp DNA PRI 24-JUL-1998 Human DNA sequence from clone 248E1 on chromosome 6q23.1-23.: Contains DOPAMINE-BETA-MONOOXYGENASE PRECURSOR, EF-1-ALPHA-2 pseudogene EST GSS and CA repeat, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel HIV proteins and peptides useful in prophylaxis or therapy of AIDS Patent: Ep 0306219-A2 21 08 MAR-1989; Location/Qualifiers
                  pseudogene
AL023578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Structural Analysis of Arabidopsis thaliana Chromosome 3. Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB019232 80818 bp
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakamura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone:MIL23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB019232.1 GI:3869071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rusche, J.R., Putney, S.D., Javaher Lynn, D., Petro, J. and O'Keeffe, T.
                                                                                                                                                                                                                                                                            84.2%;
Similarity 100.0%;
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14707 c
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/chromosome="3"
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188 c 188 g
                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MIL23"
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Pred. No. 2.36e+01;
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Pred. No.
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2.36e+01;
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3, P1 clone: MIL23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL Submitted (24-JUL-1998) E-mail enquiries: humquery@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Jun 16, 1998 this sequence version replaced gi:318366.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above. This sequence is the
entire insert of clone 248EI. This sequence has been finished
according to sequence map criteria as follows. An attempt is made
to resolve.all sequencing problems, such as compressions and
repeats, but not necessarily within known annotated human repeat
sequence elements (e.g. Alu). Where the sequence is ambiguous,
there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of
human chromosome 6, constructed by the Sanger Centre Chromosome 6
Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer Institute by the group of Pieter de Jong. For furthe details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/HGP/Chr6
248E1 is from the library RPCI1 constructed at the Roswell Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tubby,B
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                                                                                                                                                                                                                                                     /note="MERIB repeat: matches 337.
complement(11062. .11329)
                                                                                                                                                                                                                                                                                        9695. .9918
/note="MIR repeat: matches 21.
complement(10955. .11329)
                                                                                                                                                                                                                                                                                                                                                                         complement(5748. .6186)
/note="MLTIC repeat: matches 466.
complement(8135. .8435)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3308. .3428
/note="MIR repeat: matches 84.
                                                                                                             12896. .18811
/gene-"dJ248E1.1"
                                                                                                                                                                                                                  /note="MERIA repeat: matches
11239. .11623
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(52. .405)
                                                                                                                                                                             12035.
                              /note="match: protein P09172"
                                                                                            join(<12896.
                                                                                                                                                                                                                                                                                                                                                                                                                                   3550. .3629
/note="2 copies 40 mer 89% conserved"
                                                       'gene="dJ248E1.1"
                                                                                                                                                  note="L1PA2 repeat:
                                                                                                                                                                                       /note="match: GSS B93863 clone 2170K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1308. .1622
/note="Alusg repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="13 copies 2 mer aa 92% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Alux repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_lib="RPCI1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             map="q23.1-23.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="248E1"
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db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                           note-"AluY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="MLT1A1 repeat: matches 365. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:3228200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .84107
                                                                                                                                                                                                                                                                                                                                        Alux repeat: matches 301. .1 of consensus" 9918
                                                                                            .13075,13375. .13477,17393. .17559
                                                                                                                                                      matches
                                                                                                                                                                                                                                     274.
                                                                                                                                                      418.
                                                                                                                                                                                                                                                                                                                   .262 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="17 copies 2 mer aa 85% conserved" complement(30532. .31375) /note="L1PA10 repeat: matches 890. .1 of consensus" complement(31234. .36025)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Alusq repeat: matches 302. .1 of consensus" complement(28733. .28872) /note="match: 3' EST N67273 clone 286400" 28865. .28898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"match: multiple ESTs; match: N48407 AA424680 N99599 C01809 AA715253; match: AA424680 AA317005 W45115 AA909388" complement(27556. .27858)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(15810. .16171)
/note="MLTIA1 repeat: matches 365. .1 of consensus"
complement(16173. .16253)
/note="MIR repeat: matches 98. .18 of consensus"
complement(16371. .16625)
/gene="dJ248E1.1"
                                                                                       /note="match: multiple ESTs; match: AA604597 AA994351 W46980 N98695 AA530889; match: T17142 R32545 AA23598 AA905700 AA618502; match: AA907610 AA233672 W47081 AA194173; match: AA965575 AA928115 AA194174 AA424574;
                                                                                                                                                                                                                                                                          /note="16 copies 2 mer ag 97% conserved"
complement(42052. .42871)
                                                                                                                                                                                                                                                                                                                                                                                    /note="MER2 repeat: matches 327. .49 of consensus" complement(38118. .38221) /note="L1MB5 repeat: matches 113. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: 5' EST D59397 clone GEN-027G03"
complement(20216. .20503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18699. .25836
                                            match: N26240 AA227906
45844. .45919
                                                                                                                                                                                                                                                                                                                                         complement(38408. .39028)
/note="L1 repeat: matches 5021. .4387 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="LIME2 repeat: matches 351..110 of consensus"
complement(37079..37437)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1 repeat: matches 5390. .631 of consensus"
complement(36534. .36770)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(14080. .14212)
/note="MIR2 repeat: matches 146. .4 of consensus"
complement(15661. .15807)
/note="MIR repeat: matches 257. .97 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="VEPVIQRGHESLVHHILLYQCSNNFNDSVLESGHECYHPNNPDA
FLTCETVIFAWAIGGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEEGLIDNSGL
RLFYTMDIRKYDAGYIEAGLMVSLFHTIPPGNPEFQSEGHCTLECLEEALEAEKPSGI
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/protein_id="CAA19040.1"
/db_xref="PID:e1312801"
                                                                                                                                                                                                                               /note="L1PA15 repeat: matches 904. .91 of consensus"
13170. .43302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluSg repeat: matches 291. .3 of consensus"
22923. .23570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVFAVLLHAHLAGRGIRLRHFRKGKEMKLLAYDDDFDFNFQEFQYLKEEQTILP'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="PID:g33555
                                                                                                                                                                                                        note="AluJo repeat: matches 1. .132 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="MLT1A1 repeat: matches 363. .4 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="MIR repeat: matches 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: Z23591 STS containing
:6503. .16535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="SPTREMBL:075647"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="16 copies 2 mer gt 100% conserved; differs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6. .16873
e="MIR2_repeat: matches 57.
                                                                                                                                                                                     .45435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .18273
                       copies 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                      .38085
                         mer
                         91% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .143 of consensus
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Eukaryota; Metazoa; Chordata; C:
Eutheria; Primates; Catarrhini;
1 (bases 1 to 144659)
                                                                    Homo sapiens
                                                                                                                                   AC006145.2
                                                                                                                                                             g4454525
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Similarity 100.0%;
16; Conservative
                                                                                              numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 253...
complement(65534...65636)
/note="MIR repeat: matches 140...
67867...68129
/note="AluJb repeat: matches 40...
complement(68162...69508)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(68162.
/gene="dJ248E1.2"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="3 copies 19 mer 84% conserved"
46880. .46977
/note="MER42c repeat: matches 1436. .1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="THE1B repeat: matches 3.
complement(64511 . 64605)
/note="MIR repeat: matches 190.
complement(65112 . 65275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="LIMD2 repeat: matches 797.complement(58257...58819)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluJo repeat: matches 302. 55798. .56085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 124.complement(52978...53258)
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complement(48895. .49097)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47400. .47501
/note="2 copies 51 mer 85% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(60488.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MER5A repeat: matches 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="match: Z79076 chromosome 6 HindIII fragment"
59224. .59349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-"L1MD2
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50006. .50087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="Alusq repeat: matches 303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluY repeat: matches 118. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="match: Z79094 chromosome 6 HindIII fragment"
                                                                                                                                                                                                                        144659 bp DNA PRI 18-MAR-199
ns PAC clone DJ0560014 from 7q21.1-q21.2, complete
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Pred. No. 2.36e+01;
0; Mismatches 0;
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                       Craniata; Ve
i; Hominidae;
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                                            Vertebrata; Mammalia;
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                           A run of A's extends from base 112507 to 112528 of DJ0560014. The data through this region differs in the number of A's represented. The submitted sequence reflects the longest run of A's in any one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-MAR-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Mar 19, 1999 this sequence version replaced gi:3980538.
SUBMITTED BY: WUGSC
                                                                                                                                                                                                          subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone was derived from human PAC library RPCI-4, prepared by pleter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from the companion of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between neighboring data submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MO 63108,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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377. .2556
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14677. .14878
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17966. .18707
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Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Mar 23, 1999 this sequence version replaced gi:4375918.
                                       Submitted (09-MAR-1999) Wellcome Trust Genome Campus, Hinxton,
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 155582)
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HTG; HTGS_PHASE1.
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26714. .27006
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22941. .24161
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25226. .25301
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24173. .25137
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Genome Sequencing Center
Department of Genetics
Washington University
St. Louis WO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu
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The sequence of H. sapiens
Unpublished (1997)
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Human PAC clone DJ404K21 from Xq23, complete sequence.
AC002449
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Submitted (20-AUG-1997) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 173767)
Waterston, R.
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AC002449.1
                                                                                                                                                                                                              SUBMITTED BY:
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Vertebrata; Mammalia;
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This record will be updated with the finished sequence as soon as it is available and the accession number will
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sutterer, C and Fronick, B. iens PAC clone DJ404K21
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The clone sequenced to the left is H\_DJ290B04. The actual start of this clone is at base position 1 of DJ404K21; actual end is at 173767 of DJ404K21. This clone is part of an unanchored island, This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate (NID: 9995449) This clone contains STS's sWXD757 (NID:g405440) and sWXD512 orientation is unknown. SOURCE INFORMATION: MAPPING INFORMATION: confirmed by from Genome Systems, Inc. (http://www.genomesystems.com). complement(11616.
/rpt\_family="MER"
complement(14472.
/rpt\_family="L1" /rpt\_family="L1"
complement(11434.
/rpt\_family="MER" /rpt\_family="L1"
complement(11071. /rpt\_family-"ALU" complement(7833. /rpt\_family-"L1" 7187. .7448 /organism="Homo sapiens" /db\_xref="taxon:9606" /chromosome="X" Location/Qualifiers /clone\_lib="RPCI-3" /clone="DJ404K21" rpt\_family="THR" \_family="MER" \_\_family="THR"
\_\_818" restriction digest. \_family-"ALU" family-"MER" .ement(8198 \_family="ALU" y="MER" .9670) .11641) .11286) .11593) repeat\_region misc\_feature repeat\_region /rpt\_family="L1"
complement(51533.
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complement(52389. complement(49482.
/rpt\_family="ALU" /rpt\_family="ALU" complement(45972. /rpt\_3534 /rpt\_family="L1" 36463. .37291 complement(30468. /rpt\_family="L1" /rpt\_1 18756. complement(14833. /rpt\_family="L1" 15777. .15808 complement(51436 complement (45130 complement (41461 /rpt\_family="L1" 41227. .41458 complement(39829 complement(34006. /rpt\_family="L1" 25871. .25936 44494 31050. .31156 complement(24561 18450 rpt\_family="ALU" /rpt\_family="L1" /rpt\_family="L1" /rpt\_family-"L1" 'note="match to EST R00201 (NID:g749937) ye71f11.r1" /rpt\_family="L1" /rpt\_family="L1" rpt\_family-"L1" /rpt\_family="L1"
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IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coll, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments. Unfinished: dJ288M22 Contig_ID: 01539 acc- Length:
17052 bp Unfinished: dJ288M22 Contig_ID: 00927 acc- Length:
47937 bp Unfinished: dJ288M22 Contig_ID: 00927 acc- Length:
4863 bp Unfinished: dJ288M22 Contig_ID: 01555 acc- Length:
1865 bp Unfinished: dJ288M22 Contig_ID: 01555 acc- Length:
1865 bp Unfinished: dJ288M22 Contig_ID: 01555 acc- Length:
1865 bp Unfinished: dJ288M22 Contig_ID: 01800 acc- Length: 1210 bp
Unfinished: dJ288M22 Contig_ID: 01180 acc- Length: 1288 bp
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Unfinished: dJ288M22 Contig_ID: 01180 acc- Length: 1281 bp
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                                                                                                                                                                                                                                                                                                                                                           Submitted (18-FEB-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Query Match 84.2%;
Best Local Similarity 100.0%;
Matches 16; Conservative
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Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

[] (basés 1 to 250)
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PCR Profile:
                                                                                                                                                                                                                                                                                                                    Primer A: TACAGCAAAACTCATGGAAAGC Primer B: TCCTGTGAACATCATTATGGTTT
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                                                                                                                                                                                                                                                                                                                                                                                    myers@shgc.stanford.edu
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul
                                                                                                                                                  Polymerization:
PCR Cycles:
                                                                                                                                                                                            Annealing:
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2 (bases 1 to 429)
5u,X.z. and Wellems,T.E.
Direct Submission
Submitted (27-JUN-1997) NIAID-Laboratory of Parasitic Diseases,
NIH, Bethesda, MD 20892, USA
Location/Qualifiers
Chloroplast Peumus boldus
                                                                                                                                                                                                                                                                                                                                                                                                                            Toward a high-resolution Plasmodium falciparum linkage map: polymorphic markers from hundreds of simple sequence repeat Genomics 33 (3), 430-444 (1996) 96299638
                                                           protein, intron sequence. AF127454
                                                                                   AF127454 921 bp DN
Peumus boldus rpl16 gene,
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1 (bases 1 to 429)
Su,X.z. and Wellems,T.E.
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Similarity 100.0%;
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/db_xref="taxon:5833"
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Best Local Similarity 100.0%;
Matches 15; Conservative
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Sherrington,R., Rogaev,E.I., Liang,Y., Rogaeva,E.A., Levesque,G., Ikeda,M., Chi,H., Lin,C., Li,G., Holman,K. et,al. Cloning of a gene bearing missense mutations in early-onset familial Alzheimer's disease
Nature, 375 (6534), 754-760 (1995)
                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                   St George-Hyslop,P.H.

Genomic structure, promoter sequence, and alternative splicing the presentlin-1 gene associated with early onset Alzheimer's
                                                                                                                                                                                                                                                                                       2 (bases 1 to 1003)
Rogaev,E.I., Sherrington,R., Rogaeva,E.I.,
Ikeda,M., Tsuda,T., Rogaeva,E., Chi,H., Hol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-FEB-1999) Biology, Univ. of Missouri-St. Louis, 8001
Natural Bridge Rd., St. Louis, MO 63121, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Circumscription and phylogeny and morphological data Unpublished
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1 (bases 1 to 921)
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Direct Submission
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                                              /map="14q24.3"
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                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PAC clone RPCI 54D12"
/dev_stage="adult"
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/gene="PS1"
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/db_xref="taxon:63812"
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    Levesque, G., Liang, Y.,
Holman, K., Rommens, J.M. ε

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Best Local Similarity 100.0%;
Matches 15; Conservative
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Direct Submission
Submitted (28-NOV-1996) A.L. Maddison, Scottish Crop Research
Submitted (28-NOV-1996) A.L. Maddison, Scottish Crop Research
Submitted (28-NOV-1996) A.L. Maddison, Scottish Crop Research
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Bournay, A.S., Hedley
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x95820.1 GI:1695191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bournay, A.S., Hedley, P.E., Maddison, A., Waugh, R. and Machray, G.C. Exon skipping induced by cold stress in a potato invertase gene
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
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3 (bases 1 to 1911)
Maddison,A.L.
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                                                                                                                               /codon_start=2
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1771. .1892
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1762. .1770
                                                                                                                                                                                                                                                                                                      /organism="Solanum tuberosum"
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<1. .20
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188 c
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EC_number="3.2.1.26"

/note="beta-fructofuranosidase"
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                 translation-"PKNWINDPNAPMYYNG"
                                                                                                                   _xref="SPTREMBL:Q43172"
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Pred. No. 8.82e+01;
0; Mismatches 0
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a 266 c
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Search completed: Sat Nov 27 15:19:43 1999 Job time: 253 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Nov 27 15:25:27 1999; MasPar time 0.62 Seconds
90.461 Million cell updates/sec

Tabular output not generated.

Title: >US-09-103-287-6
Description: (1-19) from US09103287.seq
Perfect Score: 19
N.A. Sequence: 1 GTTACAAATATTTATAAAGAAG 19
Comp: CAATGTTTATATATTTCTTC

Scoring table: TABLE jmetric
Gap 60

Nmatch STD: Dbase 0; Query 0

Searched: 1052 seqs, 1486975 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: HIV-NA8

HIV-NA8 1:H\_PRI 2:H\_UNA 3:H\_VIR

Statistics: Mean 7.179; Variance 1.586; scale 4.525

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 2 2 3 3 3 3 3 4 4 4 4 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
100000000000000000000000000000000000000	Score
5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	% Query Match
1396 3983 42983 4684 4684 4687 1773 2583 312583 31773 1179 9170 1119 9170 11512 1512 1512 1522 1550	Length
<b></b>	BG
HIVNH52 HIVSF2B13 HIVSC HIVP896 HIVOYI HIVGESF HIVGESF HIVGESF HIVZCAM4E HIVZCAM4E HIVZCAM4E HIVZCAM40E HIVZDB08 HIVZDB08 HIVZDB08 HIVZDB08 HIVZDB08 HIVZDB08 HIVZDB08 HIVZDB08 HIVZDB08	ID
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## ALIGNMENTS

RESULT 2 LOCUS DEFINITION	Db 1100 tt    Qy 2 TT	Query Match Best Local Matches	pept pept.ps pept.ps pept pept pept pept ORIGIN	FEATURES pept pept.ps	TITLE JOURNAL STANDARD COMMENT	LOCUS DEFINITION ACCESSION SEGMENT SOURCE ORGANISM REFERENCE AUTHORS	RESULT 1
HIVSF2B13 3983 bp ss-RNA VRL 18-SEP-1992 Human immunodeficiency virus type 1, isolate SF13, tat, rev, vpU,	ttacaaatatta 1111            TTACAAATATTA 13	Query Match 63.2%; Score 12; DB 3; Length 1396; Best Local Similarity 100.0%; Pred. No. 1.18e+00; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	589 879 vpr polyprotein (AA at 589) 1091 1159 vpu protein (premature stop 1091 1336 vpu protein (premature term 860 > 1074 tat protein, exon 2 (first 999 > 1074 rev protein, exon 2 (first 502 a 230 c 329 g 335 t	form to/span description 71 295 vif polyprotein (AA at position 293) 71 649 vif polyprotein (prema	Hunsmann, G. Characterization of a new German HIV-1 isolate: HIV-1NH5 Characterization of a new German HIV-1 isolate: HIV-1NH5 Unpublished (1992) full staff_entry full staff_entry Kindly provided prior to publication in computer-readable form by Arne Falsst, Deutsches Primatenzentrum (DPZ), Abteilung fur Virologie und Immunologie, Kellnerweg 4, W-3400 Goettingen,	HIVNH52 1396 bp ss-DNA VRL 22-SEP-1992 Human immunodeficiency virus type 1, clone NH52, vif, vpR, vpU, tat regions. M00000 2 of 3 Human immunodeficiency virus type 1 (HIV-1), clone NH52. Human immunodeficiency virus type 1 Viridae: ss-RNA enveloped viruses; Positive strand RNA virus; Retroviridae; Lentivirinae. 1 (bases 1 to 1396) Weidt,G., Faisst,A.C., Sauermann,U., Lueke,W., Jentsch,K.D. and	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome).
M17450
                                                                                                                                                                                           Kindly made available in computer readable form by Marv Reitz, N.C.I., Bethesda, MD 20892 U.S.A. This isolate was taken from California AIDS patient in 1984. There is an in-frame stop at position 3212 of the envelope coding sequence; the nef cds is uncertain beyond position 4049. A in-frame stop codon, 'taa,' found at positions 4224-4226 in the nef cds..
                                                                                                                                                                                                                                                                                                                               Gurgo, C., Guo, H.-G., Franchini, G., Aldovini, A., Collalti, E., Farrell, K., Wong-Staal, F., Gallo, R.C. and Reitz, M.S. Jr. Envelope sequences of two new United States HIV-1 isolates Virology 164, 531-536 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIVSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The SF13 viral isolate was recovered from the same individual that produced SF2 (see <HIVSF2>), but five months later when the individual developed KS and PCP. The increased pathogenicity and wider host range of SF13 is studied in depth in [1]: two as changes in tat and 22 as changes in env, going from SF2 to SF13, are of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheng-Mayer,C., Shloda,T. and Levy,v....
Host range, replicative, and cytopathic properties of human
tymenopaficiency virus type 1 are determined by very few amino acid
                                                                                                                                                                                                                                                                                                                   full staff_review
                                                                                                                                                                                                                                                                                                                                                                                                                     DNA.
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Similarity 100.0%;
12; Conservation
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J. Virol. 65, 6930-6941 (1991)
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                                                                                                                            /note="genomic mRNA" <1..>4273
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          /codon_start=1
join(541..755,3089..3179)
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The authors point out that this sequence is unusual because it both macrophage-tropic and extremely cytopathic in lymphocytes: they contend that the virus is unusual in so far as it is the first well-characterized infectious molecularily cloned macrophage-tropic HIV-1 strain derived from peripheral blood.
                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1 provpr, vpu, env, tat, rev and nef genes, from strain 89.6.
                                                                                          An infectious molecular clone of an highly cytopathic strain of HIV-1 J. Virol. 66, 7517-7521 (1992)
                                                                                                                                             Human immunodeficiency virus type Viridae; ss-RNA enveloped viruses;
                                                                                                                                                                                                                                                                        M96155
                                                                              full staff_review
                                                                                                                                                                                                                                        proviral DNA
                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1 (HIV-1), clone p89.6
                                                                                                                                                                                                                                                                                                                                       HIVP896
                                                                                                                                                                                           Retroviridae; Lentivirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 63.2%;
Similarity 100.0%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1447
                                                                                                                                                                         (bases 1 to 4684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="3' LTR"
4249..>4273
/note="R repeat 3' (
a 760 c 1053 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="envelope polyprotein (premature stop at 3212)"
/codon_start=935
3089..3179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   772..864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 756..3088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="re
756..3088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="tat, rev, nef subgenomic mRNA intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="tat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="vpr protein"
/codon_start=270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=3507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="tat protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="nef protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="vpu protein (premature termination)"
codon_start=772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oin(680..755,3089.
'note="rev protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_
                                                                                                                                                                                                                                                                                                                                    4684 bp ss-RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _start=680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         premature stop (tag) in env cds"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12; DB 3; I
Pred. No. 1.18e+00;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                copy"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon 2 (first expressed exon)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (AA at 3091)"
                                                                                                                                                                                                          Positive strand
                                                                                                                             unusual macrophage-tropic and
                                                                                                                                                                                                                                                                                                      proviral DNA encoding es, and 3' LTR, clone p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4273;
                                                                                                                                                            Friedman, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                          RNA virus;
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                                                                                                                                                            Kolson, D.L.,
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p89.6
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FEATURES
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YITTSIRNKYKKYALFARLDVPIENYNNTKYRNHRCNTSVITQACDKYSFQDIPIH
YCVPAGFAMLKCNNKTFINGSGPCTNVSTVQCTHGIRPVYSTQLLNGSLAEBDIVIRS
ENFTDNAKTIIVQLNESVYINCTRPNNNTRRLLSIGPGRAFYARRNIIGDIRQAHCNI
SRAKWNYTLQQIVIKLREKFRNKTIAFNQSSGGDPEIVMHSFNCGGEFFYCNTAQLFN
STWNVTIGGTNGTEGNDIITLCGCRIKQIIMMQKVGKAMYAPPTGQIRCSSNITGLLL
TRDGGNSTETETEIFRPGGGDMRDNWRSELYKYKVPRIEPIGVAPTRAKRRTYQREKR
AVGIGAVYLGE LGAAGSYMGARSVTLTVQARLLLSGIVQQQNNLLRA LEQQHNLQLT
WGEIKOLQARVLALERYLRDQOLMGINGCSGKLICTTSVPWWSSNKSVDDWNNMT
WMEWEREIDNYTDYIYDLEKSGOTQDEKNEKELLLLDKWAFDIIMWLMYIRLF
IMIVGGLIGLRIVFAVLSIVNRYRGGYSPLSFQTLLEARRGDRAFGGERDRD
MSGPLYNGFLALFWYDLRNLCIFLYHLRNLLLILTRAKGEDRAEGGERDRD
SGPLYNGFLALFWYDLRNLCIFLYHLRNLLLILTRAKGEDRAEGGERDRD
SGSPLYNGFLALFWYDLRNLCIFLYHLRNLLLILTRAKGEDRAEGGERDRD
SGSPLYNGFLALFWYDLRNLCIFLYHLRNLLLILTRAKGELLAEGGERDRD
SGSPLYNGFLALFWYDLRNLCIFLYHLRNLLLLILTRAKGELAEGGERDRD
SGSPLYNGFLALFWYDLRNLCIFLYHLRNLLLLITTRAKGELAEGGERDRD
SGSPLYNGFLALFWYDLRNLCIFLYHLRNLLLLITTRAKGELAEGGERDRD
SGSPLYNGFLALFWYDLRNLCIFLYHLRNLLLLITTRAKGELAEGGERDRD
SGSPLYNGFLALFWYDLRNLCIFLYHLRNLLLLITRAKGELAEGGERDRD
SGSPLYNGFLALFWYDLRNLCIFLYHLRNLLLLLITRAKGELAEGGERDRD
SGSPLYNGFLALFWYDLRNLCIFLYHLRNLLLLLITRAKGENEALTYWNLLLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mrvkeirknwqhlrggilllgmlmicsaakektwvtiyygvpvw
REATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLGNVTENFNMWKNNMVDQ
MHEDIISLWDESLKPCVKLTPLCVTLNCTNLNITKNTTNPTSSSWGMMEKGEIKNCSF
                                                                                                                                                 / translation="MGGKWSKRRAEGWQTIREEMRRAEPAEPAADGVGAVSRDLARHG
AITSSNTNNADIAHLEAQEEGEVGFPVREQVPLERMTYKAADLSHFLKEKGGLEGIV
HSQKRQDIIDLWYHTQGFFPDWQNUTPGGGIRVPLTFGWCYKLVPVEPDEGENNRED
NSLLHPANQHGVEDSERQVLVWRFDSRLAFHHVARELHPEYFKN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
2718..3752
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HIYETYGDTWTGVEALIRILQQLLFIHFRIGCRHSRIGIIQHRRTRNGASKS"
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ESTNPRISSEVHIPLGDAKLVVTTYWGLHTGERDWHLGQGVSIEWRKKRYSTQVDPGL
ADRLIHLYYFDCFSDSAIRKSILGHIVSPSCEYQAGHNKVGSLQYLALAALTTPRRIK
/rpt_type=other
/note="U3 region"
                                                                            4049..4502
                                                                                                                                                                                                                                                                                                                                                                          3757..4371
                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="glycoprotein 41"
/gene="env"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="glycoprotein 120"
/gene="env"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YWSQELKNSAVSLLNATAIAVAEGTDRVIKIVQRACRAIRNIPTRIRQGLERALL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="envelope polyprotein"
/gene="env"
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/translation="MAGRSGDSDEDLLKTVRLIKFLYQSNPPPSLEGTRQARRNRRRR
                                                                                                                                                                                                                                                                                                                                'gene="nef"
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ISYGRKKRRQRRRPPQDSQTHQVSLSKQPSSQPRGDPTGPKEQKKKVERETETDPVH"
join(939..1014,3339..3613)
                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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|oin(800..1014,3339..3429)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MLSLQILAIVALVVAAIIAIVVWSIVFIEYRKILRQRKIDRLID
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REFERENCE
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            American isolate SF2 and the European virus HAN(across the genome). This is the first report of a virus from Africa that clusters with North American rather than Zairean viruses: OYI and SF2 differ by approximately 7% in envelope. The single C -> S substitution at residue 22 of the OYI tat protein renders it inactive, but may not account for the avirulence of the virus. The pattern of envelopes the mutation and nef start is not what is typically encountered. A possible mutation from a 'g' to an 'a' at position 5006 produced the triplet 'ata' instead of the usually conserved start codon for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sibling sequences for OYI(397) are available (see 1989:I-A-181).
Location/Qualifiers
<5373..5587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished AIDS Res. H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIVOYI 9190 bp ss-RNA
Human immunodeficiency virus
M26727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OYI, designated elsewhere as isolate 397, was taken from a healthy Gabonese presenting an atypical Western Blot. Tree analysis (see Part III) reveals that the sequence is closely related to the North
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kindly provided in computer-readable form by Simon Wain-Hobson, Pasteur Institute, Paris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wain-Hobson,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1 (HIV-1), isolate OYI proviral DNA (also designated gab397).

1 (bases 1 to 9190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.2%;
Similarity 100.0%;
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bp dc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coding region.
                                                                    IGGIGGFIKVROYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQLGCTLNFFISFI
ETVPVKLKPCKNGPKVKQWELTEEKIKVLIEICTEMEKEGKISKVGDENPYNPVFAI
KKKDSTKWRKLVDERELNKRTQDFWEVOLGIFHPAGLKKKSVTVLDVGAYFSVPLD
KDERKYTAFTIPSINNETPGIRYQYNVLPQGWKGSPAIFOSSMTKILEPFRKONPDIV
IYQYMDDLYVGSDLEIGQHRTKIEELRQHLLRWGFTTPDKKHQKEPPFLMMGYELHPD
KMTVQPIMLPEKDSWTVNDIGKLVGKLNWASQIYAGIKVKNLCKLRGTKAITEVIFL
                                                                                                                                                                                                                                                                                                                                                                                     /note="tat protein, exon 2 (first expressed exon)"
<5512..5587</pre>
TEEAELELAENREILKEPVHGVYYDPSKDLVAELQKQGQGQWTYQIYQEPFKNLKTGK
YARMRGAHTNDVKQLTEAVQKITQESIVIWGKTPKFKLPIQKETWEAWWTEYWQATWI
PEWEFVNTPPLVKLWYQLEKDPIVGAETFYVDGAANRETKLGKAGYVTDRGRQKVVSL
                                                                                                                                                                                                                                 /translation="ffredLafpQGKAREFSSEQTRANSPTSRELRVWGRDNNSPSEA GADRQGTVSFNLPQITLWQRPIVTIKIGGQLKEALLDTGADDTVLEEMNLPGRWKPKM
                                                                                                                                                                                                                                                                                                                                        <1628..4639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4600..4684
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                                                                                                                                                                                                                                                                                                           /note="pol polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_lib="subgenomic lambda pahge library of HMW"
849 c 1145 g 1111 +
                                                                                                                                                                                                                                                                                                                                                                /note="rev protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Organism="Human immunodeficiency virus type 1"/ore="Human peripheral blood mononuclear cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hum. Retroviruses (1990) In press
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/note="R region"
                                                                                                                                                                                                                                                                                      codon_start=
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Pred. No. 1.18e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                exon 2 (first expressed exon) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type 1, isolate OYI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Labsialation="mtargtrknyQrlwrwgtmllgmlmicsaaenlwvtvygvpw /Labsialation="mtargtrknyQrlwrwgtmllgmlmicsaaenlwvtvygvpw /Labsialation="mtargtrknyQrlwrwgtmlpwpopwtchgnytenepwkknnyvpq keatttlecasbaraxatevhnywathacvptdpwtpssclenatmitssswetmækgelk wcgryttlisladdreverleverdpwtpssclenatmitssswetmækgelk ncsryttsibdmorsyalfykldylpidkndykfrllcntstitgalpidkdyrgitsibepi pmhyctpagfailkcndkkfngtgpctnvstvqcthgikpvstqlllngslaeevi i rsswetnakiiivolnksveinctrennvtrkrisidpepraffytkqiigdirqah chisswetnitieqiatklrkofernktiafdreggepivmhsfncgskitglicolkchisgraffyltaarstyvitilecrikqivnmwodygkamyapfisqqircsskitgllltradgepiplcharstyvgrek ravghlagatelgydraffkarrvorek ravghlagatelgydraffkarrvorek ravghlagatelgydraffkarrvorek ravghlagatelgydraffkarsmitivoarollegiplogophilakswsiksluslikginger ravghlagatelgydraffkarrvorek ravghlagateleggerd ravghlagatelgydraffkarrvorek ravghlagateleggerd ravghlagatelgydraffkarrvorek ravghlagatelgydraffkarrvordek ravghlagat
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KIEEEDOKKKKKAQQTAADTGNISQVSQNYPTYOLLGOQWHOD IS PRTINAWYKVYVE
EXAFSPEVIPWFSALABGATPODLINTMLINTVGGHQAMQMLKETINEEAAEMDRLHPY
HAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKRWIILGLNKIVRM
YSPTSILDIRGGPKEPFRDYVDRFYKTLRAEQASQDVKNWMTETLLVQNANPDCKTIL
KALGPAATLEEMMTACQGVGGFGHKARVLAEAMSQUNSVTYMMCGNFKNQRKTVKCF
NCGKEGHIAKNCRAPKKGCWKCGKEGHQMKDCTERQANFLGKUWPSHRGRPGNFLQN
REPPTAPPAESFGFGEETTTPPQKQEPIDKGLYPLTSLRSLFGNDPSSQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESTHPRISSEVHIPLGDATLVVTTYWGLHTGEREWHLGOGASIEWRKKRYSTQVDPGL
ADQLIHTYYFDCFSESAIRNAILGNIVSPRCEYPAGHNKVGSLQYLALAALIKPKKIK
PPLPSVTKLTEDRWNKPQKTKGHRGSHTMNGH"
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KEKYVLAWVPAHKGIGGNEQVDKLVSAGIRKVLFLDGIDKAQEHEKYHSNWRAMASD
FNLPPVVAKEIVASCDKCQLKGEAMHGQVDCSPGIWQLOCHLLEGKIILAVHVASGY
IEAEVIPAETGQETAYFILKLAGRWPVKTIHTDNGSNFTSTTVKAACWWAGIKQEFGI
PYNPQSQGVVESMNNELKKIIGQVRDQAEHLKTAVQMAVFIHNFKRKGGIGGYSAGER
IVDIIATDIQTKELQKQITKIQNFRVYYRDSREPLWKGPAKLLWKGEGAVVIQDNSDI
                                                                                                                                                                                                                                                                                                                                                                                                                               RDRSGRLVDGFLALIWDDLRSLCLFSYHRLRDLILIVARIVELLGRRGWEVLKYWWNL
LQYWSQELKNSVISLLNATAIAVAEGTDRVIEIVQRAYRAFLNIPRRIRQGLERALL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVVPRRKAKIIRDYGKQMAGDDCVASRQDED"
join(5373..5587,7918..8008)
/translation="MGGKWSKCSMKGWPTIRERMKRAELQPPEPAAEGVGAASRDLEK
HGAITSSNTAATNADCAWLEAQEDEEVGFPVRPQVPLRPMTYKGALDLSHFLKEKGGL
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ISYGRKKRRQRRRAPQDSKTHQVSLSKQPASQPRGDPTGPKESKKKVERETETDPED"
join(5512..5587,7918..8192)
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YIYETYGDTWEGVEAIIRILQQLLFIHFRIGCQHSRIGITRQRRARNGASRS"
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                                                                                               /codon_start=:
                                                                                                                                                                                                                                 'note="rev protein,
                                                                                                                                                                                                                                                                                                                                     'note="tat protein, exon 3 (AA at 7919)"
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/codon_start=1
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                                                                                                                                                                                                                                      (AA at 7920)"
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CDS

Sg

CDS

exon

SdS exon

HIVSF2

9737 bp ss-RNA

VRL

01-MAR-1989

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LOCUS
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                                                Query Match
Best Local S
Matches 1
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JOURNAL
STANDARD
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Best Local
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                       6082 ttacaaatatta 6093
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                                                                                                                                                                                                                                                                                                                                                        The JRCSF and JRFL env nucleotide sequences differ by at least 3%; further characterization of them is forthcoming (Peng,S. et al., Nature 1990, in press). Both manifest insertions in nef previously reported for HIVBRVA.

reported for HIVBRVA.

from. to/span description
790 2304 gag polyprotein
2085 5108 pol polyprotein (NH2-terminus uncertain: AA at
                                                                                                       ຫຸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kindly provided in computer-readable form by Irvin Chen, UCLA School of Medicine, Los Angeles. JRCSF and JRFL (see <HIVJRFL) were isolated from cerebral spinal fluid and brain tissue of the patient JR, who died with Kaposi's sarcoma and severe AIDS encephalopathy (Science 236, 819-822, 1987). Both clones are infectious, but JRFL productively infects macrophages while JRCSF does not. (Peripheral blood was not available from the patient).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M38429 M38429 MINA from extracellular virus taken from cerebral spinal fluid (1986). Infectious clone.

1 (bases 1 to 9540)

Koyanagi, S., Chen, I.S.Y.et al.
Unpublished (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIVJRCSF · 9540 bp ss-RNA VRL Human immunodeficiency virus type 1, isolate
                                                h 63.2%;
Similarity 100.0%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 63.2%;
Similarity 100.0%;
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                                                                                                       terminus
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                                                                                               EGLIYSQKRQDILDLMVYHTQGYFPDWQNYTPGPGIRYPLCFGWCFKLVPMDPDQVEE ANEGENNSLLHPISLHGMDDPEKEVLVWKFDSRLAFRHMAREVHPEYYKDC" 9176...9171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="poly-A signal"
1630 c 2202 g
                                                                                                                                                                                                                                                                             5631
5861
6056
8456
6056
                                                                                                                 R repeat 5' copy
Spl binding site III
Spl binding site II
Spl binding site I
Spl binding site I
primer (Lys-tRNA) binding site
2308 g 2116 t
                                                                                                                                                                                                              nef protein
5' LTR
                                                Score 12; DB 3; Let Pred. No. 1.18e+00; 0; Mismatches 0;
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                                                                                                                                                                                                                                                                 protein,
                                                                                                                                                                                                                                                                                          protein,
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No. 1.18e+00;
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exon
exon
                                                                                                                                                                                                                                                                2 (first expressed exon)
3 (AA at 8367)
2 (first expressed exon)
3 (AA at 8368)
                                                                          Length 9540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                   Indels
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                                                   0,
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STANDARD
COMMENT
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 · ' intron
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                                        exon
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Nucleotide semisor ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1 (HIV-1), isolate ARV-2, integrated proviral DNA and circular unintegrated DNA from cells; clones lambda-[7A,7D,8A,8B,9B]. Infectious clone. 1 (bases 1 to 9737)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               full staff_review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 227, 484-492 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence and expression of an AIDS-associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete proviral genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ARV-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variations were observed between the clones used for sequencing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            occurs at position 332 in 7A and 9B; "a" occurs in 8A. occurs at position 340 in 7A and 9B; "a" occurs in 8A. occurs at position 4233 in 8A; "g" occurs in 8B. occurs at position 4677 in 8A; "c" occurs in 8B. occurs at position 6215 in 7D; "g" occurs in 7A and 9B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="R repeat 5'
455..9652
                                                                                                                                                                                                                                                               /note="gag polyprotein"
/codon_start=791
4233..4233
                                                                                                                                                                                                                                                                                                                                                                                                 /note="tat, rev, nef subgenomic mRNA"
637..654
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="genomic mRNA"
455..9652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Sp1 binding site I"
454..551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Sp1 binding site II" 400..409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Sp1 binding site III" 389..398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="g in 7A,9B; a in 8A" 378..387
                                                                                                                                                                                         5048..5626
                                                                                                                                                                                                                                                                                                                                                            /note="primer (Lys-tRNA) binding site'
745..5783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="g in 7A,9B; a in 340..340
   /note="rev protein,
6055..8383
                                                                                                                                                                                                                            4677..4677
                                                          /note="
                                                                                                                                                                    'note="vif protein"
                                                                                                                                                                                                         note-"t in 8A; c in
                                                                                                                                                                                                                                              /note="a
                                                                                                                                                                                                                                                                                                                                       'note="tat, rev, nef subgenomic mRNA intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(5840..6054,8384..8474)
note="tat protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="pol polyprotein (NH2-terminus uncertain; AA
/ng2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation,
                                                                                            codon_start=5566
                                                                                                              'note-"vpr protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=5979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"rev protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=5840
|oin(5979..6054,8384..8658)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=2092/
                                                                                                                                                     codon_start=5048
                                    e="tat protein, exon 2 (first expressed exon)"
                                                                                                                                                                                                                                          in 8A; g in 8B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      сору"
                 exon 2 (first expressed exon)"
                                                                                                                                                                                                           8B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolate ARV-2/SF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human
                                                      BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
STANDARD
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Best Local Similarity 100.0%;
Matches 12; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6080 ttacaaatatta 6091
                                                                                                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TTACAAATATTA 13
                                                                                                                                                                                                                                                             previously characterized agm strains cluster with other grivets. See related tantalus isolate sequences in a cocession number that isolate sequences in the company of the cocession numbers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simian immunodeficiency virus proviral DNA, isolate TAN-49 fr
Ugandan tantalus monkey (Gecopithecus tantalus).
Simian immunodeficiency virus
Viridae: ss-RNA enveloped viruses; Positive strand RNA virus;
                                                          193
                                                                                                                                                                                                                                                                                                                Identification of a new subgroup of SIVagm in tantalus monkeys Virology (1993) In press full staff_review
Kindly submitted prior to publication by Dr. Vanessa Hirsch, Immunodeficiency Viruses Section, NIAID/NIH, Twinbrook II, Rockville MD 20852. SIVagm-tan strains cluster with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5' terminus of LTR-U3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIVAGMT49 1773 bp ds-DNA VRL 09-JUN-1993 Simian immunodeficiency virus, isolate TAN-49, complete gag cds.
                                                                                                                                                                                                                                                                                                                                                                                                                              Hirsch.V.M., McGann,C., Dapolito,G., Goldstein,S., Biryawaho,B., Lakwo,T. and Johnson,P.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retroviridae; Lentivirinae.

1 (bases 1 to 1773)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L19253
                                                                                                                                                                                                                                                           rivets. See related tantalus isolate sequences 17, 27, 40, (accession numbers L19250-L19252, L19254).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3445 a
                                                  594 a 375 c 480 g nt upstream from the gag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9628..9633
/note="mRNA polyadenylation signal"
a 1738__ 2377 g 2177 t
                                                                                                                                                                                                                       Location/Qualifiers 195..1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="envelope polyprotein"
/codon_start=6233
8384..8474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9555..9652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6055..8383
/note="tat, rev, nef subgenomic mRNA intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="tat cds intron 6055..8383
                                                                     /sequenced_mol="DNA"
375 c 480 g
                                                                                                                                             /organism="Simian immunodeficiency virus"
/cell_line="CEMss"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6071..6187
                                                                                                                                                                                    /gene="gag"
l..1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="nef protein"
/codon_start=8802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="vpu protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="rev
                                                                                                              'proviral
                                                                                                                               'haplotype="na"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="tat protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="a in 7D; g in 7A,9B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=6071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="rev protein,
57.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat 3' copy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cds intron
Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12; DB 3; Ler
Pred. No. 1.18e+00;
0; Mismatches 0;
                                                    cds start
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                                            Human immunodeficiency virus type 1, US3 envelope glycoprotein gene, tat gene, rev gene, vpu gene, and nef gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 2583)
Breuer, J., Douglas, N.W. and Daniels, R.S.
Sequence analysis of env genes of ten HIV-2 isolates and potential
identification of domains susceptible to cross neutralizing antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolate HIV2CAM4E, complete U05356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV2CAM4E 2583 bp ss-RNA VRL 02-AUG-199
                   env gene; envelope glycoprotein; nef gene; rev gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                envelope
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HIV2CAM4E (U05356)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 2
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                                                                                                                                                                                                                                                                                                                                                                                                                    57.9%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viridae; ssRNA enveloped viruses; Positive strand
                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Retroviridae; Lentivirinae;
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AM4E (U05356) HIV2CAM5E (U05357) I
sequences cluster with HIV-2 subtype
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PROAWCWFKGEWKGAMKEVKOTLLEHPRYKGAN I INNI RLAEDEKGSDPEVAXMWTNC
RGEFLYCNMTWELNWVENRTGGPQHNVVPCHI ROI I NTWHKVGKNVYLPPREGELVCN
STVTSLIANIDMRNDSTNI TESAEVAELY RLELGDYKLI EVTP I GFAETDQKRYSPAP
TRSKRGVFVLGF LGFLAAAGTAMGTASLT LSAQSRTLLAG I VQQQQLLDVVERQQEM
LRLTVMGTKNI LQARVTA I EKYLKDQAQLNSWGCVFROVCHTTVPWNNDSLTPMNNNT
WQEWELRTRYLDANI SQLLEQAQ I QQEKNMYELGKLNSWDDFSNWFDLTSWIRY I QYG
VYI VVGI VVLRI VI Y I YQMI SALRKGY REVESSPFGY LQQI HI HITDKBQPARGETEED
VGDNVGJ VVLRI VI Y I YQMI SALRKGY REVESSPFGY LQQI HI HITDKBQPARGETEED
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QFNMTGLQRDKVKRYNETWYSKDVVCDTNNTNTNKTDNQSTCYMNHCNTSVITESCDK
HYWDTMRFRYCAPPGFAILRCNDTDYSGFKPNCSKVVAASCTRMKETQTSTWFGFNGT
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/translation="MACGKSQLLIAILLTSTCLIYCAQYVTVEYGIPAWRNASIDLFC
/translation="MACGKSQLLIAILLTSTCLIYCAQYVTVEYGIPAWRNASIDLFC
ATKNRDTWGTIQCLPDNDDYQEIPLNVTEAFDAWNYTITEQAIEDVWNLFETSIKPCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKAAYLQYGCEWIQEAFQAFARTARETLAGAWRNLWEAMGRLGRGILAVPRRIRQGAE
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/note="NCBI gi: 520432"
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/organism="Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'isolate="HIV2CAM4"
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7.89e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2583;
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HIV2CAM6E (U05358)
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                                                                                                                                                                                                                                                                                                                                                                                                                             SIVAGMIYO appears to lack a vpR coding region. [1] suggests the this may account for SIVAGMIYO'S lack of pathogenicity. The ercods contains an in-frame stop codon at positions 8077-8079, sinto the in-frame stop codons found in the SIV macaque and HIV-2 ROD35 envelope coding regions, except that SIVAGMIYO'S stop coding found 96bp downstream from the 3' splice junction of tat an interv, which is the location of the stop codon in the other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miki,K., Kitamura,T. and Hayami,M.
Sequence of simian immunodeficiency virus
monkey, a new member of HTV/SIV group
Nature 333, 457-461 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simian (African green monkey) immunodeficiency virus, extra-
chromosomal closed-circular DNA, TYO-1 clone lambda-SAH12.
1 (bases 1 to 9170)
Fukasawa,M., Miura,T., Hasegawa,A., Morikawa,S., Tsujimoto,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIVAGMTYO. 9170 bp ss-RNA VKL VLTDAK-1307 Simian (African green monkey) immunodeficiency virus, isolate TYO-1, complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mascola, J.J., Louwagie, J.J., McCutchan, F.E., Fischer, C.L., Hegerich, P.A., Wagner, K.F., Fowler, A.K., McNeil, J.G. and Burke, D. Two antigenically distinct subtypes of human immunodeficiency vir type 1: viral genotype predicts neutralization serotype J. Infect. Dis. 169, 48-54 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1 blood DNA.
Human immunodeficiency virus type 1
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was obtained from a lambda clone derived from African green monkey imported from Kenya.
                                                                                                                                                                                                                                                                               [1] finds that SIVAGMTYO is approximately equally distantly related to the HIY-1's and the HIY-2/SIV (macaque) group; over a "conserved" stretch of the pol protein, TYO is only 87% similar to AGM385 and 82% similar to AGM266, the latter two differing by 20%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 full staff_review
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1 (bases 1 to 3120)
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                                          /codon_start=1634
join(5546..5763,7984..8068)
/note="tat protein"
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Human immunodeficiency virus type 1"
|cell_type="lymphocyte"
/codon_start=5546
join(5703..5763,7984..8177)
                                                                                                                                                                             <1634..4819
                                                                                                                                                                                                        /note="5/ LTR"
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529 c 754 g
                                                                                                                                                'note="pol polyprotein
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Pred. No. 7.89e+00;
0; Mismatches 0
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                                                                                                                                                   (NH2-terminus uncertain;
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                                                                                                                              ACCESSION
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Best Local Similarity 100.0%;
Matches 11; Conservative
                                                        ORGANISM
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                                                                   Simian immunodeficiency virus PCR-amplified DNA extracted from cocultured PBMCs derived from a wild female asymptomatic sabaeus African green monkey captured in its natural habitat of Senegal.
                                                                                                                                         SIVSABIC 10036 bp ss-RNA VRL 25-MAY-1994
Simian immunodeficiency virus (SIVagm) complete genomic sequence,
African green monkey isolate SIVagmSAB-1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Cap site of genomic RNA.
                                   Simian immunodeficiency virus Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                           3172 a
roviridae; Lentivirinae. (bases 1 to 10036)
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220..237
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1720 c 2263 g 2015 t
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/note="3' LTR"
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/codon_start=5236
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/codon_start=432
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/codon_start=5703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=8201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note-"
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/codon_start=5770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="primer (Lys-tRNA) binding site"
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Pred. No. 7.89e+00
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STANDARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was obtained as part of a study designed to determine the breadth of genetic variation of SIV infecting African green monkeys. With this aim in mind, Jin et al. PCR-amplified, cloned and sequenced the LTR and partial envelope region from 12 isolates (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1, tan40, and tan-49). These isolates were derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conclude that an ancestor of the sabaeus virus was a recombinant with two breakpoints: one roughly at codon 310 of gag and the ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phylogenetic analysis suggests that each AGM species is infected with a distinct subtype of SIVagm. Interestingly, the sabaeus vith a distinct subtype of SIVagm. Interestingly the sabaeus vertex serious seems to be a mosaic of many viruses infecting different primate species [1]. Virus sab-1 forms a distinct lineage in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virus sab-1 was derived from a wild female asymptomatic sabaeus African green monkey. She was caught in her natural habitat of Senegal and susequently exported to the United States. From the point of capture and throughout the study, she was housed in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 different African green monkey species inhabiting various
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/prodict="GAG Oolyprotein"
/prodict="GAG Oolyprotein"
/translation="MGASNSVLSGRKLDAFESVRLRPNGKKKYKLRHLVWASKELDRF
/translation="MGASNSVLSGRKLDAFESVRLRPNGKKKYKLRHLVWASKELDRF
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KVKEEVPAEMTESATATSSGQTKELQAKKKNEPTVTPSGGSRNYPIVSVNNQWVHQPL
SPRTLAMWYKYLEEKKFSAEVVPMESALAEGAIPYDINQMLNAVGEHQGALQIVKDVI
NEEAADWDLRHPPPQQPPAQGYLRDPQGSDIAGTTSTIOGQIEWTTRAQNAVNVGNIV
NEEAADWDLRHPPPQQPPAQGYLRDPQGSDIAGTTSTIOGAIFNTAGANAVNVGNIV
NEEAADWDLRHPPPQQPPAQGYLRDPQGSDIAGTTSTIOGAIFNTAGANAVNVGNIV
VOLGI PHPAGLOQREQITVLDIGDAYFSCPLDPDFOKYTAFTI PSVNNREPGIRYOYK
VLPGGWKGSPTIFOTTANKILGEFROKNPOVDTYQYMDDMLIASDRPKABELYMYQQL
RDYLETWGFEYPEKKEVGKDPYLMYGYELYPKWQLOBITLPBREEMTYNDIOKLVGK
LNMASOIYTGIKTKHLCRLIRGARPLTEIVOMTEEAELLEENROILROKOQGQYYDP
                                                                                                                                                         IEGQKVTALLDTGADDSVIQGIELGDNWKPRIIGGIGGCINVKAYHNQEVKIEDKTCK
ATILVGETPVNIIGRNVLAQLGVTLNLTQREIEPIKVHLKPGQDGPRIROWPLSKEKI
EALKAICEDLEKQGHLERIGPENPYNTPVFAIRKKDKTQWRILMDFRQLNKSTQDFQE
                                                                                                                                                                                                                                                                  /product="POL protein"
/translation="FFRVWPLGQRETQEFPSDLHQTNSSPNGTGLQQAGGKLVCRQTS
DQRTRARRSSNSPVKAVCCSGETAETAVAKPLATTEPLRGGLQLPQVSLWRRPMKTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGWIILGLQKCVKMYNPVNILDIKQGPKEPFKDYVDRFYKALRAEQTDPAVKNWMTQS
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/organism="simian immunodeficiency virus"
/specific_host="African green monkey"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1FVQQGARPRGPLGGRGRPLNPN1KCYNCGKPGHLARFCKAPRRQGCWKCGS
                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="N-terminal uncertain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1017..2681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liqnanpdcktvlkglgmnptleemltacqgiggaqhkarlmaeamtaafqqqtvgn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="NCBI gi: 466230"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="sabaeus subtype"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone="SAB-1/MJ8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           putative TAR 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robertson, D.L., Mueller, M.C., Barn, J.S., Shaw, G.M., Sharp, P.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI gi: 466231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barre-Sinoussi, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hahn, B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the sabaeus viral
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LTR
BASE COUNT
ORIGIN
                                                                                                                     Query Match
2257 caaatattaaa 2267
                                                                                           y Match 57.9%;
Local Similarity 100.0%;
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                                                          Conservative
                                                                                                                                                                                                                                                  EQVPSAQG"
9270..100
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KTYAPPREGHLECNSTATALYYELNYNSKNRTNYTLSPQIESIWANELGDYKLYEIKP
KTYAPATKVRRYTGPEROKRVFYLGFLGFLGAAGAAMGAAALITVQSQQLLAGILQQ
QKNLLAAVEQQQQMLKITIWGVKNLNARVTALEKYLEDQARLNIWGCAFRQVCHTTVL
WKYNNTPDWENNTWQEWERQIEKYEANISRILEQAHEQEQKNLDSYQKLVSWSDFWSW
DLTKWFGWMKIAIMYIAGIIVARVLLVIIGILRKFRKGYAPLSSLPSSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="ENV protein"
/translation="MKLLTVLLMLSGCWSLVWLVQYVTVFYGIPVWKNSSVQAFCKTP
/translation="MKLLTVLLMLSGCWSLVWLVQYVTVFYGIPVWKNSSVQAFCKTP
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PCVKLSPMCIKMNCYRLEGGAATTTSPSTSTARPEVVSVGFNDSVIEQEMEKEQAMNC
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                                                                                                                                                                                                                                                                                                                                          /product="NEF protein"
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ECAKSLROGLIRQGDSSTEEGVKMKHQGRQPSWYDEDEEEVGFPVRFCLPLRAMTYK
LAIDFGHFLKEKGGLEGIYYSERRKKILDLYALNEWGIVDGWQNYTDGPGTRYPKCFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YWDTFRLRYCAPAGYALLRCADTDYSGHKACRNVTVSACTRLINTTVSTGIGINGSYVANRTEIWQKNGNSNDSVIIRLNRYFNLTIRCRRPGNKTVLPVTIMAGLVFHSQKYNTR
LKQAWCWFGGNWRGAWKEVKETIVRLPPKKYSGTNDTNKIFLQRQWGDPESEFFFFNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="REV protein"
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RQQVIHLAERILETPVSQIDHLAQEFDQLYLDNLQQPPSLPPGHPTENQTANSSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="TAT protein"
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KKALGIRYVERPRRAKKISHNQVSLHN"
join(6411..6474,8683..8918)
/note="NCBI gi: 466234"
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/product="YDY Drotein"
/product="YDY Drotein"
/translation="MASGGWLPPVGGDPPKDPPKNPREEIPGWLETWDLPREPFDEWL
/translation="MASGGWLPPVGGDPPKDPPKNPREEIPGWLETWDLPREPFDEWL
RDMLQDLNSEAQCHFPRNLLFRLWWNIYEEPAIDHGQTRLEGWYKYCRILQKALFVHM
KGRCCKPKTHPAYGPGAGGPPPGLGGASGGAASAAPGL"
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AVYYVDGAANRRISKEGKAGYITDRGDQKVVALENTTMQKAELILLALRDSGSKVNI
ITDSQYAMGIIAGEPTESDNNIVQQIIEELIKKEAVYIAWVPAHKGVGGNEEIDKVS
QGIRQVLFLDRIEEAQEEHDKYHANWRSMQQEFGLPAIVAKEIVAACPKCQIKGESVH
GQVDASPGVWQMDCTHLEGKIIIVAVHVASGFIEAEVIPQETGKATAHFLLKLASRWP
                                                                                                                                                                                                                                                                                                             WCFKLVPVDLSEEAKNSENHCLLHPAQVAYEDDAWKETLVWKFDPLLAVDYVAWRLHP
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ESPPPSLVEYCGRTSH"
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TADHIIHWSYFPCFTDRAVQQAIRGEKYLWCKHQVGHQPTGQVPSLQYLALRVYTNGL
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DAERLETAVIMAVHIHNFKRKGGIGGYSAAERLINIIHTELETKTLQQKISKIQNFRV
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                                                                                           Pred.
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                                                              Mismatches
                                                                                              No. 7.89e+00
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                                                                                                                         DB 3;
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COMMENT
                                 REFERENCE
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                                                                                                                                                             ACCESSION
                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.6%;
Best Local Similarity 100.0%;
Matches 10; Conservative
           AUTHORS
                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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This sequence was obtained as part of a study designed to determine the breadth of genetic variation of SIV infecting African green monkeys: With this aim in mind, Jin et al. PCR-amplified, cloned and sequenced the LTR and partial envelope region from 12 isolates (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1, tan40, and tan-49). These isolates were derived from different African green monkey species inhabiting various
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

1 (bases: 1 to 1478)
Shibuya; H., Irie, K., Ninomiya-Tsuji, J., Goebl, M.G., Taniguch
                                                                                                              Homo sapiens
                                                                                                                                                                                                            HUMMSS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 a 194 c 268 g 2
approximately 727 bp downstream
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simian immunodeficiency virus PCR-amplified DNA extracted from cocultured PBMCs derived from a wild asymptomatic tantalus African green monkey captured in its natural habitat of Uganda.

Simian immunodeficiency virus
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simian immunodeficiency virus (SIVagm) partial envelope sequence, African green monkey isolate SIVagmTAN-40.
                                                                                                                                    Human cDNA clone MSS1 (from HeLa cDNA library)
                                                                                                                                                                                           Human mRNA for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 13, 2935-2947 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         African green monkey.
habitat of Uganda.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYAYELGRYKLIEIKPIGFAPTEVRRYYGPTREKRVPFVLGFLGFLGRAGAAMGATAT
ALTYOSQQLLAGILQQQKNLLAAVEQQQQMLKLTIMGVK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="Tlklrycapagfallkcrdtnyagfgicnnvsvvsctglmntti ssafglingsqaenfelwqktensndsviiklmkyqlkikcirgnmytpvtmag Lvehsqxxnyklpaketenggwkenstrivklpaketenggryntergengtwlragm pregelektenggryntergengtyppekorlckkrtyv achtengsbsgksvnvegntctpekorlckkrtyv achtensvvndwytlskktyappregelectstytsiiasldynnknmynvtlanien
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/product="envelope protein"
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/note="tantalus subtype"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="simian immunodeficiency virus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                           1478 bp ss-mRNA
or the MSS1 cellular factor, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 10; DB 3; 1
Pred. No. 4.19e+01
0; Mismatches (
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     Taniguchi, T.
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REFERENCE
AUTHORS
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ORIGIN
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RS Grez.M. Dietrich, D., Balfe, P., Von Briesen, H., Maniar, J.K., Mahambre, G., Delwart, E.L., Mullins, J.I. and Ruebsamen-Waigmann, H. Genetic analysis of human immunodeficiency virus type 1 and 2 (HLV-1 and HLV-2) mixed infections in India reveals a recent spread of HLV-1 and HLV-2) from a single ancestor for each of these viruses at J. Virol. 68, 2161-2168 (1994)

ARD This sequence was obtained as part of a study to determine the genetic breadth of HLV-2 variation in India. In this study, blood samples were obtained from four patients from Bombay. India (D166, D808, D868, and D1024) and from one patient from Goa, India (D1071); each of the five patients was serologically dually reactive. The mean genetic divergence of the set of four sequences from Bombay was 7.3%, while the sequence from Goa was from 7 to 10.5% different from each of the Bombay sequences. The entire set of Indian sequences, including both the Bombay and Goa sequences, diverged from eleven non-Indian HLV-2 sequences by 23%. Because of the similarity of the Indian sequences, Grez et al. suggest that similar HLV-2 strains
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These data kindly submitted in computer readable form by Kenji
Trie, Department of Molecular Biology, Faculty of Science, Nagoya
University, Chikusa-Ku, Nagoya 464-01, Japan. The MSS1 protein
University, Chikusa-Ku, Nagoya 464-01, Japan. The MSS1 protein, which
Is reported to be 42% similar to the human TBP-1 protein, which
binds the HIV tat protein in vitro. Endogenous MSS1 enhances
tat mediated transactivation, leading the authors of [1] to conclude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 2 from PCR-amplified DNA extracted from uncultured PBMCs derived from a patient from Bombay, India whose sera was dually reactive (HIV1/HIV2).

Human immunodeficiency virus type 2

Viridae; ss-RNA enveloped viruses; Positive strand RNA virus; Retroviridae; Lentivirinae.
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GRLDRKIEFSLPDLEGRTHIFKIHARSMSVERDIRFELLARLCPNSTGAEIRSVCTEA
GMFAIRARRKIATEKDFLEAVNKVIKSYAKFSATPRYMTYN"
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IKQVEDDIQQLLKKINELTGIKESDTGLAUDLAADKQTLOSEQPLQVARGTKI
NADSEDPKYINVKQFAKFVVDLSDQVAPTDIEEGMRYGVDRNKYQIHIPLPFKIDFI
VTMMQVEEKPDVTYSDVGGCKEQIEKLKEVVETFLLHERRFVNLGIEPEKGVLLEGPP
GTGKTLCARAVANRTDACFIRVIGSELVQKYVGEGARMVRELFEMARTKKACLIFFDE
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product="MSS1 protein"
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TWFLNWVENKTANQTWHNYVPCHIKQIINTWHKVGKHYYLPPREGELTCNSTVTSIIA
                                                                                                                                                                     NIDGGNQTNITFSAEVGELYRLGIGDYKLVEITSIGFAPTSEKRDSSAHGRHRE"
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-geneseq35  1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  14:part14 15:part15 16:part16 17:part17 18:part18  19:part19 20:part20 21:part21 22:part22 23:part23  24:part24 25:part25 26:part26 27:part27 28:part28  29:part24 35:part33 31:part31 32:part23 33:part33  34:part34 35:part35 36:part36 37:part37 38:part38  39:part39 40:part40 41:part41 42:part42 43:part43  44:part44 45:part45 46:part46 47:part47 48:part48  49:part44 55:part50 51:part51 52:part52 53:part53  54:part54 55:part55 56:part56 57:part57 58:part58  59:part59 60:part60	Minimum Match 0% Listing first 45 summaries	271905 seqs, 107135622 bases x 2	Dbase 0; Query 0	TABLE jmetric Gap 60	>US-09-103-287-6 (1-19) from US09103287.seq 19	generated.	Nov 27 15:24:13 1999; MasPar time 21.10 Sec	n.a. database search, using Smith-Waterman algorithm	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	[MT)

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5504 5625 6178 8201 11879 12011 15109

Nucleic acid sequence pJG4-5-CDK-BP cDNA cl

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Streptococcus pneumon Enterococcus faecalis Staphylococcus aureus Clone bp783\_3 isolate

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V83540 V74355 V18273 V18272 V83561 V83533 V83533

HPIV-3

JS isolate wil FRhl cp45 vacc

Staphylococcus PCR-generated region Enterococcus faecalis

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Nucleotide sequence o Plasmid p3/7(131) enc Plasmid p3/7(131)2G e Plasmid p218(131) enc

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. numan gene signature Human brain Expressed DNA encoding DNA encoding a Staphy Partial nucleotide se UDP-N-acetylmuramate: Staphylococcus aureus MurC polynucleotides 9.94e-02 9.94e-02 9.94e-02 9.94e-02 9.94e-02 9.94e-02 3.98e+00 3.98e+00 3.98e+00 Pred. No V99652 standard; DNA; 19 BP.
V99652;
17-MAR-1999 (first entry)
MurC polynucleotides amplifying primer.
MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide;
bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine;
immunogen; drug; genetic immunisation; PCR primer; ss. bacterial infections

Disclosure; Page 13; 39pp; English.

Disclosure; Page 13; 39pp; English.

The invention relates to a UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoded by the S. aureus MurC gene. Host cells containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. bacterial (especially S. aureus) infections. They are also useful against Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for Synthetic. Staphylococcus New isolated MurC polypeptide from Staphylococcus aureus and nucleic acid - useful in diagnosis, treatment and prevention Burnham MKR, Wallis NG; WPI; 99-062655/06. EP-889123-A2. 07-JAN-1999. 26-JUN-1998; 305064. 03-JUL-1997; US-052720. (SMIK ) SMITHKLINE BEECHAM CORP.

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19 619 660 1351 2424 299 439 1767 2524 58 58 58 58

V99652 V53479 V80065 V99650 V74703 T22923 Q60017 T75076 V74671

DNA encoding aspartyl Staphylococcus aureus

infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The MurC polypeptide is also useful for

Result

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Description

SUMMARIES

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Mean 4.586; Variance 2.920; scale 1.570

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                                               RESULT
                                                                                                                                                                                                                           PT New nucleic acid sequences from Staphylococcus aureus WCHU29 - PT useful in vaccines and for treatment of bacterial infections of e.g. PT respiratory tract and central nervous system PS Claim 1; Page 146; 390pp; English.

CC finction, and represents a DNA Sequence of the invention.

CC function, and represents a DNA Sequence of the invention.

CC function, and represents a DNA Sequence of the invention.

CC (NCIMB 40771). Host cells containing the DNA sequences are used to CC produce polypeptides or fragments. The proteins are used in the treatment CC of disease, for inducing an immune response by administering them, to CC produce antibody and/or T-cell immune response. Antagonists of the CC conditions which may be treated include bacterial infections, especially crespiratory, cardiac, gastrointestinal, central nervous, eye, kidney, CC curinary tract, skin, bones and joints. The proteins can also be used to CC cidentify antimirrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection.
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V80065 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to identify modulators or specific receptors; in rational drug design and as an immunogen for vaccines. The MurC gene sequences useful in antisense/ribozyme therapeutics; to detect mutant MurC gene; for chromosomal mapping; to determine bacterial serotype; and for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. Black MT, Burnham MKR, Hodgson J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ward JM;
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24-SEP-1997; 307485.
24-SEP-1996; US-027032.
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V53479 standard;
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C'he invention relates to a UDP-Wacetylmuramate:L-alanine ligase (Murc polypeptide) encoded by the S. aureus Murc gene. Host cells containing an expression system comprising the Murc gene can be used for the recombinant production of the polypeptide. Appoints or the Murc polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. competitive polypeptide are useful for inhibiting the polypeptide e.g. competitive polypeptide are useful for inhibiting the polypeptide e.g. competitive polypeptide are useful for inhibiting the polypeptide e.g. the acterial (especially S. aureus) infections. They are also useful against the liobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The Murc polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for rational articles, to dentify modulators or specific receptors; in rational articles, to dentify modulators or specific receptors; in rational
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Sequence
EP-889123-A2.
07-JAN-1999.
26-JUN-1998; 305064.
03-JUL-1997; US-052720.
(SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                    UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoding MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine immunogen; drug; genetic immunisation; ds.
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Partial nucleotide sequence of the MurC gene.
MurC gene; UDP-N-acetylmuramate:L-alanine lig
bacterial; infection; H. pylori; cancer; ulce
immunogen; drug; genetic immunisation; ds.
                                                                                                                                                                                                                                                                                       V99650;
17-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated MurC poly
nucleic acid - useful
bacterial infections
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(SMIK ) SMITHKLINE BEECHAM
(SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                               Staphylococcus
                                                                                                                                                                                                                                                                                                                             V99650 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug design and as an immunogen for vaccines. The MurC gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant MurC gene; for chromosomal mapping; to determine bacterial serotype; and for genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunisation. The present sequence represents a partial nucleotide
sequence (MurC ORF) of the MurC gene.
Sequence 660 BP; 233 A; 83 C; 120 G; 224 T;
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Similarity 100.0%;
19; Conservative
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US-052720.
                                                                                                                          Location/Qualifiers
22..1335
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Pred. No.
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                                                                                      (MurC polypeptide)"
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Matches 1
                                                                                            Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
Claim 1; Page 1287-1288; 3271pp; English.
This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
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Staphylococcus aureus contig SEQ ID #392.
Computer readable medium; vaccine; S.aureus infection; immunodetection;
Cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Berash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
   the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are
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                                                                                                                                                                                                                                                                                                                                                                          WPI; 97-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
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01-JUN-1994; J01916.
11-NOV-1994; J0-355504.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1246; 2245pp; Japanese. A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
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Sequence 2424 BP; 839 A; 302 C; 462 G; 759 T;
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                                                                                                                                                                                                                                                     determined (esp. using primers and probes derived sequences) as a means of diagnosing abnormal cell recognising different cell types.

Sequence 299 BP; 93 A; 48 C; 45 G; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsubara K, Okub
WPI; 95-206931/27.
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                                                                                                                                                                                                                                                                                                                                                                             The appearance frequency of a given GS in a cDNA library
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                                                           134
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                                                                                                                                                            Local Similarity 100.0%;
                                    ctttaatatttgtaac 149
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CTTTAATATTTGTAAC
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Similarity 100.0%;
19; Conservative
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                                                                                                                              Conservative
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                                                                                                                       Pred.
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Pred. No. 9.94e-02;
0; Mismatches 0;
                                                                                                                                                        Score 16; DB 22;
Pred. No. 3.98e+00;
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                                                                                                                              Mismatches
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                                                                                                                                                                                      Length 299
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                                    by amino acid sequence homology to Bacillus subtilis tRNA synthetase encoded by the tyr5 gene. The enzyme catalyses the aminoacylation of tRNA-Asp, by a two step mechanism. The first step involves formation of a stable enzyme:aspartyl adenylate complex resulting from the specific binding and reaction of ATP and L-Aspartate. Subsequently, the 3' terminal adenosine of enzyme-bound tRNA-Asp reacts with the aminoacyl adenylate, leading to the esterification of the tRNA and release of AMP. Vectors comprising the DNA (or polynucleotides having at least 70 % identity to it) can be used for the recombinant production of the enzyme. The enzyme or its related DNA (through gene therapy) is used to induce an immunological response in a mammal to generate antibodies to protect against disease. The antibodies protect against invasion of bacteria, e.g. by blocking adherence of bacteria to damaged tissue, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          markers for human genes transcribed in-vivo, facilitate tagging of most human genes

Example 4; Page 268: 500pp; English.

The Expressed Sequence Tag was isolated from a human brain cDNA
library as part of a large set of ESTs which can be used as markers
for human genes transcribed in vivo. They can be used to facilitate
tagging of most human genes, for mapping locations of expressed genes
on chromosomes, for individual or forensic identification, for mapping
locations of disease-associated genes, for identification of tissue
                                                                                                                                                                                                                                                                                                       DNA encoding aspartyl-tRNA synthetase from Staphylococcus aureus WCUH 29 - useful for protection against bacterial infections Claim 4; Page 18; 31pp; English.

The present sequence encodes a novel aspartyl tRNA synthetase protein from Staphylococcus aureus strain WCUH29 (NCIMB 40771), which is relat by amino acid sequence homology to Bacillus subtilis tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK) SMITHKLINE BEECHAM Hodgson JE, Lawlor EJ; WPI; 97-365940/34.
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19-JAN-1996; GB-001096.
30-OCT-1996; GB-022617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus. EP-785265-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding aspartyl-tRNA synthetase from Staph. aureus. tRNA synthetase; Bacillus subtilis; tyrs; immunological response; antibody; bacterial infection; adherence; damaged tissue; wound h skin; protection; vaccine; ds.
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r75076 standard; DNA; 1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type, and for prepn. of antisense sequences, probes and constructs. EST01999 has a "marginal" coding probability as evaluated using the coding-region prediction program CRM. See also Q59041-Q61440. Sequence 439 BP; 101 A; 96 C; 81 G; 160 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUI Adams MD, Moreno RF, Venter WPI; 93-272882/34.
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Human brain Expressed Sequence Tag EST01999.
Human brain Expressed Sequence Tag EST01999.
Gene transcription product; genetic markers; tagging; in vivo;
transcription; mapping; locations; chromosomes; chromosomal; s
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12-FEB-1994; US-837195.
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Similarity 100.08;
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                         connective tissue caused
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enter CJ;
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. No. 3.98e+00;
Mismatches 0;
                         by mechanical, chemical
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                                                                                                                     PS Claim 1; Page 1244-1245; 3271pp; English.

PS Claim 1; Page 1244-1245; 3271pp; English.

CThis sequence represents one of 5191 Staphylococcus aureus DNA sequences confite invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access comemory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the Staureus DNA sequences allows putative functions to be assigned so commercial therapeutic or condustrial importance can be obtained. Specifically, sequences which are clikely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against Staureus infection. The composition against Staureus infection. The computer is a sample. Staureus is implicated in numerous human diseases, including cellulities, eyelid infections, food poisoning, osteomyelitis, concluding cellulitis, eyelid infections, scaled skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating computer readable medium.

Sequence 2524 BP; 876 A; 321 C; 517 G; 746 T;
                                                             Query Match
Best Local S
Matches 1
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Best Local Similarity 100.0%;
Matches 16; Conservative
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07-JAN-1997;
05-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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                             1704 gttacaaatattaaag
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(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus
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V74671;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-S.aureus vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA;
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GTTACAAATATTAAAG
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Similarity 100.08;
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1767 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
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Pred. No. :
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-hes 0;
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                                                                                          Length 2524;
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RESULT 10 ID T40041 standard;

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PS Claim 8; Page 143-144; 178pp; English.

CC T40032-T40042 represent exons of the wild type human presentlin-1 (PS-1)

CC sequence (see T40028 and T40029 for the two CDNA forms of PS-1). The PS-1

CC form represented by T40029 results from alternate splicing of the genomic

CC DNA sequence. T40031 represents the coding sequence for wild type human

CC PS-2. The presentilins are a family of highly conserved integral membrane

CC proteins with a common structural motif, common alternate splicing

CC patterns, and common mutational hot spot regions. Mutations in PS genes

CC are implicated in familial Alzheimer's disease (AD) and possibly other

CC diseases such as cerebral haemorrhage, schizophrenia, depression etc., so

CC detection of mutations in these sequences can be used for diagnosis of

CC containing antisense sequences, antibodies selective for mutant forms of

CC containing antisense sequences, antibodies selective for mutant forms of

CC expression are potentially useful for treatment of AD etc. Transgenic

CC animals are useful as models for drug screening. The antibodies can also

CC be used e.g. for affinity purification and in immunoassavs.
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31-OCT-1996.
29-APR-1995; US-431048.
R 28-APR-1995; US-431048.
R 28-JUN-1995; US-496841.
R 31-JUL-1995; US-509359.
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
PA (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
PA (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
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Best Local S
Matches 1
                                15-JAN 1998.
04-JUL-1997; CA0475.
02-JAN 1997; US-034590.
05-JUL-1996; US-021673.
12-JUL-1996; US-021700.
08-NOV-1996; US-029895.
(HSCR-) HSC RES & DEV LP.
(UTOR ) UNIV TORONTO GOVERNING COUNCIL.
Fraser PE, Rommens JM, St George-Hyslop PH
WPI; 98-286355/25.
                                                                                                                                                                                                                                                                                                                       Human presentilin-1 gene exon 12 and flanking regions.

Presentilin-1; PS1 gene; human; familial Alzheimer's disease; FAD;

cerebral haemorrhage; schizophrenia; depression; epilepsy;

mental retardation; diagnosis; therapy; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; excepression; antibody; gene expression modulator; therapy; ss.
 New isolated mutant presenilin-1 products for use in detection, d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be used e.g. for affinity purification and in immunoassays. Sequence 1003 BP; 292 A; 188 C; 193 G; 313 T;
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                                                                                                                                                                                                                                                                                                               HOMO
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20-JUL-1998 (first entry)
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                                                                                                                                                                                                                                                                                                               sapiens.
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Similarity 100.0%;
15; Conservative
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Pred. No.
0; Misma
 -1 genes -
diagnosis
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J. 1.31e+01;
Thes 0;
                                                      PH;
useful for developing and therapy of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1003;
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RESULT
ID V7
AC V7
DT 16
DE St
                                                                                                                                                                                                                                                                                                                        PT DNA construct contg. gene of interest controlled by cotton fibre produced construct contg. gene of interest controlled by cotton fibre produce cells expressing genes affecting pigmentation produce cells sequence is the Racil promoter construct, pcgN4735, isolated from cotton fibre genomic clone 15-1. DNA constructs containing cotton fibre genomic clone 15-1. DNA constructs containing cotton fibre cells with altered phenotype, especially altered colour. Genes involved in the production of melanin (e.g. tyrosinase colour. Genes involved in the production of melanin (e.g. tyrosinase colour. Genes involved in the production of melanin (e.g. tyrosinase condition of mono-oxygenase genes possibly in conjunction with a ctryptophanase gene) are of interest. The promoters of the invention are creliable and permit expression of a protein selectively in cotton fibre confict qualities such as fibre strength, length, colour and dyability cas required. The construct and methods can also be used for the plant hormone. In particular, fibres from a plant producing coloured confibres may be used to produce yarns and/or fabrics that do not require dyeling.

Sequence 3045 BP; 1063 A; 450 C; 366 G; 1162 T;
                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 1
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Best Local S
Matches 1
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This genomic DNA sequence comprises exon 12 plus flanking regions of the human presenilin-1 (ApS1) gene. Flanking genomic sequences (see T99661-71) for exons 1-13 of the ApS1 gene, as well as ApS1 cona clones (see V04666-67), are provided. Mutations in the human presenilin genes have been linked to the development of familial Alzheimer's disease (FAD). Presenilin nucleic acids and proteins can be used in screening and diagnosing FAD, identifying and developing therapeutics for treatment of FAD, and in producing cell lines and transgenic animals useful as models of FAD. Sequence 1003 BP; 292 A; 188 C; 193 G; 313 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cotton fibre promoter clone Rac13 construct, pCGN4735. promoter; fibre-specific; transcriptional factor; promoter; altered phenotype; colour; melanin; indigo; ss. Gossypium hirsutum cv. coker 130. W09640924 A2.
16-MAR-1999 (
Staphylococcus
                                          V74407
                                                              V74407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CALJ ) CALGENE INC.
Mcbride K, Pear JR, Perez-Grau L,
WPI; 97-052325/05.
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07-JUN-1995; US-480178.
01-JUL-1996; ZA-005572.
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                                                              standard;
                                                                                                                                                                                                                                 78.9%;
Similarity 100.0%;
15; Conservation
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Similarity 100.0%;
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                                                              DNA; 11050
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Pred. No.
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Pred. No. 1.31e+01;
0; Mismatches 0;
                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                 1.31e+01;
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Сþ 8

(first entry)

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or condustrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The CC saureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-S.aureus vaccines
Claim 1; Page 577-583; 3271pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide(s) and proteins derived stored on computer readable medium and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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toxic shock syndrome;
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Sequence
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d infection; food poisoning; osteomyelitis; therapy;
urgical wound infection; scalded skin syndrome;
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different types.
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Best Local :
Homo sapiens.

W09845437-A2. []

15-OCT-1998.

10-APR-1998; U06956.

10-APR-1997; US-837312.

(GEMY) GENETICS INST IN
                                                                                                                                           EST clone IJ942.

EXPressed sequence tag; secreted protein; haematopoiesis regulator; Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; has tissue growth; activin; inhibin; dene therapy; thrombolysis; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
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V89012;
12-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene signature; messenger RNA; mRNA; human; cloning; mapping; non-biased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8069 ttacaaatattaaag
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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12-JUL-1996
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DR WFI; 99-070078/06.

PT New polynucleotides encoding human secreted proteins - derived from PT e.g. human blood, kidney, foetal lung, placenta, testes, brain, PT ovary, pituitary, retina and colon cDNA libraries

PT ovary, pituitary, retina and colon cDNA libraries

Cclaim 1; Page 588; 641pp; English.

CC The present sequence represents an expressed sequence tag (EST), and is color proteins encoded by them are predicted to are all secreted EST sequences isolated from a variety of human tissue cources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and canimals, although no supporting data is given. Suggested activities and activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haemostatic and inflamentary anti-inflamentary.
                                                                                                                                           Query Match 73.7%;
Best Local Similarity 100.0%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                           Sequence
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68 tctttaatatttgt 81
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Pred. No. 4.20e+01;
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Sequence 151, Application US, Sequence 151, Application US, Patent No. 5840540  GENERAL INFORMATION: FRASER, PAUL 1  TITLE OF INVENTION: GENERAL TIPLE OF INVENTION: GENERAL TIPLE OF INVENTION: TO AN APPLICANT: FUSTA, HURW. STREET: High Street TO AN NUMBER OF SEQUENCES: 183 CORRESPONDENCE ADDRESS: ADDRESSEE: TESTA, HURW. STREET: High Street TO CITY: Boston  STATE: MASSICHMENT: HIGH STREET TO ANDRESSEE: TESTA, HURW. STREET: HIGH STREET TO STATE: MASSICHMENT: FORM: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy discomputer: LAPPLICATION DATA: APPLICATION NUMBER: US, FILING DATE: 10-NOV-199 CLASSIFICATION: 435 PRIOR APPLICATION UMBER: US, FILING DATE: 10-NOV-199 CLASSIFICATION UMBER: US, FILING DATE: APPLICATION HURBER: US, FILING DATE: APPLICATION INFORMATION NAME: PICHERY, SERVING DATA: APPLICATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1003 base pair: TYPE: nucleic acid STRANDENESS: single TOPOLOGY: linear	489 1 489 1 489 1 489 3 1198 3 1198 3 1198 3 1198 3 1196 1 1469 4 1497 3 1745 1 1774 4 1795 3 2020 3 2020 3 2020 3 2020 3 3203 3 3203 3 3203 3 3203 3 3408 3 5496 1
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Patent No. 5457090

PROTEASE NEXIN-I VARIANTS

NUMBER OF SEQUENCES: 7

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/924,294

PILING DATE: 03-AUG-1992

PROTECTION DATA:
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TITLE OF INVENTION: RECOMBINANT PURIFIED PROTEASE NEXIN NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
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PATENT NO. 5495001

APPLICANT: MCGROGAN, MICHAEL P.; SCOTT, RANDY W.; BAKER,
                                                                                                                                                                                                                                              SEQ ID NO:1
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Sequence 2198 BP; 536 A; 477 C; 451 G; 565 T; 169 other;
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SEQUENCE 1003 BP;
                                               413 AAATATTAAAGAAG 426
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APPLICATION NUMBER: 542,484
FILING DATE: 21-JUN-1990
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FILING DATE: 24-AUG-1993
APPLICATION NUMBER: 25,450
FILING DATE: 13-MAR-1987
APPLICATION NUMBER: 871,501
FILING DATE: 06-JUN-1986
APPLICATION NUMBER: 870,232
  AAATATTAAAGAAG 19
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ence 2198 BP;
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Similarity 100.0%;
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Matches 1
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Best Local Similarity 100.0%;
Matches 14; Conservative
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01-JAN-1900
01-JAN-1900
Patent No. 5495001.
Patent No. 5495001
Patent No. 549500
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/:
APPLICATION NUMBER: US/:
FILING DATE: 21-JUN-1990
SEQ ID NO:1:
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Patent No. 5187089
APPLICANT: SCOTT,
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Sequence 2201 BP; 537 A; 480 C; 449 G;
                                                                                                                                                                                                    5457090-3 STANDARD; DNA; UNC;
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Sequence 2198 BP; 534 A; 476 C; 455 G; 564 T; 169 other;
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01-JAN-1900
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Local Similarity 100.0%;
hes 14; Conservative
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APPLICATION NUMBER: US/
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 111,111
FILING DATE: 24 - AUG-1993
APPLICATION NUMBER: 25,450
FILING DATE: 13 - MAR-1987
APPLICATION NUMBER: 871,501
FILING DATE: 06 - JUN-1986
APPLICATION NUMBER: 870,232
FILING DATE: 03 - JUN-1986
ID NO:8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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Pred. No. 3.30e+00;
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Pred. No. 3.30e+00;
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Best Local Similarity 100.0%;
Matches 14; Conservative
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Best Local S
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/N
FILING DATE: 21-JUN-1990
SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5187089.
Patent No. 5187089
APPLICANT: SCOTT, RA
TITLE OF INVENTION:
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                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,155A
FILING DATE: 02-UUN-1994
CT-ASSIFICATION: 435
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Local Similarity 100.0%;
les 14; Conservative
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FILING DATE: 03-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 542,
                                                                                                                                                                                                 APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: CDK4 Binding Proteins
NUMBER OF SEQUENCES: 95
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION
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                                                                                                                  COUNTRY: USA
ZIP: 02109
                                                                                                                                          CITY: Boston
STATE: MA
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            CLASSIFICATION:
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N: PROTEASE NEXIN-I VARIANTS WHICH INHIBIT
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Pred. No.
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Pred. No. 3.
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3.30e+00;
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Best Local S
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REGISTRATION NUMBER: 36,709
REFERENCE_DOCKET NUMBER: MII-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-75941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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SEQUENCE 8201 BP; 2258 A; 1887 C; 2003 G; 2053 T; 0 OTHER.
SEQUENCE 345 BP; 121 A; 49 C; 68 G; 107 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXXX
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                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
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Local Similarity 100.08;
                                                                                                                        NAME: McMasters David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480
TELECOMMUNICATION INFORMATION:
                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/393,305
FILING DATE: 22-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 ACAAATATTAAAGA 17
                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
                                  FEATURE:
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STREET: 000.
STRY: Seattle
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
          NAME/KEY:
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                                                               TYPE: nucleic acid
                                            STRANDEDNESS:
TOPOLOGY: lir
                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                             Washington
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                                                                                                                                                                                                                                                                                                   USA
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Rauch, Charles
VENTION: EPITHELIUM-DERIVED T-CELL FACTOR
       CDS
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                                             linear
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              345
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US/08393305
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Pred. No. 3.30e+00;
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Score 13;

DB 1;

Length 345;

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RESULT

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Patent No. GENERAL I

APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

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Query Match 68.4%;
Best Local Similarity 100.0%;
Matches 13; Conservative
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          Sequence 12, Application US/08726817 Sequence 12, Application US/08726817 Patent No. 5707616
                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 1..345
SEQUENCE 345 BP; 124 A;
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Sequence 13, Application US/08393305
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                                                                                US-08-726-817-12 STANDARD;
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SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic actd
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,305
FILING DATE: 22-FEB-1995
FILING DATE: 22-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,963
REFERICE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
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ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Washington
 INFORMATION:
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Eisenman, June
Fung, Victor
Rauch, Charles
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                                                                                DNA; UNC;
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0; Mismatches 0;
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Pred. No. 1.30e+01;
0; Mismatches (
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                                                                                                                                                                                            Sequence 13, Application US/08726817 Sequence 13, Application US/08726817 Patent No. 5707616
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 1..345
SEQUENCE 345 BP; 121 A; 49
                                                                                                                                                                            Patent No. 5707616
GENERAL INFORMATION:
                                                                                                                                                                                                                                                  XXXXXX
                                                                                                                                                                                                                                                               US-08-726-817-13 STANDARD; DNA; UNC; 345 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/726,817
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                     282 AAATATTAAAGAA 294
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                                                                                                                                                                                                                                                                                                                                                                         68.4%;
Local Similarity 100.0%;
les 13; Conservative
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                          APPLICANT: Eisenman, June APPLICANT: Fung, Victor APPLICANT: Rauch, Charles
                                                                                                                                                 APPLICANT: Grabstein, APPLICANT: Anderson, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                   CORRESPONDENCE ADDRESS:
                                                                                             TITLE OF INVENTION:
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                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: | linear
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                                         STREET:
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                                                      ADDRESSEE:
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Seattle
: Washington
RY: USA
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COUNTRY:

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FEATURE:

TOPOLOGY:

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Query Match
Best Local :
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SEQUENCE 345 BP; 124 A; 50 C; 64 G; 107 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08726817
Sequence 4, Application US/08726817
Patent No. 5707616
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      XXXXXX
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FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 AAATATTAAAGAA 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 68.4%;
Local Similarity 100.0%;
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                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,817
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US 08/393,305 FILING DATE: 22-FEB-1995 ATTORNEY/AGENT INFORMATION:
                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                             APPLICANT:
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                                                  CLASSIFICATION:
                                                           APPLICATION NUMBER: US/01 FILING DATE: 04-OCT-1996
                                                                                                                                                                ZIP: 98104
                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                        CITY: Seattle
STATE: Washing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: 480052.409C2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 base pairs
                                                                                                                                                                                                                                                              Rauch, Charles
VENTION: EPITHELIUM-DERIVED T-CELL FACTOR
                                                                                                                                                                           USA
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Eisenman, June
                                                                                                                                                                                                                                                                                                                           Grabstein, Kenneth
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04-OCT-1996
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Pred. No. 1.30e+01;
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Query Match 68.4%;
Best Local Similarity 100.0%;
Matches 13; Conservative
SEQUENCE 489 BP; 162 A; 81 C; 92 G; 154 T; 0 OTHER
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Sequence 4, Application PC/TUS9403793
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PCT-US94-03793-4 STANDARD; DNA; UNC; 489
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                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         NAME: Launer, Charlene
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rauch, Charles TITLE OF INVENTION: Inter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                   TOPOLOGY: 11
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STREET: 5
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Washington
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Seattle
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Eisenman, June
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IBM PC compatible
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Pred. No. 1.30e+01;
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Best Local Similarity 100.0%;
Matches 13; Conservative
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Best Local Similarity 100.0%;
Matches 13; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 28,655
REFERENCE/DOCKET NUMBER: 283
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                              Sequence 1, Application US/08535733
Sequence 1, Application US/08535733
Patent No. 5660824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XXXXXX
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6 AAATATTAAAGAA 18
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6 AAATATTAAAGAA 18
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APPLICANT: Quinn, LeBris
APPLICANT: Grabstein, Kenneth
APPLICANT: Troutt, Anthony B.
TITLE OF INVENTION: Muscle-Trophic Factor
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7, Word 5.1a
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,733
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
                                                                                                Score 13; DB 2; Length 489; Pred. No. 1.30e+01; 0; Mismatches 0; Indels
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Pred. No. 1.30e+01;
0; Mismatches 0
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	402; scale 4.431	; Variance 1.	Mean 6.213	ics:	Statist
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·	s, Biocomputing Research Unit. iversity of Edinburgh, U.K. by Oxford Molecular Ltd	Collins, 998 Unive rights by	.1A J (c) istri	Release 3 Copyright D	
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## ALIGNMENTS

		JOURNAL COMMENT	AUTHORS TITLE	REFERENCE	SOURCE ORGANISM	ACCESSION NID VERSION	RESULT 1 LOCUS DEFINITION
cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html	Contact: Kobert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.	Unpublished (1997)	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 551)</pre>		SUBUNIT (HUMAN); MKNA sequence.  AA583407  92368016  AA583407.1 GI:2368016	AA583407 551 bp mRNA EST 08-SEP-1997 nn42b04.s1 NCI_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086511 3' similar to 9b:L07395 PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC

FEATURES

Seg primer: -40m13 fwd. ET from Amersham High quality sequence stop: 340. Location/Qualifiers

07-NOV-1994

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Dictyostelium discoideum.
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AU037905 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSE439, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y. The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                          89.5%;
Similarity 100.0%;
17; Conservet
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99156227
On Jan 5, 1998 this sequence v
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T = 'Dictyostellum discoideum cDNA project in Japan'.
Location/Qualifiers
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/dev_stage="slug"
39 c 16 g 109 t 6 others
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/clone=lib="NCI_CGAP_GC5"
/tissue_type-"germ cel1 tumor"
/lab_host="SOLR (kanamycin resistant)"
93 c 100 g 178 t
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/clone="SSE439"
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1 (bases 1 to 253)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Rabaktchis,C. and Tessier,A.

Sebastiani-Rabaktchis,C. and Tessier,A.
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                                                 Homo sapiens
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Single read. 19 T removed at sequence 5'end
Genexpress_library_ldt: C; Genexpress_sequence_idt: alc-leg05
Seq primer: (-21)M13_universal.
Location/Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: 33160778698
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1, rue de l'Internationale, BP60 91002 EVRY Cedex,
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/Organism="Homo sapiens"
/Note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; Sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
/db.xref="taxon:9060"
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/dev_stage="3 months old"
33 c 37 g 82 t
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/clone="c-leg05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="normalized infant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                           298 bp
                                                                                                                                                                                                                                                    adult (K.Okubo) Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16; DB 8; 1
Pred. No. 8.02e-03
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sapiens cDNA
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Best Local Similarity 100.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1877535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI383567 324 bp mRNA EST 18-MAR-1999 tc45e41.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2067596 3', mRNA sequence.
AI383567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: kousaku@imcb.osaka-u.ac.jp
Human Gene Slynature, 3'-directed DNA sequence. We are not
submitting the same cDNA sequence redundantly to DDBJ since 1993.
For the abundance information of clones with this sequence in this
library and as well as in other 3'-directed libraries, see '
http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones
represented by this GS sequences is also found there.
10001
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Okubo,K.

BodyMap; human gene expression database
Unpublished (1995)
On Apr 14, 1993 this sequence version re
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 324)
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AI383567.1 GI:4196348
                                                                                                                                                         High quality sequence stop: 313.
Location/Qualifiers
                                                                                                                                                                                                Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Tel: 06-877-5111(ex.3315)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_msp="958B12; 5; 5p15.31-5p15.33"
/clone_lib="Human adult (K.Okubo)"
/dev_stage="adult"
48 c 45 g 102 t 10
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Pred. No. 8.02e-03;
0; Mismatches 0
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Best Local Similarity 100.0%;
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Tumor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3188852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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AI474210
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Location/Qualifiers
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                    129
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                                                                                                            /organism="Homo sapiens"
/organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
/note="Organ: mixed site of linker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
/clone="IMAGE:2115399"
/clone="IMAGE:2115399"
/clone="IMAGE:2115399"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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               pregnant uterus"
/lab_host="DH10B"
44 c 52 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
41 c 50 g 108 t
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                                                                              /tissue_type="Pooled human melanocyte, fetal heart,
                                                                                                   clone_lib="Soares_NhHMPu_S1"
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Pred. No. 8.02e-03;
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Query Match Best Local Similarity

84.2%;

Score 16; Pred. No.

DB 27; 8.02e-03;

Length 330;

be

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JOURNAL COMMENT
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SOURCE
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 9
                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
Tumor Gene Index
                                                                                                                                                                                                                               AA988210 350 bp mRNA or98h07.sl NCI_CGAP_Lu5 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research 932 Clopper Road, Gaithersburg, MD 20878 Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T05047 346 bp mRNA EST02935 Fetal brain, Strata clone HFBCQ35, mRNA sequence
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 3018699423
Email: mdadams@tigr.org
Seq primer: M13-21.
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1 (bases 1 to 346)
               Unpublished (1997)
                                                                           Eutheria; Primates; 1 (bases 1 to 350)
                                                                                                                         Homo sapiens
                                                                                                                                                                                                                 mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                       AA988210.1 GI:3173574
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Similarity 100.08;
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Jan 19, 1998 this sequence version replaced gi:2150481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: LambdaZAP-II; 17-18 wk gestation, female; oligo-dT + random primed cDNA synthesis; lambdaZAP-II vector, 1.0kb average inser size."
/db_xref-"ATCC (lnhost):81784"
/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism≃"Homo sapiens"
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Pred. No.
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Stratagene (cat#936206) Homo sapiens cDNA
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Best Local Similarity 100.0%;
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             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                           National Cancer Institute, Cancer Genome Anatomy Project (Tumor Gene Index Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:2044387.
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 369)
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                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 291.
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                                                                                                                                                                                                                                                                                                                                                                                                                     numan.
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Location/Qualifiers
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Lu5"
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Pred. No. 8.02e-03;
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                                                                                                                                       vector to vector length is 498
Seg primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 360.
                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpubl
On Apr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 380)
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AA122490.1 GI:1681553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
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Similarity 100.08;
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Apr 14, 1993 this sequence version replaced gi:785754.
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/note-"Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. From M2 cells, a highly metastatic derivative of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1562498"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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Pred. No. 8.02e-03;
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Best Local Similarity 100.0%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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On Apr 14, 1993 th
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Emmert-Buck, M.D., Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robert_Strausberg@nih.gov
                                                                                                                                                                /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was provided to the Not I and Eco RI sites of the modified pT7T3 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the K-1735 (mouse) melanoma. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
/tissue_type="carcinoid"
/lab_host="DH10B"
61 c 65 g 13
                                                                                                                        constructed by Bento Soares and M. Fatima Bonaldo. /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Stratagene mouse melanoma (#937312)"
/tissue_type="melanoma"
/dev_stage="M2 cells"
                                                                        /clone_lib="NCI_CGAP_Lu5"
                                                                                               /clone="IMAGE:1883194"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="SOLR (kanamycin resistant)"
65 c 55 g 134 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:584489"
                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this sequence version replaced gi:716440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16; DB 36;
Pred. No. 8.02e-03;
0; Mismatches 0
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Best Local
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Best Local
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   12
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI369619 410 bp mRNA EST 16-FEB-1999 gy70h02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017395 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
On Jan 14, 1998 this sequence version replaced gi:1797674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 410)
1 (bases 1 to 410)
1 (Chases 1 to 410)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CG
                                                                                                                                                      h 84.2%;
Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Similarity 100.0%;
16; Conservative
                                                                                                                               16;
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                                                                                                                                                                                                                                                                                                150
                                                                                                                               Conservative
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/db_xref="taxon:9506"
                                                                                                                                                                                                                                                                                   /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
64 c 67 g 128 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:2017395"
/clone_lib="NCI_CGAP_Brn25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double-stranded cDNA was ligated to Eco RI rs (Pharmacia), digested with Not I and cloned into
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Pred. No.
0; Misma
                                                                                                                                                             Score 16; I
                                                                                                                               . No. 8.02e-03; Mismatches 0;
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                                                                                                                                                                                           DB 26;
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                                                                                                                                                                                       Length 410;
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by Bento
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SOURCE
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Best Local Similarity 100.08;
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                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                  TTACAAATATTAAAGA 17
                                                                                                                                                                                                                                           R07577 415 bp mRNA EST ye97b09.s1 Soares fetal liver spleen lNFLS IMAGE:125657 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST56978 Infant brain Homo sapiens cDNA containing L1 repeat, mRNA sequence.
AA349916
1 (bases 1 to 415)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 12, 1
Other_ESTs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 414)

Adams,M.D., Kerlavage,A.R., Fields,C. and Venter,J.C.
                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93364420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature Genet. 4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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SSTs: EST56977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/note="Organ: brain; Vec
Site_2: NotI"
                                                                                                                                                                                          GI:759500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="infant"
73 c 83 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Infant brain"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="ATCC (inhost):150864"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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Pred. No. 8.02e-03;
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Best Local Similarity 100.0%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                     AA900060 424 bp mRNA EST 05-FEB-1999 UI-R-E0-da-f-02-0-UI-S1 UI-R-E0 Rattus norvegicus cDNA clone UI-R-E0-da-f-02-0-UI 3' similar to > gi|2863157|gb|AA800202|AA800202 EST189699 Normalized rat heart, Bento Soares Rattus sp. cDNA 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High qality sequence stops: 208 Source: IMAGE Consortium, LLNL The clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1682 Std Error: 0.00
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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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                                                                                                                                                                                         Eukaryota;
Eutheria; F
                                                                                                                                                                                                                         Norway rat.
Rattus norvegicus
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Insert Size: 1682
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Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                        97044477
                                                                                                     Genome Res. 6 (9),
                                                                                                                        discovery
                                                                                                                                                       Bonaldo, M.F.,
                                                                                                                                                                                                                                                                            AA900060.1 GI:4232549
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                                                                                                                                       Normalization and subtraction: two
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/lab_host="DH10B (ampicillin resistant)"
73 c 84 g 123 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares fetal liver spleen lNFLS"
                                                                   1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:125657"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
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                                                                                                                                                       Lennon, G. and Soares, M.B.
                                                                                                       791-806 (1996)
                                                                                                                                                                                       Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
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Pred. No. 8.02e-03;
0; Mismatches 0;
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Search completed: Sat Nov 27 15:23:49 1999 Job time: 225 secs.
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Best Local Similarity 100.0%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult 12-Day-Embryo library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this cDNA sequence: 1-32, PAT_rich#Low_complexity Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Research Genetics The following repetitive elements were found in
                                                                                                                                                                                                                                                                                                                                               136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Sprague-Dawley"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: NotI; Site_2: EcoRI; This library
consists of a mixture of individually tagged normalized
libraries constructed from 8, 12 and 18 day embryo. The
tag is a string of 3-5 nucleotides present between the
Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture."
                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="embryonic"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10116"
/clone="UI_R-E0-da-f-02-0-UI"
/clone_lib="UI-R-E0"
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DESON HINTER TOPA SILL

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Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llni.gov) for further information.
MGI:688758
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 384.

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se.  lus  y Metazoa; ( Rodentia; 1 1 to 489)  Hillier,L., Kucaba,T., Kucaba,T., Kucaba,T., Ku, Stel B., Wylie,T, R. HHMI Mouse ed (1996) , 1998 this	0 40 10		37	14	20	27	26	23	27	26	o o	ω ω 5	34	15	10	9	23	ο G	26	ا س	် ပ	2 0	18	20	18
Chordata; Sciurognat Sciurognat , Allen,M., , Lacy,M., , Lennon, , Lennon, , EST Proje sequence	mRN/ mouse ', mRN/	ALIGNMENTS	$\vdash$											AA579079									00	0454 <i>3</i> 88717	A77887
raniata; Vertebrata; Mamm i; Muridae; Murinae; Mus. Bowles,M., Dietrich,N., Le,M., Martin,J., Morris, n,F., Underwood,K., Moore ., Soares,B., Wilson,R. a t	1 macrophage (#937306) Mus musculus 1 sequence.		1D037011098 Cosmi 3.4	υ W	ωω	ω	ມເມ	ωu	υ	ωu	υω	ww	ω		ω	ມພ	ωι	υ	ωı	u u	ω (	w c	4a03.sl NCI_CGAP_GC 3.4	-R-C1-)z-a-08-0-01.8 3.4 51d04.s1 NCI_CGAP_Pr 3.4	j42d07.sl Soares_feta 3.4
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Best Local Similarity 100.0%;
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1 (bases 1 to 493)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,; Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. Washd-NCI human EST Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1405126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ac07c03.s1 Stratagene lung (#937210) IMAGE:855748 3' similar to gb:X57809
                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 424.
                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                  /note="Organ: blood; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"/db_xref="taxon:1000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Stratagene mouse macrophage (#937306)"
/tissue_type="macrophage"
/dev_stage="WEHI-3 cell line"
/lab_host="SOLR (kanamycin resistant)"
138 c 121 g 134 t
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
121 c 164 g 124 t
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                                                              /sex="male"
                                                                                   /clone_lib="Stratagene lung
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g4370343
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Clemson University
100 Jordan Hall, Clemson University, Cl
Tel: 864 656 5737
Fax: 864 656 4293
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A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ399316 506 bp DNA GSS 05-MAK-1999 mgxb0008L21f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0008L21f, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                               than 25% genome coverage. High density are available upon request." /db_xref="taxon:5138"
                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater
                                                                                                                                                                           /tissue_type="Protoplasts"
/lab_host="E coli DH10B"
131 c 96 g 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Magnaporthe grisea"
/strain="70-15"
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/clone_lib="CUGI Rice Blast BAC Library"
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Pred. No. 1.47e-02;
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Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein,P., Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                    AI295400 603 bp mRNA EST 01-DEC-1998
LP09018 5prime LP Drosophila melanogaster larval-early pupal pOT2
Drosophila melanogaster cDNA clone LP09018 5prime, mRNA sequence.
AI295400
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Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA786907 516 bp mRNA EST 31-JUL-1998 m7b0lal.r1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone m7b0lal 5', mRNA sequence.
                                                                         Eukaryota; Metazoa; Arthropoda;
Pterygota; Diptera; Brachycera;
Drosophilidae; Drosophila.
1 (bases 1 to 603)
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We anticipate the future release
Genetics Stock Center
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Fax: 405 325 7762
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On Jan 19, 1998 this sequence version replaced gi:2150589.
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Prade,R. and Roe,B.
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Eukaryota; Fungi; Ascomycota; Euascomycetes;
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                                                                                                                                                                             fruit fly.
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Similarity 100.0%;
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Location/Qualifiers
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XhoI; 5' end of cDNA cloned into EcoRI site of pBlueScript
3' end of cDNA cloned into XhoI site of pBlueScript"
/db_xref="taxon:5072"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Emericella nidulans"
/strain="FGSC A26"
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Muscomorpha; Ephydroidea;
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1 (bases 1 to 147)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuq: Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thorisian, T., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mg73d12.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:438647 5', mRNA sequence.
AA051068
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University of California Berkeley
539 LSA, Beskeley, CA 94720-3200, USA
Fax: 510 643 9947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ဝ္ပ
                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                      Unpublished (1996)
On May 5, 1995 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: http://www.fruitfly.org/EST, e
Sequence is the complete cDNA Insert.
Plate: 90 row: B column: 6
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                                    Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 135.
                                                                            MGI:263983
                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
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/note-"Organ: whole body; Vector: pOT2; Site
Site_2: xhol; Sized fractionated cDNAs were
ligated into pOT2. Plasmid cDNA library.
Location/Qualifiers
1. .147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male and female"
/dev_stage="larvae-pupae"
/lab_host="DH5-alpha"
151 c 197 g 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:7227"
/clone="LP09018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="LP Drosophila melanogaster larval-early pupal
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Pred.
0; M
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. No. 1.47e-02;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 est@fruitfly.berkeley.edu
                                                                                                                                                                                                                                                                                                           replaced
                                                                                                                                                                                                        Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 603;
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                                                                                                                                                                                                        MO 63108
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                                                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 GCAGTCGCGTGCG 20
                                                                                                       Seq primer: MIDREL
High quality sequence stop: 95.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 215)
1 (bases 1 to 215)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
Washington University School of Medicine
                                                                                                                                                                                    Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further:
                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-Merck EST Project Unpublished (1995)
On Apr 18, 1995 this sequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R97568 215 bp mRNA EST 11-SEP-1995 yq57g07.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:199932 5', mRNA sequence.
                                                                                                                                                                                                                                                          High quality sequence stops: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R97568.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g983228
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Similarity 100.0%;
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/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
lst strand cDNA was primed with a Pac I - oligo(dT) primer
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/dev_stage="13.5-14.5dpc total fetus"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/14 g 18 t
                                                                          /organism="Homo sapiens"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="Soares mouse embryo NbME13.5 14.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    this sequence version replaced gi:775517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13; DB 35;
Pred. No. 3.46e-01;
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                                                                                                                                                                                            information.
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RESULT LOCUS

SOURCE KEYWORDS VERSION

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FEATURES

pSPORT1;

Site\_1: NotI; Site\_2: SalI; 1st

COMMENT

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REFERENCE
AUTHORS
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Best Local (
                                               source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;

Cyprinoidea; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 220)

Clark, M.; Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M.,

Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,

Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,

Person, B., Schurk, R.,

Person, B., Schurk, R.,

Ritter, E.; Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
                                                                                                                                                                                                         Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@qenomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                              Trace considered overall poor quality Possible reversed clone: similarity on Seq primer: T3 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Stephen L. Johnson
Washidgton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R. and Wilson, R. WashU Zebrafish EST Project 1998 Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI397401 220 bp mRNA EST 05-FEB-1999 fb22903:y1 zebrafish WashU MPIMG EST Danio rerio cDNA 5' simil: TR:P79101 P79101 CLEAVAGE AND POLYADENYLATION SPECIFITY FACTOR PROTEIN: ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Oct 6, 1998 this sequence version replaced gi:3712226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zebrafish
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                                                                                                                                                                                            www.rzpd.de)
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                                                                      quality sequence stop: 1.
Location/Qualifiers
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/note="Vector: pSPORT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH108 (ampicillin resistant)"
37 c 54 g 59 t 8 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares fetal liver spleen lNFLS'
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/map="19q13.2"
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Pred. No. 3.46e-01;
0; Mismatches 2;
                                                                                                                                          on wrong strand
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double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORTI vector (BRL), Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck

oligo(dT)15 primer

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RESULT
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Best Local Similarity 100.0%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                               source
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                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seg primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 282.
                                                                                                                                                                                                                                                                                           Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 296)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Washu-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
AA233357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA233357 296 bp mRNA EST 28-FEB-1997 zr29d07.rl Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664813 5' similar to TR:G986918 G986918 A10 ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ဝှ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="26 somite embryos, adult livers, shield
stage embryos"
/note="Organ: brain; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="XL1-blue MRF"
47 c 44 q 5
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                                                   /organism="Homo sapiens"
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                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             this sequence version replaced gi:716893
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Pred. No. 3.46e-01;
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Best Local
Query Match 65.0%;
Best Local Similarity 100.0%;
Matches 13; Conservative
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AA882998
                                                                                                                                                                                                                                                                                                                                                                     Av. Gral Paz entre Albarellos y Constituyentes, cp(1650) San Martin, Prov. de BS AS. Argentina Tel: (54-1)752-9639 or (54-1)752-0021 Fax: (54-1)752-0021 or (54-1)752-9839 Email: dsanchez@inti.gov.ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Sanchez D.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Apr 14, 1993 this sequence version replaced gi:692606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene discovery through expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 303)
Verdun, R.E., Di Paolo, N.C., Urmenyi, T.P., Frasch, A.C.C. and Sanchez, D.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    San Martin)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trypanosoma cruzi.
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Similarity 100.0%;
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                                                                                                                                                                                          /note="cDNA library constructed with oligo dT primed
epimastigote mRNA and cloned in pt7t318D phagemid wi
modified polylinker (PHARMACIA)"
/db_xref="taxon:5693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligo dT. Uninduced, exponentially growing neuroepithelial cells (Ntera-2/cl.Dl). Average insert size: 1.0 kb; Uni-ZAP xR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                      /map="X q11.2-q12; 737E12; 16"
/clone="575"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="neuroepithelial cells"
/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
70 c 95 g 56 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3' -3' adaptor sequence: /db_xref="GDB:5426844"
                                                                                           /clone_lib="T. cruzi epimastigote normalized
/cell_type="epimastigote"
52 c 63 g 121 t 4 others
                                                                                                                                                                                                                                                                            /strain="Cl-Brenner"
                                                                                                                                                                                                                                                                                          /organism="Trypanosoma cruzi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Stratagene NT2 neuronal precursor 937230"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:664813"
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                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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Score 13; DB 20;
Pred. No. 3.46e-01;
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LOCUS AI045436 351 bp mRNA EST DEFINITION UI-R-C1-jz-a-08-0-UI.s2 UI-R-C1 Rattus norvegicus
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Best Local Similarity 100.0%;
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. washU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNI; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA778878 317 bp mrNA EST 05-FEB-1998 23/42607 ISOARES_fetal_liver_spleen_lNFLS_S1 Homo sapitens cDNA clone IMAGE:452941 3' similar to gb:U15537_rna2 PROTEIN-TYROSINE PHOSPHATASE 1C (HUMAN); mrNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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//Organism="Homo Sapiens"
//Organism=
//Organ
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="20 week-post conception fetus"
/lab_host="DH108 (ampicillin resistant)"
97 c 80 g 96 t
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/clone="IMAGE:452941"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13; DB 18;
Pred. No. 3.46e-01;
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Query Match 65.0%;
Best Local Similarity 100.0%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
Oligo-dT track served to identify it as a clone from the normalized
adult Spleen library. CDNA Library Preparation: M. Fatima Bonaldo,
ph.D. Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics The following repetitive elements were found in this cDNA sequence: 24-90, >ID4#SINE/ID Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UI-R-Cl-jz-a-08-0-UI 3', mRNA sequence. AI045436
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University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    brain, liver, kidney, heart, spleen, overy, and muscle. The UI-R-EI library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CI) was constructed as follows: PCR amplified cDNA inserts from UI-R-CO clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-CO library in the form of single-stranded circles. The remaining single-stranded cloum chromatography, converted to double-stranded circles and electroparated into DHIOR
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/note="Vector: pf7f3D-Pac (Pharmacia) with a modified /note="Vector: pf7f3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C1 library is a subtracted library derived from the UI-R-C2 library, which is a subtracted library derived from the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library consisted of a mixture of individually tagged normalized constructed from rat placenta, adult lung, being libraries constructed from rat placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                         double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C1 library. This procedure has been previously described
                                                                                                                                                                                                                                                                                                                                                                                                (Bonaldo, Lennon and Soares,
                                                                                                                                               /lab_host="DH10B (Life Technologies)"
111 c 94 g 94 t
                                                                                                                                                                                                    /dev_stage="Adult"
                                                                                                                                                                                                                                             /clone="UI-R-C1-jz-a-08-0-UI"
/clone_lib="UI-R-C1"
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Score 13; DB 22;
Pred. No. 3.46e-01;
0; Mismatches 0
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                                                           Length 351;
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Best Local Similarity 100.0%;
Matches 13; Conservative
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                                                                                                                                                                                                              GCGACTGCAGGAC 3
                                                                   AA806951 366 bp mRNA EST U/-AFK-LYYD OC34A03.s1 NCI_CGAP_GCB1 HOMO SAPIENS CDNA CLONE IMACE:1151564 3' similar to gb:U15537_rna2 PROTEIN-TYROSINE PHOSPHATASE 1C (HUMAN)
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nz51d04.sl NCI_CGAP_Pr12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:2044705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 362)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AA887173.1 GI:3002281
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                                           AA80695
                                                               mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
  AA806951.1 GI:2876527
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .362
/organism="Homo sapiens"
/organism="Wector: pawP10; mRNA made from metastatic prostate
/note="Vector: pawP10; mRNA made by oligo-dT priming.
lesion of the bone, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
Non-directionally cloned. Library made by D. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
78 c 113 g
                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="metastatic prostate bone lesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="NCI_CGAP_Pr12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:1291303"
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Pred. No. 3.46e-01;
0; Mismatches 0;
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Homo sapiens cDNA clone IMAGE:1291303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2150480
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1 (bases 1 to 366)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA)

Tumor Gene Index.
                 Mus musculus
                                                                                                 AI503863
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Seq primer: -40m13 fwd. ET from /
High quality sequence stop: 135.
Location/Qualifiers
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.ilnl.gov/bbrp/image/image.html
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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Similarity 100.0%;
13; Conservative
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D., I
Ph.D., Gerald Marti, M.D.
CONA Library Preparation: M. Bento Soares, Ph.D.,
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                                   nouse mouse.
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/db_xref="taxon:9606"
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/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center
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1 (bases 1 to 372)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,

Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,

Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

Waterston,R. and Wilson,R.

The WashD-NCI Mouse EST Project 1999

Unpublished (1999)

Unpublished (1999)

Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Seq primer: Primer name ambiguous
High quality sequence stop: 370.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                  h 65.0%;
Similarity 100.0%;
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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SEQUENCE
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01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
CELL DIVISION CONTROL PROTEIN 27.
CDC27 OR SNB1 OR YBL084C OR YBL0718.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
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MEDLINE; 95009933.
LAMB J.R., MICHAUI
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COLD SPRING HARB
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JENCE 703 AA; 81959 MW; 31B09B6D CRC32;
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                                                                                    essential components of the yeast cell SYMP. QUANT. BIOL. 56:663-673(1991).
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38; Mismatches 59
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DOMAIN 358
MUTAGEN 613
SEQUENCE 758 AA;
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SGD; L0000266; CDC27.
PFAM; PF00515; TPR; 5.
CELL DIVISION; CELL CYCLE;
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EMBL; z35845; G536136; -.
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Search completed: Wed Nov 24 02:26:02 1999 Job time: 272 secs.

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bution rights by Oxford Molecular Ltd  Smith-Waterman search, using a protein database en backtranslated into n.a. using IUPAC symbols  24 02:12:01 1999; MasPar time 153.50 Seconds 24 02:12:01 1999; MasPar time 153.50 Seconds ated.  103-287-3 from US09103287.seq ATTTAAAGATTCGGATGACA
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	FACTOR VIII.	MYO-3 PROTEIN.	NISB.	MA-P17 (FRAGMENT).	COSMID C26E6.	COSMID C26E6.	MICROTUBULE BINDING PR	MASTERMIND.	EG:66A1.2 PROTEIN.	C49H3.5 PROTEIN.	PUTATIVE TRANSCRIPTION	HYPOTHETICAL 54.7 KD P	$\Box$		ъ	HISTIDINE KINASE C.	HYPOTHETICAL 86.5 KD P	HOMEOBOX-CONTAINING PR	ASPARAGINE-RICH ANTIGE	THYMIDINE KINASE (TDK)	KINETOPLAST APOCYTOCHR	CONSERVED HYPOTHETICAL	HYPOTHETICAL 39.1 KD P	LECTIN-LIKE PROTEIN.	FACTOR VIII.			IMMUNOGENIC PROTEIN P3	
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## ALIGNMENTS

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RESULT	OLT 1
ID	067373 PRELIMINARY; PRT; 454 AA.
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, Di	(TREMBLREL. 07,
ָ קלו	01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
DE	UDP-N-ACETYLMURAMATE-ALANINE LIGASE.
GN	MURC.
SO	AQUIFEX AEOLICUS.
8	BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX.
RN	
RP	SEQUENCE FROM N.A.
RC.	STRAIN=VF5;
RX	MEDLINE; 98196666.
RA	DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RA	, OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M.,
RA	FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
RT	
RT	aeolicus.";
RL	NATURE 392:353-358(1998).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=VF5;
RA	DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RA	OVERBEEK R.,
RA	FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
RL	SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR	EMBL; AE000736; G2983764;
KW	LIGASE.
SQ	SEQUENCE 454 AA; 50893 MW; 1207F9CE CRC32;
ō	Query Match , 9.5%; Score 313; DB 2; Length 454;
Ве	cal Similarity 39.4%; Pred. No. 4.64e-23;
M.	Matches 117; Conservative 54; Mismatches 121; Indels 5; Gaps 5;
Дb	H N V Y N A L A A T G V A L E L G V S F
Dt	TAYAAYGCNYTNGCNGCNACNG-GNGTNGCNYTNGARYTNGGNGTNWSN
ΟV	121 CCATACAGTTTTAAATGCATTAAGTGTAATTGCGATTAGTTAATTTAAAGAAAG
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RESULT

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AC 084767;

DT 01-NOV-1998 (TREMBLREL 08, CAE
DT 01-NOV-1998 (TREMBLREL 08, LAS
DT 01-NOV-1998 (TREMBLREL 18, LAMME
RA CSTEPLENG R.S., KALMAN S., LAMME
RA MITCHELL W.P., OLINGER L., TATU
RA DAVIS R.W.;
RI "Genome Sequence of an Obligate
RA MITCHELL W.P., OLINGER L., TATU
RA DAVIS R.W.;
RI SCIENCE 0:0-0(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN-D/UW-3/CX;
RA STEPLENS R.S., KALMAN S., LAMME
RA STEPLENS R.S., KALMAN S., LAMME
RA MITCHELL W.P., OLINGER L., TATU
RA DAVIS R.W.;
RL SUBMITTED (MAY-1998) TO EMBL/GE
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Mismatches 173;
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ANNOTATION UPDATE)
ASE AND D-ALA-D-ALA
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Q., KOONIN E.
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Q1-NOV-1996
Q1-NOV-1996
Q1-AUG-1998
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                                                                                                                                                                                                                                                                                                          MITOCHONDRION.
SEQUENCE 373
                                                                                                                                                                                                                                                                                                                                       CARDAZZO B., RINALDI T.,
SUBMITTED (FEB-1996) TO
EMBL; U49822; G1236921;
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CARDAZZO B., PELLIZZARI
SUBMITTED (FEB-1996) TO
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EMBL/GENBANK/DDBJ DATA BANKS
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LAST SEQUENCE UPDATE)
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Pred. No. 4.44e-03;
36; Mismatches 51
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IRESULT
ID 990523;
AC P90523;
DT 01-MAY-DT 01-MAY-DT 01-NOV-DE PUTATIVOS DICTYOS OC EUKARK(RN [1])
RP SEQUENC RC STRAIN-RX MEDLINE RX MEDLINE RX MEDLINE RA CHANG WRT "Ident! WE RA CELL 87 DR PEAM; E SQ SEQUENC
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"Identification of the cell fi
CELL 87:471-481(1996).
EMBL; U68754; G1685115; -.
PFAM; PF00320; GATA; 1.
SEQUENCE 872 AA; 99101 MW;
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01-MAY-1997
01-MAY-1997
01-NOV-1998
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J. MOL. BIOT
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01-NOV-1996
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EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM.
                                                                                                                                                                     SEQUENCE
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BL; X95275; E220242; -.
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DTA; ALVEOLATA; APICOMPLEXA;
                                                                                           h 5.0%;
Similarity 35.5%;
59; Conservative
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7998 (TREMBLREL. 08, LA
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larity 36.9%;
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Q88439;
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01-NOV-1996
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SUBMITTED (SEP-1998) TO EMBL
EMBL; Z98547; E1325396; -.
SEQUENCE 4550 AA; 534109
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PETRZIK K
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STRAWBERRY VEIN BANDING V.
VIRUSES; RETROID VIRUSES;
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D EMBL/GENBANK/DDBJ
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).76e-03;
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.52e-03;
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                                                                                                                                                                                                            CRC32;
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BANKS
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RESULT 8
ID 025802;
AC 025802;
DT 01-NOV-1996
DT 01-NOV-1996
DT 01-NOV-1996
DE FRAMESHIFT.
GN RPOD.
OS PLASMODIUM E
OC EUKARYOTA; A
RN [1]
RP SEQUENCE FROJ
RC STRAIN=C10;
RX MEDLINE; 963
RA WILSON R.J.M
RA ROY A., WHYT
RT "Complete ge
RT Plasmodium f.
RI J. MOL. BIOL
DR EMBL; X99275
SQ SEQUENCE 9
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                                                                                TAMBLEEL. 06, C.

1-AUG-1998 (TREMBLEEL. 07, LAS

NADH DEHYDROGENASE SUBUNIT 6.
ONCHOCERCA VOLVULUS.

MITOCHONDRION.
EUKARYOTA; "
FILAPT"
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 5
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MEDLINE; 96346169.

MILSON R.J.M., DENNY P.W., PREISER P.R., RANG,

WILSON R.J.M., DENNY P.W., PREISER P.R., RANG,

ROY A., WHYTE A., STRATH M., MOORE D.J., MOOR

"Complete gene map of the plastid-like DNA of

"Complete gene map of the plastid-like DNA of

"Lasmodium falciparum.";

Plasmodium falciparum.";

J. MOL. BIOL. 261:155-172(1996).

EMBL; X95275; E220245; -...
                                                                                                                                   ULT 9
047574 PRELIMINARY;
047574;
01-JUN-1998 (TREMBLREL. 0
01-JUN-1998 (TREMBLREL. 0
01-AUG-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                             1783
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                   KEDDIE E.M., UNNASCH T.R. SUBMITTED (JUL-1997) TO EEMBL; AF015193; G2735938;
                                                   SEQUENCE FROM STRAIN-FOREST;
                                                                                                                                                                                                                                                    1901
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FIN*RCTT RT N FIN * 1
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59; Conser
                                                             FROM N.A.
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(TREMBLREL.
                                                                                                                                                                              PRELIMINARY;
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                                                                                 eTAZOA; NEMATODA; SECERNENTEA;
ONCHOCERCIDAE; ONCHOCERCA.
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                               T.R.;
TO EMBL/GENBANK/DDBJ
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44; M
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LAST ANNOTATION UPDATE)
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                                                                                                                                   SEQUENCE UPDATE)
ANNOTATION UPDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                   162; DB 5;
No. 1.64e-02
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 CRC32;
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MOORE P.W., WILLIAMSON D.H.;
NA of the malaria parasite
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                                DATA BANKS
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                                                                                           SPIRURIA;
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RESULT
AC Q9
RESULT
ID 01
AC 01
DT 01
DT 01
DT 01
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Best Local S
Matches 4
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Best Local
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SEQUENCE FROM N.A.

MEDLING: 96400190.

KUTISH G.F., LI Y., LU Z., FU

"Analysis of 76 kb of the chi-
positions 182 to 258.";

POSITION 223:303-317(1996).

EMBL: U44580; G1620080; -.

SEQUENCE 277 AA; 30772 MW;
JLT 11
015791
015791;
01-JAN-1998
01-JAN-1998
01-NOV-1998
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098460;
098460;
01-FEB-1997
01-FEB-1997
01-NOV-1998
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VIRUSES; DSDNA VIRUSES, NO RNA STAGE;
                                                                                                                                                                                                                                                                                                                                                                     348
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CGACGTTTAACACCACAAA
T F N T T K
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TGGTNYTNGAYTTYATHAAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Similarity 47; Conserv
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                                                                    PRELIMINARY;
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LAST SEQUENCE ANNOTED
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Pred.
33; M
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Pred.
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1. No. 4.57e-02;
. ___+ches 50;
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. No. 2.74e-02;
Mismatches 60;
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ANNOTATION UPDAT
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PHYCODNAVIRIDAE;
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330-kb genome:
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(TREMBLREL.) (TREMBLREL.)

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EMBL; AF030692; GZ642514; -.
SEQUENCE 2708 AA; 322929 MW; 6F4
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                                                         MUNGALL K., LAWSON D., BARRELL B.;
SUBMITTED (SEP-1998) TO EMBL/GENBANK/DDBJ
EMBL, Z98647; E1325392; -
SEQUENCE 1532 AA; 186754 MW; B3F0FC43
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EMBL; AF030693; G2642516; -.
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Best Local Similarity 37.4%;
Matches 43; Conservative
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066201;
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01-AUG-1998 (TREMBLREL 07, CREATED)
01-AUG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL 07, LAST ANNOTATION UPDATE)
01-AUG-1998 (TREMBLREL 07, LAST ANNOTATION UPDATE)
SIMILAR TO GROES PROTEIN (FRAGMENT).
SERRATIA RUBIDAEA.
SERRATIA RUBIDAEA.
SERRATIA, PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
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STRAIN-JCM 1240;
HARADA H., ISHIKAWA H.;
J. GEN. APPL. MICROBIOL. 43:355-361(1997).
EMBL; AB008143; D10.6146; -
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Pred. No. 2.05e-01;
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B7840	W51835	AQ110	N62159	AA688	AI34367	AA48202	R4370	AI027	W9546	AI216	R97582	AA923	AU00361	R2231	T93588	AA229	C92129	AA912	AQ38558	AQ04584	AQ34584	AU04001	AI22078	C28215	AQ10889	AQ059	AQ06472	C90922	AI111	в9896	C9387	C91268	3 AQ060967	C9426
21TF TAMU Arabid	9e10.s1 Soares_se	-HSP-23	2e07.s1 Soares_mu	4g04.sl NCI_CGAP_	6b10.x1 NCI_CGAP_	8g03.s1 NCI_CGAP_	9e12.sl Soares in	6a09.x1 Soares_pa	2c08.sl Soares_fe	2all.xl NCI_CGAF	9a06.rl Soares f	7h11.s1 NCI_CGAP	03619 Bombyx mor	6c11.s1 Soares p	7g03.s1 Stratagene	5f02.r1 NCI_CGAP_F	129 Dictyostelium	9d06.s1 NCI_C	I11-133L5.TV	I11-35L5.TJ R	I11-126I1.TJ	40013 Dictyos	2d07.x1 Soare	28215 Rice call	IT-HSP-2378A17.	IT-HSP-2348N2.	S_2214_B1_C08_M	90922 Dictyoste	I-R-Y0-me-g-06-	IT-HSP-2280A9.T	93878 Dictyostelium	91268 Dictyostelium	2356J16.TR	94261 Dictyostelium
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## ALIGNMENTS

FEATURES Source	TITLE JOURNAL COMMENT	VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 1 LOCUS DEFINITION ACCESSION
Contact: Eun M.Y.  Department of Cytogenetics National Inst. of Agri. Sci. and Tech, RDA  Suwon, Kyunggido, Korea  Tel: 82 331 290 0301  Fax: 82 331 290 0307  Email: myeun@sun20.asti.re.kr Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr  Location/Qualifiers  1. 252 /organism-"Oryza sativa"	Nanm, B.H., Kim, V.K., Cheong, J.J., Kim, S.I., Hahn, T.R., Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.  Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)  On Jan 14, 1998 this sequence version replaced gi:1797457.	92801165 AA754459.1 GI:2801165 EST. Oryza sativa. Oryza sativa. Elikaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza. 1 (bases 1 to 252)	AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence.

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FEATURES
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Best Local Similarity
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Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
                                                                Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
                                                                                                                                                        Department of Cytogenetics
National Inst. of Agri. Sci.
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
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                                                                                                                                                                                                                                                                              Contact: Eun M.Y.
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/organism="Oryza sativa"
                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 ot
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5.01e-61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Moon, E.P.,
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Best Local S
Matches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATATTTAGATAAATTAGGCATGAAAAATGCGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVVKKYHVVBBGCHBTDSKCKTMWMTNKHVMTSTTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTGATAATGCTG-TTGTTTTATTTATGGGTGCAGGTGATATTCAAAAATTACAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTGATAAAATTGAAGGTGCATCGTTAATTAATGAAGATTCTATTA-ATGTATTAGAACA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGAAATTTTTGGATCAATTAGAGAAAA-TACTG-GCGCATTAACGATACAAGATTTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRATRSYTCVRKYCVMWMTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMWCWBHYNTKCTASGWHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWBVBNTKVDVGNHTRCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 247)
Nahm, B.H., Kim, J.K., C
Kim, W.T., Kim, W.Y., Ya
Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                              Department of Cytogenetics National Inst. of Agri. Sci. Suwon, Kyunggido, Korea Tel: 82 331 290 0301
                                                                                                                                                                                                                                                                                                                                                                                                                              Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
On Jan 14, 1998 this sequence version version versions.
                                                                                                                                                                      Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.:
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA754458 247 bp mRNA EST 20-JAN-1997SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza
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                                                                                                                                                                                                                                                                                                                                                                                   Contact: Eun M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poaceae; Oryza.
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similarity 14.4%;
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           14, 1998 this sequence
/organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
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/tissue_type="immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c · 12 g 35 t 179 ot
                                                                                                                                                   location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52; DB 17; Le
Pred. No. 6.06e-39;
108; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                        Tech,
                                                                                                                                                                                                bhnahm@bioserver.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252
                                                                                                                                                                                                                                                                                                                                        RDA
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123 CDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDKTDSDCGGGCWRKVTY 182
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Local Similarity 12.9%;
hes 29; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAATTGCGATTAGTTATTTAGAGAAGCTAGATGTTACAAATATTAAAGAAGCATTAGAAA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTATGATCACTTCCTGTCTCCACAATATGGTGACCATA-CAGTTTTAAATGCATTAGCTG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYTVBWYYARSKYGYGTBYYSWNVDTNTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBTAY 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DCTMNTVWRGCCCCBAWMNKHTHMMTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNAHC 62
                                                                                                                                                                                                                                                          Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA754458 247 bp mRNA
97SN1784 Rice Immature Seed Lambda
cDNA clone 97SN1784, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
On Jan 14, 1998 this sequence version replaced gi:1797455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Loases 1 to 247)

1 (bases 1 to 247)

Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Nahm, B.H., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
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Oryza sativa
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                                                           /organism="Oryza sativa"
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/cultivar="Milyang23"
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XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
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/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
16 c 21 g 34 t 169 others
                                                 /map="6"
                                                                                                                                                                                                                                           Location/Qualifiers
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                                /clone="97SN1784"
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Pred. No. 4.21e-36;
       Immature
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       Seed
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    ZAPII cDNA Library"
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AUTHORS
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                                                                                                                                                                                         Query Match 5.5%;
Best Local Similarity 15.3%;
Matches 19; Conservative
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Best Local Similarity 14.7%;
Matches 33; Conservative
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TTCTCTTGGATGGTGCATAATCATCTACAATAACTTGATTTGCAATTGTAGTTTCATT
                                               RSYWGYWGSMSGCYGMTKRYYRYSWTGWTKWTTWWYMWSMTRWTMTTYTTWWTWRTTKTW 1644
                                                                                                CTGCAACAACTTCT-TTATGTGGATATTTCTTTCGTGCTG-TGTCAATTGTAGCACTAAT 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF034173 2275 bp mRNA EST AF034173 Human mRNA (Tripodis and Ragoussis) clone ntcon2 contig, mRNA sequence. AF034173
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Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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Division of Medical and
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On Jan 19, 1998 th
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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1 (bases 1 to 2275)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     floor, Guy's Tower, London il: nikos@nki.nl.
                                                                                                                                                                                                                                                                                                                438
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/lab_host="E. coli SOLR"
16 c 21 g 34 t 169 ot
                                                                                                                                                                                                                                                                                                         /clone_lib="Human mRNA (Tripodis and Ragoussis)" 619 c 470 g 599 t 149 others
                                                                                                                                                                                                                                                                                                                                                          /map="6p21.3"
/clone="ntcon2 contig"
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                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Pred.
106; M
                                                                                                                                                                                       Score 36; DB 20;
Pred. No. 3.18e-17;
66; Mismatches 37
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No. 4.21e-36;
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239

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RESULT LOCUS

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SOURCE KEYWORDS VERSION

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                                                                                                                                                                                                                                                                                                   1612 WTKWTTWWYMWSMTRWTMTTYTTWWTWRTTKTWWWWWWTTCWTMRKRGAGTTTTGG 1667
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                                                                                                                                                                                                                                                                                                                                                                       TYTYWYCWCCTSMKSASCAMMRWMGYMGSRSSRSYWGYWGSMSGC-YGMTKRYYRYSWTG 1611
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B50349.1
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g2707735
                                                                                                                                                                                          B50349 439 bp DN CIT-HSP-351C15.TV CIT-HSP
Kim,U.-J., Adams,M.D. and Simon,M.I.
Determination of clone end sequences
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1 (bases 1 to 2275)

Tripodis, N. and Ragoussis, J.

Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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                               Primates; Catarrhini; Hominidae;
1 (bases 1 to 439)
                                                                              Homo sapiens
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7th floor, Gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
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On Jan 19, 1998 this sequence version replaced gi:2045115
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                                                               Eukaryota; Metazoa; Chordata; Vertebrata;
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Similarity 14.8%;
26; Conservative
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                                                                                                                                GI:2602586
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619 c     470 g     599 t     149 others
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/db_xref="taxon:9606"
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Pred. No. 5.7
87; Mismatcl
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Homo sapiens genomic clone 351C15,
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Lepidoptera; Bombycoidea; Bombycidae; Bombyx.

1 (bases 1 to 727)

Chimada m Okano.K. and Maeda, S.
                                                                                                                   Genome Research Group
National Institute of Radiological Sci
Anagawa 4-9-1, Inage, Chiba 263-8555,
Email: kmita@uxxs64.nirs.go.jp
PROJECT = 'CREST project by JST'.
Location/Qualifiers
                                                                                                                                                                                                                                                                   Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S. Establishment of cDNA database of Bombyx mori Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU005149 Bombyx mori
                                                                                                                                                                                                                       Contact: Mita K
                                                                                                                                                                                                                                                      On Jan 14, 1998 this sequence version replaced gi:1797828
                                                                                                                                                                                                                                                                                                                                                                                        domestic silkworm
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AU005149
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Class: BAC ends.
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Callech Genome Research Lab
California Institute of Technology
Division of Biology, MS 147-75, Pasadena, CA 91125,
Tel: 626 796 7066
Fax: 626 395 4901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosomes
Unpublished (1997)
Other GSS: CIT-HSP-351C15.TP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ung@ash.tree.caltech.edu
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 4.2%;
Similarity 72.6%;
45; Conservative
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      251
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/strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="ws30310"
/clone_lib="Bombyx mori p50(Daizo)"
a 104 c 123 g 249 t
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                                                                                      /organism="Bombyx mori"
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.: 115 c 75 g
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/clone="351C15"
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/note="Vector: pBeloBAC11;
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p50(Daizo)
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Pred. No. 1.26e-07;
0; Mismatches 17;
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                                                                                                                                                                                      Sciences
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RESULT 9
LOCUS
DEFINITION
ACCESSION
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JOURNAL
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Best Local Similarity 71.7%;
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                           526 CTTTATCAAAAACCCAAATTTTTGGGCACAAATGCCNTCCNAAACTGTAAAT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 3.8%;
Local Similarity 83.8%;
hes 31; Conservative
                                                                                                                                                                                                                                                                           53 CTTTATCCGTAATTTGAAATATTTGAGCATAAATGTCATCCGAATCTTTAAAT 1
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PT1.3_05_D12.r tumor1 Homo sapiens
A1525758
                                                                                                                                                                    D56970 208 bp mRNA EST 28-AUG-1995 HUM240G07B Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-240G07 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Washington
Department of Molecular Biotechnology, Box 357730, University of
Washington, Seattle, WA 98195
Tel: 5106280100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu.J. and Hood.L.
Prostate Cancer Expression Profiling by cDNA Sequencing Analysis
Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3137680.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 208)
Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,
                                                                                                                                    g963592
                                                                                                                                                        cDNA clone
D56970
                                                                                                                                                                                                       D56970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Guyang Matthew Huang
Leroy Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 768)
1 (bases 1, Ng.W., Farkas,J., Chen,L., Liang,H.A., Gordon,D.,
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                                                                  Homo sapiens
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                                                                                     human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             huanggm@yahoo.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/note="Organ: Prostate; Vector: pBluescript; Directional cDNA library was constructed using Lambda ZP II kit (Stratagene). mRNA was extracted from a frozen prostate tumor tissue (Mayo Clinics)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/map="6p21.3"
                                                                                                                      GI:963592
                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="tumor1"
163 c 191 g
                                                                                                                                                                                                                                                                                                                                          Score 25; DB 28; Length 768
Pred. No. 2.23e-04;
0; Mismatches 15; Indels
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Pred. No. 2.23e-04;
0; Mismatches 6
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   Kuga,Y.,
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                                                      Mammalia;
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   Nagata, M.,
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Best Local Similarity 78.9%;
Matches 30; Conservative
                                               Query Match
Best Local
                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 TWTTCATACGTAAAATTTTCGGATTAATTTGTGAAAAT 145
1 (bases 1 to 273)
Yoshino,R., Morio,T. and Tanaka,Y.
Developmental cDNA in Dictyostelium discoideum
Unpublished (1997)
On Jan 14, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C94261 273 bp mRNA
C94261 Dictyostelium discoideum
discoideum cDNA clone SSK635, mF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho,
Tel: 0886-65-2888
Fax: 0886-37-1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okúno,Ś., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y. Fujiwara et al. (1995)
Unpublished (1995)
On May 5, 1995 this sequence version replaced gi:797884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum Eukaryota; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g3218876
C94261.1 GI:3218876
                                                                                                                                                                                                                                                                                                                                                      Contact: Hideko Urushihara
Institute of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 542 Std Error: High quality sequence stop: 271.
                            3.6%;
Similarity 73.1%;
38; Conservation
                                                                                                                                                                                                                                                                                                                     3-3-10 Ten-nodai, Tsukuba, Ibaraki 305,
                                                                                                                                                                                                                                                                                                                                      University of Tsukuba
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                                                                                                                                                                                                                                                                                         PROJECT =
                                                                                                                  100
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                                                                                                                                                                                                                                                                   d402hu@sakura.cc.tsukuba.ac.jp
T = Dictyostelium discoideum cDNA
 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GEN-240G07"
                                                                                                                /clone_lib="Dictyostelium discoideum
/dev_stage="slug"
41 c 27 g 105 t
                                                                                                                                                                                                                    /strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Clontech human aorta polyA+ mRNA (#6572)" 30 \text{ c} 26 \text{ g} 75 \text{ t} 16 \text{ others}
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                                                                                                                                                                     /clone="SSK635"
                                                                                                                                                                                                    /db_xref="taxon:44689"
                                                                                                                                                                                                                                    /organism="Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                         this sequence version replaced gi:1797461.
                                               Score 24;
Pred. No.
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Pred. No.
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                                 Mismatches
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mRNA sequence.
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                                               DB 21;
2.36e-03;
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2.36e-03;
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                                                               Length 273;
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                                 Indels
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                                                                                                                                                   (H.Urushihara)"
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652

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sapiens

GSS 30-JUL-1998 genomic clone 2356J16

KEYWORDS SOURCE ORGANISM

ACCESSION DEFINITION

VERSION

REFERENCE

AUTHORS

COMMENT

JOURNAL TITLE

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Query Match 3.6%;
Best Local Similarity 74.0%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                               28 CAATGGTAGTTTCAATAAAGCATGGTTTCACACCACCAGACAATCATAAT 77
                                                                                                                                                                                                                                                                                                             CAATTGTAGTTTCATTGAAACGACGTTTAACACCACCAAACGTTTCTAAT 199
   Yoshino, R., Morio, T. and Tanaka, Y. Developmental cDNA in Dictyostelium Unpublished (1997)
                                                                                                                                                                                             C91268 282 bp mRNA EST (91268 Dictyostelium discoideum SS (H.Urushihara) discoideum cDNA clone SSJ728, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 bp DNA
CIT-HSP-2356J16 TR CIT-HSP Homo
genomic survey sequence.
A0060967
                                                                                           Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                               g3060634
C91268.1 GI:3060634
                                                                        Eukaryota; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_GSSs: CIT-HSP-2356J16.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jnpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               imates; Catarrhini; Hominidae;
(bases 1 to 276)
                                                     (bases 1 to 282)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="Sperm"
66 c 41 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="2356J16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/note="Vector: pBeloBAC11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib-"CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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                      discoideum
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Dictyostelium
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                                                                                                                                                                                                                                                                                                                                    Contact: Motonobu Yoshida
Research Institute of Food Science
Kinki University
Nakamachi 3327, Nara 631, Japan
Email: yoshidadews06.nara.kindai.ac.jp
Dictyostellum discoldeum cDNA project in Japan.
Location/Qualifiers
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C93878 Dictyostelium discoideum SS
discoideum cDNA clone SSL820, mRNA
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Unpublished (1998)
On Jan 19, 1998 this sequence version replaced gi:2151736.
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Dictyostelium discoideum
Eukaryota; Dictyosteliida; Dictyostelium.
1 (bases 1 to 294)
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3-3-10 Ten-nodai, Tsukuba, Ibaraki
Email: d402hu@sakura.cc.tsukuba.ac.
Location/Qualifiers
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Institute of Biological Sciences
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Similarity 73.1%;
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/dev_stage="slug"
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/strain="AX4"
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Search completed: Sat Nov 27 12:32:26 1999 Job time: 1172 secs.
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1 (bases 1 to 339)

Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: M13 Reverse Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/clone_lib="CIT-HSP"
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh; U.K. Distribution rights by Oxford Molecular Ltd
srch_pp protein - protein database search, using Smith-Waterman algorithm
n on: Wed Nov 24 00:49:16 1999; MasÞar time 10.17 Seconds 449.783 Million cell updates/sec bular output not generated.
tle: >US-09-103-287-4 scription: (1-215) from USO9103287.pep rfect Score: 1495 quence: 1 FKDSDDIYAQIFQITDKGTAGDIQKLQNAYLDKLGMKNAF 215
oring table: PAM 150 Gap 11
arched: 170751 seqs, 21266608 residues
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tabase: a-geneseq35 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part25 26:part26 27:part27 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38 39:part39
atistics: Mean 31.787; Variance 165.505; scale 0.192
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tide.  anine ligase; Murc polypicer; ulcer; gastritis; \n.  n.  taphylococcus aureus and treatment and preventior treatment and preventior aureus Murc gene. Host trising the Murc gene can lypeptide. Agonists or the folypeptide are also rections. They are also ections. They are also to treat in-dwelling devenum treatments to pre wound treatments to pre house for treation disease, for respecific receptors; in receptors; in the bacterial serotype; an eppresents a partial sequencers.	A. chrysogenum phosph Staphylococcus epider Helicobacter polypept Secreted protein clon Typl protein.  Rat brain glutathione 9 S. pneumoniae GlmU OR Phosphoglycerate kina 1 portion of B fragment Recombinant botulinum Glutathione S-transfe Bovine RSV strain A 5 E. maxima Em70-1 anti Eukaryotic cell growt T iniveum Cyclosporin Serpulina hyodysenter Hemolysin.  Rabbit excitatory ami 1 Hemolysin.  Rabbit excitatory ami 1 Hemolysin.  Rabbit opidina protein G 1 protein encoded by Hu Human huntingtin prot 1 previously undescribe 1 previously undescribe 1
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MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide;
bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine;
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96.3%;
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                                                                                                                         Score 1434; DB 39;
Pred. No. 8.46e-105;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                          determine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a protein from Streptococcus pneumoniae.

C. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against commoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid care used to detect Streptococcus infection (by usual hybridisation or camplification methods), also for isolating Streptococcus genes or their callelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive cimmunisation (optionally coupled to a toxin). Vaccines are administered, ce.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae. WO9818930-A2. 07-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protective or therapeutic vaccines, and for diagnosis Claim 11; Page 73; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choi GH, Hromockyj
WPI; 98-272224/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W55120
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Choi GH, Hromockyj A, Johnson LS,
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                                                   386 plldhdnavyvfmgagdiqtyeysf-erl
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les 92; Conser
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VLEQFDNAVVLFMGAGDIQKLQNAYLDKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 651; DB 33;
Pred. No. 3.14e-41;
54; Mismatches 60
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This sequence represents a Staphylococcus aureus protein of unknown function, and is encoded by a DNA sequence of the invention.

The DNA sequences were isolated from Staphylococcus aureus WCHU29

(NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides.

Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                              H. pylori cytoplasmic protein, Olep30520orf27.

Vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; cytoplasmic; outer membrane; cell wall; biosynthesis.
  Claim
The pa
                                                                                                                                                                                                                                                      19-DEC-1996.
06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
                                                                                                                                                                                                                                                                                                                                                                                              cytoplasmic; outer m
Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    especially useful Sequence 46 AA;
                                                                                  Helicobacter pylori nucleic acid sequences polypeptide(s) - useful for vaccines to tr
                                                                                                                                              N-PSDB; T67859.
                                                                                                                                                                     Berglindh OT, Smi
WPI; 97-052306/05.
                                                                                                                                                                                          (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                 WO9640893-A1.
19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W20606 standard; protein; 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; V53479
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Lonetto MA, Nicholas RO, Pratt JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-1997; 307485.
24-SEP-1996; US-027032.
(SMIK ) SMITHKLINE BEECHAM CORP
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  present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invleqfdnavvlfmgagdiqklqnayldklgmknaf
                 ococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100.0%; 37; Conservative
                                                        e(s) - useful for vaccines to
and to detect Helicobacter
  sequence is
  a Helicobacter
                                                                                                                                                                                                   Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265; DB 34;
No. 5.35e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knowles DJC,
Reichard RW, Rosenberg
pylori cytoplasmic
                                                                                     treat
                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215
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                                                                                                             related
                                                                                     or
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  protein
                                                                                  H. pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      involved in outer membrane or cell wall biosynthesis.

(The protein may be used in a vaccine to prevent or treat

H. pylori infection or to identify H. pylori polypeptide binding

compounds, useful as potential H. pylori life cycle activators or

inhibitors. The genomic sequence of H. pylori (ATCC 55679) was

determined from overlapping contigs generated by mechanically

shearing the bacterial DNA. The sequences were analysed for ORF of

at least 180 nucleotides, and the predicted coding regions defined

by computer evaluation. To identify likely H. pylori antigens for

vaccine development, the amino acid sequences predicted from

covarious ORF were analysed for significant homology to other known

or exported membrane proteins. Having identified and determined

to sequences of interest, particular regions can be isolated from

u maint her now manificant for recombinant columns to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                             Helicobacter pylori nucleic acid sequences and related proteins used for diagnostics and therapeutics claim 18; Page 131; 235p; English.

This sequence represents an H. pylori cytoplasmic protein involved in outer membrane or cell wall biosynthesis. This sequence showed homology to N-acetylmuramate-Alanine ligase.

Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequence is a corresponding proteins, are
                                                                                                                                                                                                                                                                                                                                                            29-MAY-1997.
15-NOV-1996;
17-NOV-1995;
also useful for generating vaccines for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. pylori cytoplasmic protein, 11253.aa.
Transmembrane; cytoplasmic; cell envelope; flagella; transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H. pylori by PCR amplification for recombinant polypeptide
                                                                                                                                                                                                                                                                                  WPI; 97-298052/27.
N-PSDB; T77043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted; periplasmic; chronic gastritis;
activator; inhibitor; bacterial life cycl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W24585 standard;
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                                                                                                                                                                                                                                                                                                                          Smith DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; antisense; inhibition.
                                                                                                                                                                                                                                                                                                                                              (ASTR ) ASTRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ekkdiyniqyilkd-gepytsf-elknlgaflvwglgehnatna-slailsaldelnlee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 15.7%;
Similarity 28.6%;
44; Conservative
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455 AA;
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133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                          "encoded by RCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "encoded by TYA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "encoded by AAS
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Pred. No. 9.34e-09;
42; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   duodenal ulcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
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polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter Claim 61; Page 335; 1481pp; English.

This sequence represents a H. pylori cytoplasmic protein involved in outer membrane or cell wall biosynthesis.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To
                                                                                                                                                                                                                              (ASTR ) ASTRA AB.
Berglindh OT, Smith
WPI; 97-052306/05.
                                                                                                                                                                                                                                                                          06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pMPX vectors to construct a series of shotgun subclone libraries. The purified DNA samples were then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W20102;
29-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                        misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis
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                                                                                                                                                                                                  Helicobacter
                                                                                                                                                                                                               N-PSDB; T67723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 QPHTFSRTQAFLNEFAES-LSKADRVFLCEIFGS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189
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                                                                                                                                                                              pylori nucleic acid sequences and related
s) - useful for vaccines to treat or prev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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166
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                                                                                                                                                                                                                                                                                                                                                                         /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Pred. No. 3.65e-08;
40; Mismatches 62
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                                                                                                                                                                                                                                                                                                                                                                                                       by TYA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection; envelope;
life cycle; activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 286;
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gshnvenalatiavaklrdvdnqtiketlsafggvkhrl 199 GDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRF

Query Match Best Local S Matches 2

Similarity 21; Conse

9.2%; larity 53.8%; Conservative

Score Pred. 7; M

re 137; DB 33; 1. No. 9.70e-02; Mismatches 11;

3 137; 3 70, 9.

Length 335;

Indels

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Gaps

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                                                     PT Nucleic acid encoding antigenic peptide(s) from Streptococcus
proper protective or their epitope-containing fragments, useful in
protective or therapeutic vaccines, and for diagnosis
Claim 11; Page-72; 118pp; English.

The present sequence represents a protein from Streptococcus pneumoniae.
The nucleic acid sequence encoding the Streptococcus pneumoniae protein
can be useful in vaccines for inducing protective antibodies against
Streptococcus pneumoniae, for treatment or prevention of infection e.g.
pneumonia, otitis media or meningitis. Probes based on the nucleic acid
are used to detect Streptococcus infection (by usual hybridisation or
amplification methods), also for isolating Streptococcus genes or their
allelic variants. The protein can be used similarly to detect specific
monitoring infections. Antibodies which bind the protein are used to
detect corresponding antigens, to purify the protein and for passive
immunisation (optionally coupled to a toxin). Vaccines are administered,
e.g. by injection, orally or through the skin, typically at 0.01-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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W55117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choi GH, Hromockyj
WPI; 98-272224/24.
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31-OCT-1996; US-029960.
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Best Local Similarity
Matches 21; Conser
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18 JUN-1996; US-665435.

14 APR-1997; US-843309.

(ELII.) LILLY & CO ELI.

HOSKINS JA, Peery RB, Skatrud PI

WPI: 99-008720/01.
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18-JUN-1996; US-665435.
(ELIL ) LILLY & CO ELI.
Hoskins JA, Peery RB,
WPI; 97-535046/49.
                                                                                                                                                                                                                                  Streptococcus pneumoniae mur D biosynthetic gene - which encodes uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligase, useful for identifying antibacterial compounds Claim 1; Column 13-16; 14pp; English.

This is the amino acid sequence of the Streptococcus pneumoniae murD biosynthesis protein. The murD gene encodes the enzyme uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligase. The nucleic acid can be used for the production of recombinant MurD protein and the implementation of large scale screens to identify new antibacterial compounds targeted at the stem peptide biosynthetic pathway involved in the synthesis of the bacterial cell wall. Structural analysis of the MurD protein will enable structure-based drug design to develop novel compounds for the treatment of antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug design; resistance;
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Biosynthesis; recombinant; antibacterial; bacterial cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W68551 standard; Protein;
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Claim 2; Columns 21-22; 13pp; English.
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Score 137; DB 37;
Pred. No. 9.70e-02;
7; Mismatches 11;
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                                                      M20436 standa
W20436;
W20436;
14-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 screen a library generated from Thai strain K1. One clone contained a 6.85 kb insert including the genomic sequence T78867. The gene comprises a 1.8 kb region encoding 3 major blocks of tetrapeptide repeats (especially the amino acid sequence VEES, VEEN, VEEI, VAPS, VAPT, etc) and a 3' hydrophobic region corresponding to a glycosyl-phosphatidyl-inositol membrane anchoring sequence. The invention relates to new polypeptides of at least 10 amino acids derived from the LSA-3 protein with the exception of the peptides W24791-4. The LSA-3 peptides can be used to raise antibodies and as vaccines for immunotherapy of malaria. Sequence 1786 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum; pre-erythrocyte; liver stage antigen; serum; prophylaxis; Thai strain; gene organisation; exon; intron; hydrophot glycosyl-phosphatidylinositol membrane anchoring sequence; antibody;
  H. pylor1 protein.
Cytoplasmic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pre-erythrocytic liver stage antigen-3 (LSA-3) protein. The encoding gene sequence was isolated by screening a P. falciparum strain T9/96 library with serum from a missionary treated by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones isolated, clone 729S was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prodn. and diagnosis
Claim 1; Fig 2A-I; 69pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum poly:peptide(s) and related nucleic acids derived from the liver stage antigen-3, useful for malaria vacci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9641877-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence corresponds to a Plasmodium falciparum strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; T78868
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                                                                                                                                                                                                                                                                                                                                   YPHKEVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKI 168
                                                                                                                                                                                                                                                                                                                                                                                       eekkevidvieevkeevattlietveqaeeksantit-eifenleenave-snenvaenl 971
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                                                                                                                                                                                                                           EGASLINEDSIN-VLEQFDNAVVLFMGAGDIQKLQNAYLDKL
                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Similarity 33; Conser
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larity 20.4%;
Conservative
                                                    (first entry)
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279..818
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                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stage antigen-3.
  prevention;
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                                                                                                             187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 135; DB 23;
Pred. No. 1.33e-01;
55; Mismatches 66
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treatment; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1786;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        malaria vaccine
     identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PT Helicobacter pylori nucleic acid sequences and related problement (s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter by infection, and to detect Helicobacter pylori protein of unknown places of the present sequence is a Helicobacter pylori protein of unknown control or the protein may be used in a vaccine to prevent or treat the protein may be used in a vaccine to prevent or treat the pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 5579) was compounded from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 cultivation. To identify likely H. pylori actigens for vaccine canalysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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Best Local Similarity 36.7%;
Matches 22; Conservative
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09-OCT-1997.

27-MAR-1997; U

06-DEC-1996; U

29-MAR-1996; U

02-APR-1996; U
Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection Claims 14,94; Page 668-669; 1145pp; English.

This sequence is a H. pylori secreted protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of the pylori in a sample and the diagnosis of H. pylori infection. Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                  (ASTR
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06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
                                                                                                                                                                                                                                                                                                                           Alm RA, Smith D
WPI; 97-503122/
N-PSDB; V24872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H. pylori ORF 05ae30220_21619067_f3_56 secreted protein.

Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
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H. pylori ORF 05ae30220_21
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N-PSDB; T67609.
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Berglindh OT, Sm
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                                                                                                                                                                                                                                                                                                                                              RA) ASTRA AB.
RA, Smith D;
97-503122/46.
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US-625811.
US-758731.
US-736905.
US-738859.
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Pred. No. 1.44e+01;
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Matches
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02-APR-1996;
25-OCT-1996;
28-OCT-1996;
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27-MAR-1997;
06-DEC-1996;
DNA act as antisense sequences, and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant
                                                                                                                                                                                     The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample, and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the
                                                                                                                                                                                                                                                                                                                       N-PSDB; V24653.
Helicobacter pylori nucleic acid sequences and encoded helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent infection and for diagnosis of H. pylori infection Claim 14; Pages 487-488; 1145pp; English.
This sequence is a Helicobacter pylori protein of unspections.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (ASTR ) ASTRA AB. Alm RA, Smith D; WPI; 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W55244 standard;
                                                                                                                                                                                                                                                                                                           function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9737044-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitor; duodenal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identification;
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; US-761318.
; US-625811.
; US-758731.
; US-736905.
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Pred. No. 1.44e+01;
21; Mismatches 31;
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CC The present sequence is a Helicobacter pylori cell envelope protein. CC The protein may be used in a vaccine to prevent or treat H. pylori CC infection or to identify H. pylori polypeptide binding compounds. CC useful as potential H. pylori life cycle activators or inhibitors. CC The genomic sequence of H. pylori (ATCC 55679) was determined from CC overlapping contigs generated by mechanically shearing the bacterial CC and the predicted coding regions defined by computer evaluation. To CC identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant CC and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide Sequence 432 AA;
                                                                                                                                                                                                                                                                    IRESULT

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Best Local Similarity 26.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-1996. U09122. 06-JUN-1996; U09122. 07-JUN-1995; US-487032. 01-APR-1996; US-630405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter claim 56; Page 1148-1149; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
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Berglindh OT, Sm
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64 KEALETFGGVKRRFNETT 81
                                          256 spilgrynlynilagvlgvkiltglpletiapllenfygvkgrl-eivhskplvvvdfah 314
   35 SPQYGDHTVLNALA-VIAISYLEKLDVTNIKEALETFGGVKRRFNETTIANQVIVDDYAH 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pylori cell envelope protein, 06cp11722orf15.
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Similarity 36.7%;
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Search completed: Wed Nov 24 00:52:56 1999 Job time: 220 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Nov 24 00:53:33 1999; MasPar time 4.20 Seconds 610.175 Million cell updates/sec

Tabular output not generated.

Title: >US-09-103-287-4

Description: Perfect Score: (1-215) from US09103287.pep 1495

Sequence: 1 FKDSDDIYAQIFQITDKGTA......GDIQKLQNAYLDKLGMKNAF 215

Scoring table: PAM 150 Gap 11

Searched:

122461 seqs, 11912985 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 29.592; Variance 156.427; scale 0.189

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	1	2	w	4	ر ت	σ	7	80	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	
Score	137	137	134	134	101	95	92	92	88	88	88	88	88	88	88	87	87	86	86	86	87	87	87	
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Description	Sequence 2,		Sequence 4,		Sequence 5,	Sequence 72	Sequence 17	Sequence 7,	Sequence 7,	Sequence 2,		Sequence 2,	Sequence 6,	Sequence 3,	Sequence 2,	Sequence 2,	Sequence 2,		Sequence 48	Sequence 46		Sequence 6,	Sequence 42	
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Sequence 2		Sequence 2		Sequence 8	Sequence 2	Sequence 2		Sequence 1		Sequence :	Sequence 1		Sequence 6	Sequence (		Sequence 6	Sequence 9	Sequence 9	Sequence 4	Sequence 4	sequence .
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## ALIGNMENTS

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MOLECULE TYPE: protein	5	H: 450	SEQUENCE CHARACTERISTICS:	INFORMATION FOR SEQ ID NO: 2:	TELEFAX: 317-276-3861		H	BE	TRATION NUMBER:	NAME: Webster, Thomas D	ATTORNEY/AGENT INFORMATION:	CLASSIFICATION: 435		APPLICATION NUMBER: US/08/843,309	LICATION DATA:	PatentIn	SYSTEM:		TYPE: F	COMPUTER READABLE FORM:	$\sim$	ĸ	•	Indianapolis	lly Corporate (	ADDRESSEE: Eli Lilly and Company	Š	SEQUENCES: 3	NVENTION: Bios			Peery, Ro	ADDITONUT: Skatrid Daii	GENERAL TRECOMARION:	Datent NO 5834270	3 3 3 3 4 4 5 5	Sequence 2, Application US/08843309			XXXXXX		US-08-843-309-2 STANDARD; PRT; 450 AA.

pneumoniae

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39

Matches

RESULT

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Query Match 9.2%;
Best Local Similarity 53.8%;
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             US-08-934-481-4
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                                                                                           276 GSHNVENALATIAVAKLRDVDNQTIKETLSAFGGVKHRL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5681694
GENERAL INFORMATION:
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                                                                  39 GDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRF 77
                                                                                                                                                                                                                          TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 450 AA; 48579 MW; 1010380 CN;
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/665,435A
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hoskins, Joann
APPLICANT: Wu, Chyun-Yen Earnest
TITLE OF INVENTION: Biosynthetic
TITLE OF INVENTION: pneumoniae
                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDHTVLNALAVIAISYLEKLDVINIKEALETFGGVKRRF 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
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Similarity 53.8%;
21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08665435A
                                                                                                                                                                                                               amino acid
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                                                                                                                     Conservative
                                                                                                                                                                                                                          450 amino acids
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             STANDARD;
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                                                                                                                   Score 137; DB 1;
Pred. No. 4.20e-02
7; Mismatches 1
                                                                                                                                                                                                                                                                                                                       39,872
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Pred. No. 4.20e-02;
7; Mismatches 11
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             PRT;
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Best Local Similarity 53.8%;
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                       Sequence 2, Application US/08934481
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                                    Patent No. 5929045
GENERAL INFORMATION:
                                                    Sequence 2, Application US/08934481 Patent No. 5929045
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                                                                                                                                                                                                                            39 GDHTVLNALAVIAISYLEKLDVINIKEALETFGGVKRRF
                                                                                                                                                                                                                                                   93 GSHNVENALATIAVAKLRGVDNQTIKETLSAFGGVKHRL 131
                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
COMPUTER: TOTALE TOTALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wallis, Nichola APPLICANT: Fueyo, Joanna L. APPLICANT: Lonetto, Michael
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lonetto, Michael A. TITLE OF INVENTION: NOVEL MURD
                                                                                                                                                                                                                                                                                                                                               LENGTH: 267 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 4000 BELL CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 215-994-2222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                  267 AA; 29079 MW; 348410 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dickinson, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PA
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Lonetto, Michael A.
                       Wallis, Nichola G.
         Fueyo, Joanna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wallis, Nichola G.
                                                                                                                                                                       STANDARD;
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Pred. No. 6.72e-02;
7; Mismatches 11
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Matches

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Query Match 9.0%;
Best Local Similarity 53.8%;
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                  US-08-736-770-5
                                                                                                                                                                                                                                                                                                                                                                                                               272 GSHNVENALATIAVAKLRGVDNQTIKETLSAFGGVKHRL 310
                                                                                                                                                                                                                Sequence 5, Application US/08736770 Patent No. 5871965
                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       39 GDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                          APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
            COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                   CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
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SOFTWARE: FastSE(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GM.
ILECOMMUNICATION TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Dickinson, Todd
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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COMPUTER:
                                                                          STREET: 3174 PO:
CITY: Palo Alto
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                                                                                                       ADDRESSEE:
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                                                                                         3174 Porter Drive
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IBM Compatible
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             Diskette
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                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Pred. No. 6.72e-02;
7; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                           Sequence 72,
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Local Similarity 29.6%;
hes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acid
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LIBRARY: GenBank
CLONE: 829177
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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                                                                                                                                                                                                          NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       APPLICANT: Matsuda, Akio
TITLE OF INVENTION: A Polypeptide Capable of Interacting
TITLE OF INVENTION: with Thrombin
NUMBER OF SEQUENCES: 80
                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
PRIOR APPLICATION DATA
                                                                                                                                                      NUNKESSEE: Birch, Stewart, KC
STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                            APPLICANT:
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SOFTWARE: FastSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                           FILING DATE:
                                                                                                                                 COUNTRY: USA
ZIP: 22046-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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             CLASSIFICATION:
                                     APPLICATION NUMBER:
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Pred. No. 1.01e+01;
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application PC/TUS9108177
GENERAL INFORMATION:
APPLICANT: Samal, Siba K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 GALTIQDLIDKIE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 INDAFGTAHRAHSSMVGVDLPQKAAGFLMKKE-LDYFAQALEAPQRPFL-AILGGAKVSD 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 KIQLIDNLLDKVN 232
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6.4%; Score 95; DB 1; I
Local Similarity 26.0%; Pred. No. 2.40e+01;
hes 19; Conservative 23; Mismatches 28
         TELEFAX: 202-96 INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 ISATIDTARKKYPHKEVVAVFQ-PHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                 NAME: Highet, David W
REGISTRATION NUMBER: 30,265
REFERENCE/DOCKET NUMBER: 20509-96711
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4854
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Bovine Respiratory Syncytial Virus NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: ADDRESS: Venable, Baetjer, Howard & Civiletti
                                                                                              APPLICATION NUMBER: US 07/608,937 FILING DATE: 05-NOV-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                      FILING DATE: 19911104
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRÁTION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                             APPLICATION NUMBER: PCT/US91/08177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/740,492 FILING DATE: 03-AUG-1991
                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                         CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LE TYPE: protein
418 AA; 44347 MW; 867507 CN;
                                                                                                                                                                                                                                                                      20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                     E: Venable, Baetjer, Howard & Civiletti
1201 New York Avenue N.W., suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418 amino acids
                                                                                                                                                                                                                                                                                  USA
                        202-962-8300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Best Local S
Matches 1
 Query Match
                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Flop Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,0901

FLING DATE: 05-JUN-1995

CLASSIFICATION: 435

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08463090B Patent No. 5801015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 SIRENTGALTIQDLIDKIEGASLINEDSINVLEQF - - DNAVVLFMGAGDIQKLQNAYLDK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 GIRDAMVGLR-EEMIEKIRSEALMTNDRLEAMARLRNEESEKMXKDTSDEVKLTPTS-EK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 LNM 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 LGM 211
                                                                             REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 6.2%;
Local Similarity 22.2%;
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Cell-Cycle Regutatory .....TITLE OF INVENTION: Human Pathogens, and Uses Related Thereto NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cottarel, Guilla APPLICANT: Damagnez, Veroni APPLICANT: 'Draetta, Guilla
                       MOLECULE TYPE: protein ENCE 411 AA; 47663 MW; 877573 CN;
                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: BUTTN: FS-1
                                                                                                                                                                                                                                                                                                                    CITY: Boston
STATE: MA
                                               TOPOLOGY:
                                                                                                                                                 REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley, Hoag & Eliot, LLP STREET: One Post Office Square
                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                         amino acid
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                    411 amino acids
                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                              linear
 6.2%;
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                                                                                                                                                                                                              US/08/463,090B
 Score 92;
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Pred. No. 3.69e+01
25; Mismatches 2
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 DB
2
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Length 411;
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APPLICANT:

Samal, Siba K

PCT-US91-08177-7

В

Matches

14;

Conservative

Best Local Similarity 24.1%;

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Sequence 7, Application PC/TUS9108177
                                                                                                                                                                                                                                                                               165 GIRDAMVGLR-EEMIEKIRSEALMTNDRLEAMARLRDEESEKMTKDTSDEVKLTPTS-EK 222
                                                                                                                                                                                                                                   151 SIRENTGALTIQDLIDKIEGASLINEDSINVLEQF-DNAVV-LFMGAGDIQKLQNAYLDK 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 05-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Highet, David W
REGISTRATION NUMBER: 30,26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 DSDDIYAQIFQITDKGTAVDVYVDGEFYDHFLSPQYGDHTVLN-ALAVIAISYLEKLD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 30,265
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Bovine Respiratory Syncytial Virus Genes NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                         JE TYPE: protein 241 AA; 27254 MW; 281214 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 241 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202-962-4854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                                                                                                                                                                                                                                                                                             Score 88; DB 3;
Pred. No. 6.51e+01
23; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 :
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                                                PRT;
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                                                456 AA
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Best Local
                                                                                                                                       Sequence
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                                           Sequence 2, Application US/08464164 Patent No. 5614195 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           105 ARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKA-DR 142
                                                                                                                                                                                                                                                                                                                                                                                                     343 LDKSAIETEVEQVLEAVDFDKN-GFI-EYSEFVTVAMDR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 LAAAALLYMGSKLTTNEETDELNKIFQKMDKN-GDGQLDKQELMEGYVELMKLKGEDVSV 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08338057 Patent No. 5795741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 LAVIAISYLE-KLDVTNIKEALET-FGGVKRRFNETTIANQVIVDDYAHHPREISATIDT 104
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APPLICANT: Tomley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 5.9%;
Local Similarity 21.2%;
es 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (301) 258-
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 456 AA; 52270 MW; 1035762 CN;
APPLICANT: Tomley, Fiona M. APPLICANT: Dunn, Paul P. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (301) 258-5200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: EP 9:
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: GOIDLEY, MARY E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                     2, Application US/08464164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, Paul P. J.
Bumstead, Janene M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                               STANDARD;
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Pred. No. 6.51e+01;
26; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34,409
                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                               456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 456;
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APPLICATION NUMBER: POFILING DATE: 19911104

CLASSIFICATION:

COMPUTER READABLE FORM:

20005

MEDIUM TYPE:

COUNTRY:

USA

Washington

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Best Local Similarity Matches 15; Conser

Conservative

5.9%;

Query Match

SEQUENCE

MOLECULE TYPE:

TOPOLOGY:

linear

TYPE:

LENGTH:

INFORMATION FOR SEQ ID NO:

TELEPHONE: 202-962-8300

SEQUENCE CHARACTERISTICS:

RESULT

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US-08-338-057-2

STANDARD;

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APPLICANT:

Bumstead, Janene M.

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Best Local :
                                          APPLICANT: Dunn, Paul P. J.
APPLICANT: Bumstead, Janene M.
APPLICANT: Bumstead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: AKRO NO. 5843722el Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Marvland
                                                                                                                                                                                                                                   Sequence 2, Application US/08668416
                                                                                                                                                                                                                                                                                                            US-08-668-416-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                  Sequence 2, Application US/08668416 Patent No. 5843722
                                                                                                                                                                                                                                                                                                                                                           105 ARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKA-DR 142
                                                                                                                                                                                                                                                                                                                                                                                 343 LDKSAIETEVEQVLEAVDFDKN-GFI-EYSEFVTVAMDR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                284 LAAAALLYMGSKLTTNEETDELNKIFQKMDKN-GDGQLDKQELMEGYVELMKLKGEDVSV 342
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Local Similarity 21.2%;
hes 21; Conservative
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NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                   atent No. 5843722 GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                         12
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JENCE 456 AA; 52270 MW; 1035762 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        LAVIAISYLE-KLDVINIKEALET-FGGVKRRFNETTIANQVIVDDYAHHPREISATIDT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Vermeulorities of INVENTION:
                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/464,164 FILING DATE: June 2, 1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Rockville
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VENTION: Coccidiosis poultry vaccine
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Pred. No. 6.5le+01;
26; Mismatches 46
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Best Local Similarity 21.2%;
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                       Patent No. 5871965
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08736770 Patent No. 5871965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                      FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                      SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESS: Inc
                                                                                                                                                                                                                                                        APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 258-5200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: June 2, 199:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                             COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                STREET: 3174 POI CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
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OPERATING SYSTEM:
                                                                           APPLICATION NUMBER:
                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Gormley, Mary E REGISTRATION NUMBER: (
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456 AA; 52270 MW; 1035762 CN;
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                                                                                                                         IBM Compatible
                                                                                                                                        Diskette
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                                                                           US/08/736,770
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Pred. No. 6.51e+01;
26; Mismatches 46;
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Best Local S
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  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 LIDKIEGASLINEDSINVLEQFDNAVVLFMGAGDIQKLQNAYL-DKL-GMKNAF 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 5.9%;
Local Similarity 24.1%;
hes 13; Conservative
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                                                                            TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 LIENTNGRLMANPEALKILSAITQPMVV-VAIVGLYRTGKSYLMNKLAGKKKGF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 03:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 592 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: McClung, Barbara G.
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1
MOLECULE TYPE:
  MOLECULE TYPE:
ENCE 3174 AA;
                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                FILING DATE: 07
CLASSIFICATION:
                        TOPOLOGY:
                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                 ZIP: 94608-2916
                                                                                                                                                                                                                                                                          COUNTRY:
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CLONE: 183002
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                                                        LENGTH:
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                                                       3174 amino acids
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                        linear
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  protein
369950 MW; 52965964 CN;
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Pred. No. 6.51e+01
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Matches 37; Conservative
 SEQUENCE
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                                                                                                                                         TELEFAX: 201 50 INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                           REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                  ORIGINAL SOURCE:
                                              ANTI-SENSE: NO
                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Weber, Gerhard
TITLE OF INVENTION: Cyclo
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APPLICANT: Schneider, Eli
                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINE 176
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                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                           STRANDEDNESS:
             STRAIN:
                      ORGANISM:
                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                 TOPOLOGY:
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                                                                                                                  ENGTH:
15281 AA; 1689051 MW; 1163257458 CN;
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                                                                                                    amino acid
           M: Tolypocladium niveum ATCC 34921
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                                                                                 unknown
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37; Mismatches
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Pred. No. 6.51e+01
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Query Match

5.9%;

Score 88;

DB 2;

Length 15281;

Db 12664 DFATEASVVDVFQTQVVANPDAL 12686
|| || || : : |:
Qy 107 KKYPHKEVVAVFQPHTFSRTQAF 129

IO/ KNIPHNEVVAVEQPHIESKIQAF 129

Search completed: Wed Nov 24 00:54:20 1999 Job time : 47 secs.

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1 2573 96 2 1309 49 2 1309 49 4 1309 49 5 324 12 6 320 12 7 38 10 0 283 10 110 283 10 111 283 10 12 283 10	Result Quer No. Score Matc	Statistics: Mean Pred. No. is the score greater than and is derived	Database: en	Post-processing: M	Nmatch STD: Dl Searched: 64	Scoring table: T/	Title: >I Description: (: Perfect Score: 26 N.A. Sequence: Comp:	Run on: Sa Tabular output not	MPsrch_tpn n.a which	Release Copyrigh	
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aphylococcus aureus 8.76c cillus subtilis UDP- 3.43c cillus subtilis comp 3.43c cillus subtilis comp 3.43c cillus subtilis rnnB 3.43c eponema pallidum sec 4.01c rphyromonas gingival 1.00c rrelia burgdorferi (1.58c ulfex aeolicus secti 2.11c cherichia coli UDP-M 4.11c cherichia coli murg 4.11c cherichia coli murg 4.11c cherichia coli K-12 4.11c coli 2 minute regio 4.11c	SCI	56; scale 0.282  coted by chance to have a of the result being printed, score distribution.	fun 4:em_htg 5:em_hum1 6:em_hum2 10:em_ov 11:em_pat 12:em_ph _sts 16:em_vi gb_htg1 20:gb_htg2 21:gb_in1 b_ov 25:gb_pat 26:gb_ph 27:gb_pl1 gb_pr2 31:gb_pr3 32:gb_ro b_sy 36:gb_un 37:gb_vi		x X X		TNGGNATGAARAAYGCNTTY 645	MasPar time 1198.35 Seconds 1491.947 Million cell updates/sec	), using a protein query ) n.a. using IUPAC symbols	puting Research Unit. of Edinburgh, U.K. d Molecular Ltd	

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## ALIGNMENTS

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	CDS	gene	FEATURES source	JOURNAL	TITLE	REFERENCE	TOTIRNAT	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	NID	ACCESSION	DEFINITION	RESULT 1
/gene="murc" /function="cell wall biosynthesis" /function="cell wall biosynthesis" /note="MurC; UDP-N-acetylmuramate-alanine ligase" /codon_start=1 /transl_table=11 /product="UDP-N-acetylmuramoy1-L-alanine synthetase"	/gene="murc" 11314	/organism="Staphylococcus aureus" /db_xref="taxon:1280" 1. 1314	Location/Qualifiers 11314	Submitted (11-NOV-1997) Channing Laboratory, Brigham and Women's Hospital and Harvard Medical School, 181 Longwood Ave, Boston, MA 02115, USA	Lowe, A.M. and Deresiewicz, R.L. Direct Submission	2 (bases 1 to 1314)	involved in cell wall biosynthesis	Lowe, A.M. and Deresiewicz, R.L.	1 (bases 1 to 1314)	Eubacteria; Firmicutes; Low G+C gram-positive bacteria;	Staphylococcus aureus	Staphylococcus aureus.	AF0340/0:1 GI:2042030	g2642658	AF034076	AFU34076 1314 bp DNA BCT 26-NOV-1997 Staphylococcus aureus UDP-N-acetylmuramoyl-L-alanine synthetase	

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LEKLDVTNIKEALETFGGVKRRFNETTIANQVIVDDYAHHPREISATIETARKKYPHK
EVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKIEG
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NKGIKILPFDANNIKEDMVVIQGNAFASSHEEKARAHQMKLDVVSYNDFLGQIIDQYT
SVAVTGAHGKTSTTGLLSHVMNGDKKTSFLIGDGTGMCLPESDYFAFEACEYRHHFLS
YKPDYAIMTNIDFDHPDYFKDINDVFDAFQEMAHNVKKGIIAMGDDEHLRKIEADVPI
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1 (bases 1 to 2320)

Varon,D., Brody,M.S. and Price,C.W.

Varon,D., Brody,M.S. and Price,C.W.

Bacillus subtilis operon under the dual control of the stress transcription factor sigma B and the sporulation transcription factor sigma H
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/note="sigma-B consensus"
1172. .1177
                                                                                                                                                                 /translation="MMSKDGINSKDFLIGTLIGGIIGATTALFLAPKSGKELRDDLGS
QAVALRDKTDKMTADAKEKGTQYVSIAKDKTSNITQLVADQSGQIMNKVKDLRDRSKS
DKTDSSTAMQMREEAMQAADETKDQVLQTKEDVKDELKDAQKQAEQLNR"
                                                                                                                                                                                                                                                                                                                                                                                                                SVSASVRENQDKINQVVGRSTWSQAAMEIWEKWKQKKKSAL"
                                             /note="open reading frame extends an additional 53 codons
(including the TGA stop) into the overlapping sequence
reported by Bolotin et"
                                                                                                                                                                                                                                                                                                                                                                  1670. .2128
/note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MIIILYLSVALIAVAFLVLVIYLSKTLKSLQLTLKNVASTLEGLEGAMKGITTETAELLHKTNRLAEDIQEKSEKLNTVVHAVQGVGASVQQFNTSMKQAAG
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VFVRNTFYDTFYIPAYGHHNVLNSLAVIALCHYEEIDSSIIKHALKSFGGVKRRFNEK
QLGDOVLIDDYAHHPTEIKVTIEAAROKYEDREIVAVEOPHTETRTOCETLDEFAESLS
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/db_xref="taxon:1423"
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l Similarity 45.2%;
272; Conservation
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Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C.,
                                   Kunst, F., Ogasawara, N.,
                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae;
                                                                                                            Bacillus subtilis
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/db_xref="GI:556017"
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                                                                                                                                                                                                                                                       215640
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Pred. No. 3.43e-125;
L23; Mismatches 207;
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                               Moszer, I., Albertini, A.M., Alloni, G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regulation de l'Expression Genetique, 28 rue du Docteur Roux, Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adannhin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bron,S., Brouillet,S., Bruschi,C.V., Caldwell,B., Capuano,V., Carter,N.M., Choi,S.K., Codani,J.J., Connerton,I.F., Cummings Daniel,R.A., Denizot,F., Devine,K.M., Dusterhoft,A., Ehrlich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-NOV-1997) I. Moszer, A. Danchin,
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                                                                                                                                                                                                                                                                                                                                                                    /translation="MKKLIVFAFIGLLSQLIDGSLGMAYGVTSTSLLLAFGITPAVAS ASVHLAEVUTTAASGVSHIKFGNVDKOUTVQLVIPGSLGAFLGAAFLSQLPGDVAKPY ISLFLLLLGGVYLIRFLFQYKPALEKKHVPLNRKQSIPLGAFAAGFADATGGGMGPVT TPILLSRKGLSPRKVVGTVDTSEFAIAVSATAGFLISLGWEDVNWLWVFSLMAGGIIA APIAAWLYQKFHPQLMGVLVGGFIILVNARTLINEWIANTAVHPLIYTAIGAIWLSAV LFVLSKIGNRNIVKTAVDVHLKEK"
                                                                                                                                                                                                                                                                                                                              complement(1020.
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SETGROFAAKNADAIFTHSNSLEETKAFYADVKSRAADEGRDPSSVRIFPGISBIVA
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                                                                                                                                                                                                                                    /db_xref="SPTREMBL:034639"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ytnI"
complement(4352. .4633)
/gene="ytnI"
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SLTKQIKKDISCVAKRELIGIMAPNKKESLLSHQELNLPDLCFYKKCNNLYGVNRGV
YNVIDNWFFETGITQVAYRRIYILSFLSFLKEDNPKVSSKYIRFGAGGLADKLNRFIS
SYVEESEENILG"
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/db_xref="PID:e2185802"
/db_xref="PID:92635413"
/db_xref="GI:2635413"
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/db_xref="GI:2635413"
/db_xref="SPTREMBL:O34980"
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KGAHAALPHNGFDFIIGASQLIVALQTIVSRNVNPLQSAILTUTVGKINGGSTWNVIPDT
VVIEGTVRTFDSEVRNQVKQRFFAVTEGISAAFSLKANVKWHSGPPFLCNDEALTGLV
RDAAHKAKLQVIDFAPSTAGEDFAXYLEHIPGSFAFFGTDGDHDWHHPAFTIDETAII
                                                                                                                                         complement(4648. .5652)
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PGTLDAFVEKVIPILQERGLYRDDYRGGTLRENLGLGIPQHQSVLHSSHH"
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/gene="ytnJ"
                                                                                                                                                                                                        complement(4648.
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                                   /function="unknown"
/note="similar to h
                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB14910.1"
/db_xref="PID:e1185805"
/db_xref="PID:g2635416"
/db_xref="GI:2635416"
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/db_xref="PID:e1185804"
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/protein_id="CAB14908.1"
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/codon_start=1
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/note="alternate gene name: ytnK"
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n_id="CAB14909.
                               to hypothetical proteins"
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Matches 27
49868 TTGATCCCCAAGCTGCTTCTCATTGAATCTGCGTTTTGACGCCCCCCAAAGGATTTGAGAGC 49927
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                                                                                                                                                                                                                                                                                                                                                                                             CTGGAGATCACCGATCGTCAGCTTTCCGGCATTCTCACGGGCTGAGCCGAAAATATCGCA 49687
                                                                      NGCNGTRTCDATNGTNGCNSWDATYTCNCKNGGRTGRTGNGCRTARTCRTCNACDATNAC
                                                                                                                   NCKNSWRAANGTRTGNGGYTGRAANACNGCNACNACYTCYTTRTGNGGRTAYTTYTTNCK
                                                                                                                                                                                                                                                                  NARRAANACNCKRTCNGCYTTNSWNARNSWYTCNGCRAAYTCRTTNARRAANGCYTGNGT 376
                                                                                                                                                                                                                                                                                                               TAAATACACAGTCGGCGCCGCTCAGGCTTTCTGCAAATTCGTCAAGGAACTGCTGCGT 49747
                                                                                                                                                                                                                                                                                                                                                                  DATNARRTCYTGDATNGTNARNGCNCCNGTRTTYTCNCKDATNSWNCCRAADATYTCRCA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAAYTGYTCNARNACRTTDATNSWRTCYTCRTTDATNARNSWNGCNCCYTCDATYTTRTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTANGCRTTYTGNARYTTYTGDATRTCNCCNGCNCCCATRAANARNACNACNGCRTTRTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        th 49.2%; Score 1309; DB 17; Similarity 45.2%; Pred. No. 3.43e-125; 272; Conservative 123; Mismatches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotations omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ./translation="MIEIKNIHKOFGIHHVLKGINLTVRKGEVVTIIGPSGSGKTTFL RCLNLERPDEGIISIBDKVINCREPSKKEVHWLRKQTANVFQOYHLFAHKTVIENVM BGLTIARKMRKQDAYALASIBDKVINCREPSKKEVHWLRKQTANVFQOYHLFAHKTVIENVM LLFDEPTAALDBELVGEVLEVMLEIVKTGATMITVTHEMEFARRVSDQVVFMDEGVIV LLFDEPTAALDBELVGEVLEVMLEIVKTGATMITVTHEMEFARRVSDQVVFMDEGVIV EQGTPEEVFRHIKKDRTRQFLRRVSPEYLFEPKEHIKEPVI"
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./db_xref="SPTREMBL:034846"
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VDRKPOIFILGGSTESAISAAKLGISTVFAYFINGEEEVLKEARRAFDAHLPPGSSAE
FHLAPAVFAAHTKEEAEKHIVSRESIKVVLKDGRKVNVGSREQAEAYLENVTEPVDII
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/db_xref="PID:e1185807"
/db_xref="PID:g2635418"
/db_xref="GI:2635418"
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/db_xref="PID:e1185806"
/db_xref="PID:g2635417"
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/codon_start=1
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HHNNDEIAGSAPEVLLGYLAASTRKIRLASGGVMLQHYSSYKVAEQFHLLSALAPGRI
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AF008220
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Connors,M.J., Mason,J.M. and Setlow,P.
Cloning and nucleotide sequencing of genes for three acid-soluble proteins from Bacillus subtilis spores
J. Bacteriol. 166 (2), 417-425 (1986)
                                          7 (bases 133624 to 134990)
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Green, C.J., Stewart, G.C., F
Nucleotide sequence of the
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J. Bacteriol. 172
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 96312354
20 (bases
                            Pero,J.
Cloning, sequencing, and characterization biotin biosynthetic operon
J. Bacteriol. 178 (14), 4122-4130 (1996)
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96144257
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transcription factor sigma H
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Microbiology 141 (Pt 6), 1433-1442 (1995)
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Grundy, F.J., Waters, D.A., Allen, S.H. and Hen
Regulation of the Bacillus subtilis acetate
J. Bacteriol. 175 (22), 7348-7355 (1993)
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Bolotin,A., Khazak,V., Stoynova,N.,
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Jin,S. and Sonenshein,A.L.
Identification of two distinct Bacillus subtilis
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Three transport systems for the osmoprotectant
operate in Bacillus subtilis: characterization
J. Bacteriol. 178 (17), 5071-5079 (1996)
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Lapidus, A., Galleron, N.,
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Local Similarity 45:2%;
hes 272; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGATAAAGCCGTTCTCATCTTCATGGGAGCAGGAGATATCCAAAAATATATGAGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGGAAAAATTCATAATGCCAAGCTGATTGAAGAAGATGACACATCTGTTTTAAAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNTGYGARATHTTYGGNWSNATHMGNGARAAYACNGGNGCNYTNACNATHCARGAYYTNA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGACGCAGCAGTTCCTTGACGAATTTGCAGAAAGCCTGAGCGGCGCCGACTGTGTGTATT 130736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGACAGAAGTATCCTGATCGGGAAATTGTCGCGGTATTCCAGCCTCATACATTTACCC 130676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGTGCTGATTGATGACTATGCCCATCATCCGACAGAATAAAAGTGACAATCGAGGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCTCTCAAATCCTTTGGGGGGCGTCAAACGCAGATTCAATGAGAAGCAGCTTGGGGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNGAYGGNGARTTYTAYGAYCAYTTYYTNWSNCCNCARTAYGGNGAYCAYACNGTNYTNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC 130918
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                                                                                                                                                                                                                                                                                                                             AE001213 14838 bp
Treponema pallidum se
AE001213 AE000520
spirochete
Science 281
                                      Complete genome sequence of Treponema
                                                    Fraser, C.M., Norris, S.J., Weinstock, G.M., White, O., Sutton, G.G., Dodson, R., Gwinn, M., Hickey, E.K., Clayton, R., Ketchum, K.A., Sodergren, E., Hardham, J.M., McLeod, M.P., Salzberg, S., Peterson, J. Khalak, H., Richardson, D., Howell, J.K., Chidambaram, M., Utterback, T., McDonald, L., Artiach, P., Bowman, C., Cotton, M.D., Fujii, C., Garland, S., Hatch, B., Horst, K., Roberts, K., Watthey, L., Weidman, J., Smith, H.O. and Venter, J.C.
                                                                                                                                                                                                                             Treponema pallidum.
Treponema pallidum
                                                                                                                                                                                                                   Eubacteria;
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(5375),
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375-388 (1998)
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Pred. No. 3.43e-125;
123; Mismatches 207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98332770
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                                                                                                                                                                                                                                                                                                                                                       /product="cell division protein, putative"
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IDCGVTLNRNSLPFDPNGAWLTSGLRIGTPAVTSLGMGPEEMKRIARLIARVLGAATP
VRTKTGALSKSAAEVPGEVRSSVCSEVRELLARFTLYPELDEPFLRAHFTRRPAGQNT
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identity: 48.52; identified
putative"
                                                                            complement(3649. .
/gene="trna-Gly-1"
                                                                                                                                                                                                                                         KQGRADVLPMGYLISGPIGTGKSFMVSAFAGEIGIPMVRLCNFQATQPGITQSNLEKT
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PDLLPIDLKRQGRAEEHLALFYPETTKEKTEIFEALKKKLRIKLKDVHVPAIIRRIKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:L43967
identity: 29.18; identified
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1788. .3584)
/gene="TP0330"
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KRERPLILLAGYSAYPRSINFRIFREIADKVGAVLMADMAHFAGLVAGGVFTGDEDPV
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AAEACALFGAEHAYVQPHSGADANLVAFWAILSRQIEMPTLSSLGVTAATHLSEEQWE
                                                                                                                                                                                              AVSGSDLEAILVRAQLTAAMENRTMVTTQDITRTIEDFIPPAYPHEIELQNLVAVLEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="tRNA-Leu-3"
complement/1700
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/protein_id="AAC65317.1"
/db_xref="PID:93322607"
                                                                                                                                                    TGKEMLPARYQHLDRSKLVADIRELKLLMGEK"
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/translation="MNNSALRAYLSTRAPDQIHSAFVAYLANLDLVAHQFPQIASDIV
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/db_xref="taxon:160"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="tRNA-Leu-3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norris, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J., Weinstock, G.M., White, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1696)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SP:P47695 PID:1046176 percent by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:556886 GB:AL009126 percent
by sequence similarity;
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Ketchum,K.A.,
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/gene="tRNA-Gly-1"
complement(3814...
/gene="TP0331"
GTQVISLGQRLVMDLNTDVQPDVEISVEDIEAHQADGGARVRVFTGSLVQTLRDRSAQ
SFVPTSGVNVSGQTGVAAGARYQVLFEGGVAYPVTMNATFRSYCLFRYEADRTRREER
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ACVLFLGGVLGYYARHRALGFLSRIVFFGRAQRTPRELSPPDATGAVRETVSLSSAQ
HEERARRTRSSASRYTLAEEKFEHTVFPGDVLVISSGGNAYELTVSRTTPHLYLDTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="TP0334"
6176. .7393
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                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GP:1842438 percent identity: 31.48; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSAAETFKSLRVLVSAHTKLIRRIEAWPLSGEKITFDFSHYRLNVGIPDTRFLYDVPP
TANVVHNELFAD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mrrrrfltlcacavhllplfpqtittasyffasysehyarlkd
YAADLAMSTGSGTRAHLMRAKVIFKYPDRLRLDFSSPAEQTIVFTGDSLTIYLPTSRV
ALVQSVAKDDTVSAASLASPHGLALMKRFYTIAYETSSSPVPLGPDSGEMVVALVLNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"T. pallidum p:
/protein_id-"AAC65327.1'
/db_xref="PID:93322617"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein; identified
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDYFGAHTYERTDAPRGEFFHTNWTGTGGDTIAGTYSI"
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FTRWNTGRLHSYLIEITAAILAHQDTDGTPLLEKILDAAGQKGTGRWTCVAALEEGSP
LTLITESVMARSLSAQKQARCKAHRVFGSPVKVSKAETLSAQQREELVSALEDALYCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="phosphogluconate dehydrogenase (gnd)"
/protein_id="AAC65319.1"
/db_xref="ptb:93322609"
/db_xref="GI:3322609"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical protein"
/protein_id="AAC65320.1"
/db_xref="PID:93322610"
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                                                                                                                                                                                                                                                                          /product="conserved h
/protein_id="AAC65321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GI:3322610"
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/gene="TP0332"
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                                                                                                                                                                                                                                                                                                      hypothetical protein"
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Wachi, M., Nagai, K.

Fukuoka

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      AUTHORS
TITLE
                                                                                                                         ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARAARTAYCCNCAYAARGARGTNGTNGCNGTNTTYCARCCNCAYACNTTYWSNMGNACNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARGCNTTYYTNAAYGARTTYGCNGARWSNYTNWSNAARGCNGAYMGNGTNTTYYTNTGYG
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                                                                                                                                   9278U/41 GI:2780741 D84504.1 GI:2780741 FtsQ; MurC; ftsQ; murC; Peptidoglycan synthesis.
                                                                                         Porphyromonas gingivalis Bacteria; Cytophagales;
                                                                                                                                                                                                                                                                                                                                             Porphyromonas gingivalis gene for MurC, cds.
         Direct Submission
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Similarity 36.9%;
75; Conservati
                                                            (bases 1 to 2454)
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ISPAVVMAIAAVGGEYGTHVYEVPFPYAFFGAVQACVLCIGCLLVRSGVRFFSRWGAV
RIWRRWGIAYTSVCRCCNTLFFVFCGLCVACVARTSLMVQQAPLQTLAQPQKLRVLTI
HLLQEPKPACTRFRVRARVLGAGYIDGASFSARGVCTYLFPAEVILQQYATDWTDDAD
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SPWGRAGGLLLALLSADSVFLSDEMRVAFRHAGLAHVLALSGMHLSLVGASATFLGRF
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TEYAFYLSTLVFPSFCFSLPSPFPFPEGEGGAFYVRLFLNALSEEVLFRAYIPERLCH
HATSCTARACGEVLSVLLFALAHRPAGSATLFAGAAGAALRVLFVREKKRSGSRARAS
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/protein_id="AAC65328.1"
/db_xref="PID:g3322618"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="PID:g3322612"
/db_xref="GI:3322612"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="comE protein, putative"
/protein_id="AAC65322.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to PID:1652202 percent identity: 27.72;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="TP0336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:3322618"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="TP0335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                      2454 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          omitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 324; DB 18; 1
Pred. No. 4.01e-15;
46; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                         Bacteroidaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .7932)
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                                                                                                                                                                                                                                                                                                                                                                   FtsQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding
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                                                                                                                                                                                                                                                                                                                                                                      partial and complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region TP0335
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                                                                                                                                                                                                                                                                                                                                                                                                      06-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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AUTHORS
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A murC gene in Porphyromonas gingivalis 381

Microbiology 141 (Pt 9), 2047-2052 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Jan 16, 1998 this sequence version replaced gi:1304183. D28916:Submitted(11-Mar-94) to by: Toshihiro Ansai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96118684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ansai,T
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   607
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EIIIGSTPNWAEKLSNLRLFMDKAIPKYGWDTFKTLNLEFKDQVVATPFPSSPLYPA'
1 591 c 575 g 681 t
                                                      AIVFFSDYSDSTRCSGLEVRVEGKTKHAFMQKVDVERDLKRLGFTPYGKPLDSIDLYR
MERNLRTNSLFRGAELYASPSGQLYLTVEQKDPLFMVVRSDTSFYVSTDRSVIVPNLQ
YAAPVLMASGDISLSLATGPLFDLIAFISDDPFWSNFFAQVHVPDNGQIILVPRLGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ftsQ"
1630. .>2454
                                                                                                                                                /db_xref="PID:92780744"
/db_xref="GI:2780744"
/translation="MSYDTRSRRYRSFSDSCQTISPNFMLKKVLYILGFFLVLAYLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRINVENAVAAMAIAHLNGVTVEELRSGIASFKGSHRRFEKVLDTERVVLIDDYAHHP
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YGAPVNPRLGSDVSLFTYSSDDRQADYFASDIMIRDGRLFFTWHYPGGQLEEVELGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="BAA24358.1"
/db_xref="PID:d1025270"
/db_xref="PID:d1025270"
/db_xref="PID:92780743"
/db_xref="FID:92780743"
/db_xref="GI:2780743"
/db_xref="GI:2780743"
/db_xref="GI:2780743"
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/translation="MKRVYFIGIGGIGMSAIARYFHAKGENVCGYDLT"
/translation="MKRVYFIGIGGIGMSAIARYFHAKGENVCGYD
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                                                                                                                                                                                                                                      /product="FtsQ"
/protein_id="BAA24359.1"
/db_xref="PID:d1025271"
                                                                                                                                                                                                                                                                                                                                                                                                                             1630. .>2454
/gene="ftsQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="murc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPLPGVTSRLILDLIENPNKTLVSKNDLLDYLHGNEIPDVV'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VELDAAIRSVREIYSGKHIMGIFQPHLYSRTADFYQDFAKSLSMLDQVVLLDIYPARE
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                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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/db_xref="GI:2780742"
/translation="YCAADLVVSRAGACSISELCLLGKPTILVPSPNVAEDHQTKNAL
                                                                                                                                                                                                                                                                                                                                                                                                note="see also AB004555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="peptidoglycan synthesis"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAA24357.1"
/db_xref="PID:d1025269"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:837"
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                                                                                                                                                                                                                                                                                                                                                                   codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTGGACATTT 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NACNCARGCNTTYYTNAAYGARTTYGCNGARWSNYTNWSNAARGCNGAYMGNGTNTTYYT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACGGCAGACTTTTATCAGGATTTTGCCCAAAAGCCTTTCCATGTTGGACCAGGTGGTTTT 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMGNAARAARTAYCCNCAYAARGARGTNGTNGCNGTNTTYCARCCNCAYACNTTYWSNMG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGTGAAATCTATTCGGGAAAACATATCATGGGGATCTTTCAACCCCATCTGTATAGTCG 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGTNATHGTNGAYGAYTAYGCNCAYCAYCCNMGNGARATHWSNGCNACNATHGAYACNGC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi (section 66 AE001180 AE000783
                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 15079)
2 (bases 1 to 15079)
2 (bases 7.C.M., Casjens, S., Huang, W.M., Sutton, G.G., Clayton, R.A., Lathigra, R., White, O., Ketchum, K.A., Dodson, R., Hickey, E.K., Gwinn, M., Dougherty, B., Tomb, J.-F., Fleischmann, R.D., Richardson, D., Peterson, J., Kerlavage, A.R., Quackenbush, J., Salzberg, S., Hanson, M., van-vugt, R., Palmer, N., Adams, M.D., Gocayne, J.D., Weidman, J., Utterback, T., Watthey, L., McDonald, L., Artiach, P., Bowman, C., Garland, S., Fujii, C., Cotton, M.D., Horst, K., Roberts, K., Hatch, B., Smith, H.O. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser.C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A., Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B., Tomb,J.-F., Fleischmann,R.D., Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van-Vugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L., Artiach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Horst, Artiach,P., Hatch,B., Smith,H.O. and Venter,J.C.
                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (12-DEC-1997) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borrelia burgdorfer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98065943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390 (6660), 580-586 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            burgdorf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic sequence of a Lyme disease spirochaete,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eubacteria; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lyme disease spirochete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE001180.1
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Similarity 40.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                       /note="hypothetical protein; identified by Glimmer;
putative"
                                                                                                                                  /gene-
/codon_start=1
/transl_table=11
/product="B. burgdorferi predicted coding region BB0813"
/protein_id="AAC67176.1"
                                                                                                                                                                                                                    /organism≃"Borrelia burgdorferi"
/db_xref≈"taxon:139"
                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                /gene="BB0813"
                                                                                                                                                                                                                                                                       1. .15079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:2688755
                                                                                                                                       "BB0813"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 320; DB 17;
Pred. No. 1.00e-14;
36; Mismatches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCT 15-DEC-1997 of 70) of the complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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/db_xref="g1:2688762"
/translation="meldkylflevlandngkrldsilikilneskasiikhirkgdirtranslation="meldkylflevlandngkrldsilikilneskasiikhirkgdirtranslikelschikelschikelschikelschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschileschi
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PID:1045895 percent identity: 31.20; sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MLLNKYFLANRNINFIVMALLESSSYISASSFISGPSAVYKYGL
SFILLATIQIPTTLIVFIIVGGRLNRESKKINAINIIDYIRHRYESDFLALMSGFVLI
FFSMFLISAQLIGGAKLIEVFWGIDYVVGLTFFAFLVFIYVFFGGFKAVAYTDLIQGF
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HCREMLEVUAKEEFWKILIIGTSLKMLDKIISKLLPNVFKIIVITDVSTROEIEKAR
ISROMGEHYVPAAAFEITSIAPNLLLNSIKVFEKSGWFFARKKNYIRSVYRPHFYEG
VLSISKRAVROIIEHCVSEYDRNYIVYDLKIKKDGNNYLFKLFILNIPLGNNLLNNTEM
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/db_xref="GI:2688771"
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                                                                                                                                                                                                          /note="similar to GB:L42023 SP:P45066 PID:1006469
PID:1221261 PID:1205384 percent identity: 28.70;
identified by sequence similarity; putative"
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/product="B. burgdorferi predicted
/protein_id="AAC67175.1"
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/protein_id="AAC67167.1"
/db_xref="pip:92688782"
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RIIMISNIFFILIILIFSLEPPNFLFFINIFAFGALEVSFFPIIVFGLYLNFVSKIAA
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322. .1656
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outative"
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'product="UDP-N-acetylmuramate--alanine ligase (murC)"
                                                                   transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="BB0817"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MMSMNFQNFSSDFFLKKILSKVKDFAISIKHKFVRVKVYALVGS"
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'db_xref="GI:2688770"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="BB0815"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="BB0814"
                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="BB0817"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTYIITNVLKYTIINILSIDIVIHKFYDKKDYLEESYEG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; identified by
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by
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'protein\_id="AAC67166.1"

gene

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/product="2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA)"
/protein_id="AAC67163.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="BB0819"
5798. .6340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="BB0820"
6376. .6576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:2688759"
/translation="mKIALSGKSGCGNTTVSGMIAKHYGLEFINYTFHDIAREHNIPF
SEFYEKEIIGRNDYYMDKYLDNRLSVLSRKNNTVLASRLAIWISKSADLKIYLYAKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLDIRNLISKYISRGNVFLNVGYKELVPSVNFTINPNYIEAISRLRDSLAHTNLNIKN
ELSLGDFLSLKGALIIDEDSEHQEEIYGLFKGVLEEALLHYNNGRSFEGENTKSDIVS
TLVLIERDLKIVKDACSDINVKLFASIKENISKLMDEFRDLNIAEEAAKMAIRLDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:L10328 PID:42721 percent identity:
                                                                                                   /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/product="B. burgdorferi
/protein_id="AAC67174.1"
/db_xref="PID:g2688769"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRAERIMTREGGMYSDVLSSTFIRDENDKKRYLAIYNIDIDDYFSETDLVIDVTNINP
NEVFELIRDEIDKRNLKKNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to identity: 38.76; i putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4935
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AADILILHNIYLSNRENFNPDELSVKLFLNIKKINKNTYFFKDVKDSINFIKSLLISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPEALGELSRKYYSIGIAGSHGKTTTTAFLGVLFNKLGLNPNVIVGSSVKDFKDNSAI
AGISNIFIVETCEYKKHFLNFSPNMLILTNVDYEHVDFFKNYEALEEAFLQYINNLKK
                                                                                                                                                      /note="similar to GP:216567 percent identity:
identified by sequence similarity; putative"
                                                                                                                                                                                                           /gene="BB0821"
                                                                                                                                                                                                                                                                                                                 KILGQAFNDVLTGKFRYSIEGR"
                                                                                                                                                                                                                                                                                                                                       translation="MTKVPLKKIQDFDGNFYELVVATIMRTEQIIDNISLAEHAIFDD/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="BB0820"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="cytidylate kinase (cmk-2)"
/protein_id="AAC67164.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="BB0819"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIMRLDSHIETFYKNLEYEICGKALEFISQEMHREITTMSNKAVDLDIKNLILNMKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity;
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YTDEILSNNKISYYDNIYEFSLKQLDRSFDLIVYSSAYNKDGLQVLLEAKELNIPILS
                                                                                                                                                                                                                                                      'gene="BB0821"
                                                                                                                                                                                                                                                                                                                                                                    'db_xref="GI:2688769"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'codon_start=1
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/db_xref="PID:g2688760"
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/db_xref="GI:2688761"
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65.1"
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29.96; identified by sequence
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by sequence similarity;
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Best Local
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                                                                                                                                           4722 TATATCTTTCAAATAGGGAAAAT 4744
                                                                                                                                                                                                                                                                                                            4602 TTTATAAGAATAAACGTATAATTTTGGATTTTATGCCTCATACCTTTACAAGAACAAAAG 4661
                                                                                                                                                                                                                                                                                                                                                                                        4542 TGGACGATTATGCTCATCCTAGGGAAATTAAAAATACTCTTTTTGGTATTAAAAATT 4601
                                                                                                                                                                                                                            4662 AATTTTTTGCCGATTTTGTTGAAGTTCTAAGTGCTGCCGATATATTTAATTTTTGCACAATA 4721
                                                                                                         443
                                                                                                                                                                                        383 CNTTYYTNAAYGARTTYGCNGARWSNYTNWSNAARGCNGAYMGNGTNTTYYTNTGYGARA 442
                                                                                                                                                                                                                                                                    323 ARTAYCCNCAYAARGARGINGINGCNGINTIYCARCCNCAYACNIIYWSNMGNACNCARG
                                                                                                                                                                                                                                                                                                                                                  263 TNGAYGAYTAYGCNCAYCCNMGNGARATHWSNGCNACNATHGAYACNGCNMGNAARA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 76; Conser
                                                                                                       THTTYGGNWSNATHMGNGARAAY 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotations omitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKRSLEVYYQTGIPISQFQKKQSSEFKNIVIIGLKRSFEDLKTRISIRINEMLNSGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:2688758"
                         15862 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 318; DB 18;
Pred. No. 1.58e-14;
44; Mismatches 83
DNA
AND
      of 109
      of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15079;
      complete
    genome
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MEDLINE
REFERENCE
AUTHORS
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SOURCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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                                                                                                                                                                                                                                   gene
                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 15862)
Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L., Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M., Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L. Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M., Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V. The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aquifex aeolicus section
AEO00736 AEO00657
g2983763
                                                                                                                                                                                                                                                                                                                                     Hypothetical indicates similarity 
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Putative indicates no similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-JUL-1997) Diversa Corporation,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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/codon_start=1
/transl_table=11
/product="putative protein"
/protein_id="AACO7332.1"
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/db_xref="GI:2983773"
/db_xref="GI:2983773"
/translation="MMGLKRILRVVRAEAHSVVEKLEDPIKITEEGLRELRKOLKEA
MEALAQVKASQIRFEREARNEKERAKALVKKAESILLQAQEGKISPEEAEKLAAELIQ
                                                                                                                                                                                                                                       233.
                                                                                                                                                                        /gene="aq_1345"
                                                                                                                                                                                                              /gene-
                                                                                                                                                                                                                                       /db_xref="taxon:63363"
233. .937
                                                                                                                                                                                                                                                                              /strain="VF5
                                                                                                                                                                                                                                                                                               ∕organism="Aquifex aeolicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics,
                                                                                                                                                                                                                                                                                                                                                            unknown function
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KVNKOIAKVDPSDTIAMLERMKEKVEEEETLAOAYEELAKOEVALDVESEAEKKLKEV
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YGLSFVIGSLIGLEIPLAVRINNMYEELKVNISSVLEKDYLGSVPAGLLYAYLFLPKL
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.2756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSLEEEVKRLIVHGIVHLLGYDHEKGGEEEKKFRELENYVLSKLSKAL" complement(5649. .6479)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MEKVLAEERIDLGRYDERFYAIVGRGDENIKFFSKFFDVRIVPRGTELIIKGEEDKVREFVNFLKAVLKREHERLTAEEVKSYAKQELKFSVEXYKIEEQPGGTELIIKGEEDKVRETVNFLKAVLKREHERLTAEEVKSYAKQELKFSVEXYLAMAAA LQHLKEGKVNKIILTHRKAKAIVFKTEFTOKKYVEALKKNDIVFGIGPAGTGKYLAANAA LQHLKEGKVNKIILTRPAVEAGEKLGFLPGTIAEKVHPYLTPLYDALYDMVDYDKANY
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                                                                                                                                                                                                                                                 Origin of mutant strain
2 (bases 1 to 1998)
Eveland, S.S., Pompliano, D.L. and Anderson, M.S.
Conditionally lethal Escherichia coli murein mutants contain defects that map to regions conserved among murein and folyl poly-gamma-glutamate ligases: identification of a ligase
                                                                                          Submitted (23-AUG-1996) Enzymology, P.O. Box 2000, Rahway, NJ 07065, US:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265
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                                                                                                                                                                                                                              Biochemistry 36 (20), 6223-6229 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 1998)
Matsuzawa, H., Matsuhashi, M., Oka, A. and Sugino, Y.
Genetic and biochemical studies on cell wall peptidoglycan
synthesis in Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.7%;
Similarity 40.9%;
74; Conservet
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Escherichia coli
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   /organism="Escherichia coli"
/strain="CGSC 5988"
/db_xref="taxon:562"
435. .1910
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/product="cytochrome oxidase d subunit
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/db_xref="PID:g2983770"
/db_xref="GI:2983770"
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'gene="cydB"
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Pred. No. 2.11e-11;
33; Mismatches 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AARTAYCCNCAYAARGARGTNGTNGCNGTNTTYCARCCNCAYACNTTYWSNMGNACNCAR 381
                                                                                                      2 (bases 1 to 2793)

Ikeda, M., Wachi, M., Jung, H.K., Ishino, F. and Nucleotide sequence involving murG and murC i region of Escherichia coli
Nucleic Acids Res. 18 (13), 4014 (1990)
                                                                                                                                                                                                       Submitted (21-APR-1990) Ikeda M., Inst. Microbiology, The University of Tokyo, Tokyo, 113, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECMURGC. 2793 bp DNA BCT LY-JUL-1993 Escherichia coli murG and murC genes for an unidentified reading frame and UDP-N-acetylmuramate:L-alanine ligase (EC 6.3.2.8)
                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
Escherichia coli
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ligase; murC gene; mu
ligase; unidentified
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Similarity 42.4%;
72; Conservative
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                                                         Location/Qualifiers
1.2793
/organism="Escherichia coli"
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/map="2mins"
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/protein_id="AAB60787.1"
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DFANVLTQVDTLLMLEVYPAGEAPIPGADSRSLCRTIRGRGKIDPILVPDPARVAEML
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497 c
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435. .1910
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28; M
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No. 4.11e-11;
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Gaps

the mra gene cluster

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620
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GRYSGFGGLAAWSLGIPVVLHEQNGIAGLTNKWLAKIATKVNQAFPGAFPNAEVGN
PVRTDVLALPLPQQRLAGREGPVRVLVVGGSQGARILNQTMPQVAAKLGDSVTIWHQS
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/db_xref="GI:42057"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HILPFYGRAYMCVDDPYIRELLPRVGRQTTTYGFSEDADVRVEDYQQIGPQGHFTLLR
QDKEPMRVTLNAPGRHALINAAAAVAVATEEGIDDEAIIRALESFQGTGRREDFIGEF
PLEFYNGKSGTAMLVUDYGHHPTEVDATIKAARAGWPDKNLYMLFQPHHEFRTRDLYD
DFANVLTQVDTLLMLEVYPAGEAPIPGADSRSLCRTIRGRGKIDPILVPDPARVAEML
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QISGSDLapnpytqqlmnlgatiyfnhrpemyrdayvyssalsadnpetynahebar
IPVIBRAEMLAELMRERHGIALAGTHGKTTTTAMVSSIYAEAGLDPTFYNGGLVKAG
VHARLGHGRYLIAEADESDASFLHLQPMVAIVTNIEADHMDTYQGDFENLKQTFINFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA36868.1"
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/protein_id="CAA36867.1"
/db_xref="PID:942055"
                                                                                                                                                                                                       translation="MTDKIAVLLGGTSAEREVSLNSGAAVLAGLREGGIDAYPVD" 676 c 858 g 639 t/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APVLTGNDL1LVQGAGNIGKIARSLAEIKLKPQTPEEEQHD'
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1203. .2678
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/transl_table=11
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/product="(UDP-N-acetylmuramate: L-alanine ligase)
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plukett,G. III.

Direct Submission

Submitted (13-0CT-1998) Laboratory of Genetics, University of Submitted (13-0CT-1998) Laboratory of Genetics, UNA Submitted (13-0CT-1998) Laboratory of Genome Project at the Wisconsin, 445 Henry Mall, Madison, WI 53706, USA This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGN). The entire sequence was independently determined from E. coli K-12 strain MG1655. Predicted open reading determined from E. coli K-12 strain MG1655. Predicted open reading
                                                                                                                                                                                                                                      frames were determined using GeneMark software, kindly supplied by Mark Borodowsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amber_gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli
                            Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli K-12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1 The unique numeric identifiers
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Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoll@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Demail: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The complete genome sequence of Escherichia coli K-12 Science 277 (5331), 1453-1474 (1997) 97426617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="leu0"
646. .1767
/gene="leu0"
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460. .474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="central position to predicted promoter: -0.5"
/bound_moiety="LexA predicted site"
complement(201. .221)
/note="No predicted promoter"
/bound_moiety="LexA predicted site"
complement(354. .368)
                                                                 /db_xref="GI:1786264"
/translation="MTHSTAMDSVFIRTRIFMFSEFYSFCFFLFYMHDKSYSSGLFLC
/translation="MTHSTAMDSVFIRTRIFMFSEFYSFCFFLFYMHDKSYSSGLFLC
IPIRERELSYTVELSMPEVQTDHPETABELSKPQLFMYDLNLLTVFDAVMQEQNITRAA
HVLGMSQPAVSNAVARLKVMFNDELFYRYGRGJQPTARAFQLFGSVRQALQLVQNELP
                                                                                                                                                                                                                                                                                                                                      P10151(290 aa) but contains 59 additional N-ter aa and C-term residues; 100 pct identical to PIR: S40589 but contains 24 additional C-term residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="central position to leuABCD promoter:
/bound_moiety="Lrp documented site"
complement(354. .368)
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/db_xref="GI:1786263"
/translation="MTHIVRFIGLLLLNASSLRGRRVSGIQH"
complement(197. .226)
rfasfsqpwydtydkqasiayqgmammsylsvysqthlvaiaprwlaeefaeslelqv
                                              GSGFEPASSERVFHLCVCSPLDSILTSQIYNHIEQIAPNIHVMFKSSLNQNTEHQLRY
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                                                                                                                                                                                                                                                               /product="probable transcriptional activator for leuABCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leucine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="central position to predicted promoter: -319.5"
/bound_moiety="TyrR predicted site"
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/bound_moiety="Lrp predicted site"
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/protein_id="AAC73186.1"
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complement(77. .163)
/note="b0075"
                                                                                                                                                                                /protein_id="AAC73187.1"
/db_xref="PID:g1786264"
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                                                                                                                                                                                                                                                                                                                   codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="central position to predicted promoter:64"
/pound_mojety="AraC predicted site"
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/note="f28; 100 pct identical to LPL_ECOLI SW: P0914
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                                                                                                                                                                                                                                                                                                                                                                                                                     note="0373; 100 pct identical
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Note: remainder Query Match Best Local : Matches

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annotations omitted

h 10.6%; Similarity 42.4%; 72; Conservative

Score 283; DB 18; Pred. No. 4.11e-11; 28; Mismatches 70;

Length 21757; Indels

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/translation="MFWSLAANCHSKIGRLMCFTHFFROTVRQAMEMLSGAEMVVRSL
IDGGVKQVFGYPGGAVLDIYDALHTVGGIDHVLVRHEQAAVHMADGLARATGEVGVVL
'VTSGPGATNAITGIATAYMDS.TPLVVLSGQVATSLIGYDAFQECDMVGISRPVVKHSF
LVKQTEDIPQVLKKAFWLAASGRPGPVVVDLPKDILNPANKLPYVWPESVSMRSY.NPT
/note="b0078"
/gene="ilvH"
3812. .4303
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GMVKQWQDMIYSGRHSQSYMQSLPDFVRLAEAYGHVGIQISHPHELESKLSEALEQVR
NNRLVFVDVTVDGSEHVYPMQIRGGGMDEMWLSKTERT"
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FPATHRQALGMLGMHGTYEANWTMHNADVIFAVGVRFDDRTTNNLAKYCPNATVLHID
IDPTSISKTVTADIPIVGDARQVLEQMLELLSQESAHQPLDEIRDWWQQIEQWRARQC
                                                                                                                                                     ,...e-central position to predicted promoter:156.5"
/bound_moiety="Lrp predicted site"
2017. 2045
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1838. 1866
Inote-"factor Sigma70; promoter 11vTHp3;
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'note="central position to predicted promoter: -39.5"
'bound_molety="Lrp predicted site"
1813. 1839
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"mote="central position to predicted promoter:136.5"

"bound_moiety="Lrp predicted site"
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/db_xref="PID:g1786265"
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Nucleic Acids Res. 11 (15), 5299-5313 (1983) 83272971 8 (bases 4274 to 6093) Leclerc,G., Noel,G. and Drapeau,G.R. Molecular cloning, nucleotide sequence, and expression of shl, a new gene in the 2-minute region of the genetic map of Escherichia coli J. Bacteriol. 172 (8), 4696-4700 (1990) 90330385 9 (bases 6088 to 7587)	Proc. Natl. Acad. Sci. U.S.A. 85 (18), 6602-6606 (1988) 88320486 6 (bases 1799 to 2187) Haughn, G.W., Squires, C.H., DeFelice, M., Largo, C.T. and Calvo, J.M. Unusual organization of the ilvIH promoter of Escherichia coli J. Bacteriol. 163 (1), 186-198 (1985) 85234358 7 (bases 2101 to 4431) Squires, C.H., DeFelice, M., Devereux, J. and Calvo, J.M. Molecular structure of ilvIH and its evolutionary relationship to	4 (bases 268 to 1130) 5 (bases 843 to 1812) 6 (bases 843 to 1812) Henikoff,S., Haughn,G.W., Calvo,J.M. and Wallace,J.C.	to 306) to and Ca leu oper lon atten ol. 149 (	Molecular, Centro de Biología Molecular, Universidad Autonoma, Canto-Blanco 28049, Madrid, Spain 2 (bases 1 to 28277) Ayala,J.A. Regulation of transcription at the 2-minute region of the genetic map of Escherichia coli	ubdivision; Ente		
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19 (bases 19464 to 21952)  Robinson,A.C., Kenan,D.J., Hatfull,G.F., Sullivan,N.F.,  Spiegelberg,R. and Donachie,W.D.  DNA sequence and transcriptional organization of essential cell division genes ftsQ and ftsA of Escherichia coli: evidence for  overlapping transcriptional units J. Bacteriol. 160 (2), 546-555 (1984) 8554557 20 (bases 21464 to 23333) Yi.O.M. and Lutkenhaus,J.  The nucleotide sequence of the essential cell-division gene ftsZ of		16 (bases 14743 to 16239)  Ikeda,M., Sato,T., Wachi,M., Jung,H.K., Ishino,F., Kobayashi,Y. and Matsuhashi,M.  Structural similarity among Escherichia coli FtsW and RodA proteins and Bacillus subtilis SpovE protein, which function in cell division, cell elongation, and spore formation, respectively J. Bacteriol. 171 (11), 6375-6378 (1989)  17 (bases 16094 to 17806)	(bases ngin-Leccleotide P-MurNAccleic Accleic Acceleic A	14 (bases 12423 to 15030) 14 (bases 12423 to 15030) Ikeda,M., Wachi,M., Ishino,F. and Matsuhashi,M. Nucleotide sequence involving murD and an open reading frame ORF-Y spacing murF and ftsW in Escherichia coli Nucleic Acids Res. 18 (4), 1058 (1990) on10700a	90328986 13 (bases 11142 to 12634) Parquet,C., Flouret,B., Mengin-Lecreulx,D. and van Heijenoort,J. Nucleotide sequence of the murf gene encoding the UDP-MurNAc-pentapeptide synthetase of Escherichia coli Nucleot. Acids Res. 17 (13), 5379 (1989)		Gomez,M.J., Fluoret,B., van Heijenoort,J. and Ayala,J.A. Nucleotide sequence of the regulatory region of the gene pbpB of Escherichia coli Nucleic Acids Res. 18 (9), 2813 (1990) 90251464 10 (bases 7316 to 10074) Nakamura,M., Maruyama,I.N., Soma,M., Kato,J., Suzuki,H. and Horota,Y. On the process of cellular division in Escherichia coli: nucleotide sequence of the gene for penicillin-binding protein 3 Mol. Gen. Genet. 191 (1), 1-9 (1983) 83296957

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Schmidt,M.G., Rollo,E.E., Grodberg,J. and Oliver,D.
Nucleotide sequence of the secA gene and secA(Ts) m
preventing protein export in Escherichia coli
J. Bacteriol. 170 (8), 3404-3414 (1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 (bases 1 to 28277)
Wang,O. and Calvo,J.M.
LTP, a global regulatory protein of Escherichia coli, binds
co-operatively to multiple sites and activates transcription
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Robinson,A.C., Begg,K.J., Sweeney,J., Condie,A. and Donachie,W.D.
Mapping and characterization of mutants of the Escherichia coli
cell division gene, ftsA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular cloning and nucleotide sequence of the mut
Escherichia coli that causes A:T to C:G transversion
Mol. Gen. Genet. 206 (1), 9-16 (1987)
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Gene 36 (3), 241-247 (1985)
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Wang,Q. and Calvo,J.M
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yama,M., Horiuchi,T. and Sekiguchi,M.
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The gene for Escherichia coli diadenosine tetra;
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mol. Gen. Genet. 205 (3), 515-522 (1986)
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Nucleotide sequence of the Escherichia
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J. Biol. Chem. 261 (4), 1778-1781 (1980
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Note: remainder Ŏ Ħ annotations omitted

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                                                                                                                                                                                                                                                                                                                                                                        Submitted (03-NOV-1998) Molecular and Human Genetics, Baylor College, of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jan 8, 1999 this sequence version replaced; 14062895.

* NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the pieces is not known and their order in this sequence record is
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Muzny,D., Arenson,A.D., Brundage,E., Carvelli,K., Chen,E., Di,W.,
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Direct Submission
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152081: gap of unknown length
159908: contig of 4827 bp in len
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1599104: gap of unknown length
159861: contig of 2910 bp in len
159904: gap of unknown length
161904: contig of 2000 bp in len
161947: gap of unknown length
163449: contig of 1502 bp in len
163492: gap of unknown length
164741: contig of 1249 bp in len
164784: gap of unknown length
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-NOV-1998) S.G.E. Andersson,
Siv.Andersson@molbio.uu.se, Dept. of Molecular Biology, University
of Uppsala, Husargatan 3, Uppsala, S-751 24, SWEDEN
On NOV 13, 1998 this sequence version replaced gi:3860788.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andersson, S.G., Zomorodipour, A., Andersson, J.O., Sicheritz-Ponten, T., Alsmark, U.C., Podowski, R.M., Naslund, A.K. Eriksson, A.S., Winkler, H.H. and Kurland, C.G.

The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsiaae; Rickettsia.

1 (bases 1 to 312430)
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Andersson, S.G.E.
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DFGSTILPSVASNYIDSKAEYENSTNLAASYNTQDIQVKQQEFDPSEASEPIDIGNTK
FTSATNHEMYKEAVSSNDKETNLTSNIITPNVPSPVISIPTAQDVNYVVPSQQSVQIY
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51340 c 52814
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gene

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SKYYTPSGRSIQAEGIEPDILLEPAKVEYPEVKKIDKRESESILKNYLKDNAKNKDS
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GSAKQARNRETQAVLPLWGKVLNVASSTLEKIINNQAIQDLEIALACGSLKNYKKENL
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KGNKFITSNMLHWYSVDNYKDDSLIELVITKIDKIFLKSFTSAAPLRDAFKGITSHIL
LPKVVIENESDLTIEHASFVTSYIPVIDHNLDFPVDAVFEINFNNITSQUKNITSLEGK
VFITFIIIFIIFCTIIISNTNYARQIIEEQLETNRNLKAQIEKVEKTSSSNTKFFANI
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1374 8126
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'transl_table=11
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CDS gene

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IALNDHTILVQTISNQTIALDSETLKTLWDHESIAEILSTSYSMIPIVQHDNVIVTYN
TGQVLALNIKNGEVKWBFETMLMDHTAIFWFDTSSILCTPVHDSMNLYIATGLGKLI
KLNLLTGSVLMQINADDIGSMSLIGNSEFINNANQIAALNPETGKVKFVADLNYEKN
DKRLKSTTFLVPFVGVDNNNQRSLNVISVDGILXNENIDSNGLKNNPHIIKIIKNIRY
YGLRSNNTLYSTDRQVIFGSQI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="RP233"
10279.
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8123. 870=
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VSKKTFEVNKDIAPYKQAYDLALAAYKDNKLTEAKDKFKNFIQKYPNNSLISNAYFWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MKTYSAKPSEIEKKWWYIDAKNYVLGRLASRVAIMLRGKHKPSF
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KKDRRIKNNQKNGDILVKTIGLDTKONKALAFNTLEBLITSSWKIKELAALEQVAI
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11279. .11352
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/db_xref="PID:e1342541"
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/gene="RP232"
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                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="RP234"
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10753. .11238
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/gene="RP231"
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Search completed: Sat Nov 27 09:58:37 1999 Job time: 1214 secs.

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472
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                                                                                                                                                                                                                                                             GCNACNATHGAYACNGCNMGNAARA-ARTA--YCCNCAYAA-RG--ARGINGINGCNGIN 351
GCNYTNACNATHCARGAYYTNATHGAYAARAT 503
                                GGAATTACAGGACAAAGTTTAGTTGATAAGAT 22329
                                                                 WSNAARGCNGAYMGNGTNTTYYTNTGYGARATHTTYGGNWSNATHMGNGARAAYACNGGN 471
                                                                                                GCGGATGCAGATATACTCTATATTACCAATATATGCTGCAGGTGAAACCCCCTATAGAA 22297
                                                                                                                                  TTYCARCCNCAYACNTTYWSNMGNACNCARGCNTTYYTNAAYGARTTYGCNGARWSNYTN 411
                                                                                                                                                 GCAACGCTTGCAACTGCTAAAAATATAGCAAATCAACAAAACGGTAAAGTTATAGCGATT 22177
                                                                                                                                                                                                                                                                                                                               ACNAAYATHAARGARGCNYTNGARACNTTYGGNGGNGTNAARMGNMGNTTYAAYGARACN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 10.5%;
Similarity 38.3%;
150; Conservative
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/gene="tRNA Met (CAT)"
complement(12284. .127)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 279; DB 17;
Pred. No. 9.94e-11;
70; Mismatches 163
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed Nov 24 00:53:13 1999; MasPar time 0.42 Seconds 196.757 Million cell updates/sec

Description:
Perfect Score:
Sequence:

>US-09-103-287-4
(1-215) from US09103287.pep
1495
1 FKDSDDIYAQIFQITDKGTA.....GDIQKLQNAYLDKLGMKNAF 215

Scoring table: PAM 150 Gap 11

Searched: 1479 segs, 387401 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: HIV-AA8 1:ALL

Statistics: Mean 42.724; Variance 87.119; scale 0.490

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

					-
· 22 23	16 17 18 19	12 13 14	110	1004001	Result No.
67 67	68 68 68	5 5 5 5 5 5 6 6 6 6	70 70 70	78 73 73 70 71	Score
444	4444 0.0.0.0.0	4444 0000	4.7	. 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	% Query Match
489 489 5	103 486 487 489	486 488 1045 91	489 492 1033	485 485 2248 2542 2642	Length
بر بر بر	4444	<b></b>	· 		## B
GAGSTN240 GAGSTN238 GAGSTN2431	GAG\$F10S1 GAG\$LBV231 GAG\$VI174 GAG\$K112 GAG\$K88	GAG\$DJ258 GAG\$VI310 POL\$VLVCG GAG\$M2S1	GAGSCI59 GAGSTN245 GAGSK124 POL\$MVP518	GAG\$VI57 GAG\$VI415 GAG\$VI415 GAG\$LBV23 ENVELOPE\$A GAG\$IC144 GAG\$VI354	ID
$\omega \omega \circ$	HIVF10S1, GAG HIVLENZ310, GAG POLYP HIVVI174, GAG POLYPROT HIVK112, GAG POLYPROTE HIVK88, GAG POLYPROTE	HIVDJ258, GAG POLYPRO HIVVI310, GAG POLYPRO VLVCG, POL POLYPROTEI HIVM2S1, GAG	HIVCIS9, GAG POLYPROT HIVTN245, GAG POLYPROT HIVK124, GAG POLYPROT HIVMVP5180, POL POLYP	GAG GAG GAC , GAC ENVEL	Description
1.60e+01 1.60e+01 1.60e+01	1.30e+01 1.60e+01 1.30e+01 1.30e+01 1.30e+01	1.05e+01 1.05e+01 1.05e+01 1.30e+01	8.39e+00 6.72e+00 8.39e+00 8.39e+00	1.29e+00 4.26e+00 4.26e+00 4.26e+00 5.36e+00 8.39e+00 6.72e+00	Pred. No.

	AC L1791 DT 20-APR-1993 DE HIVVI415, GAG POLYPROTEIN	TUS	Qy 45 NALAVIAISYLEKLDYTNIKEALETEGGYKRENETT 81	Query Match 4.9%; Score 73; DB Best Local Similarity 27.0%; Pred. No. 4.26 Matches 10; Conservative 15; Mismatche	TRANSI	DT 20.ADR-1993 DT 20.ADR-1993 DE HIVVI32, GAG POLYPROTEIN FT PEPT 1 >385 GAG POLYPROTEIN (PREMATURE TERMINATION) CC -!-5':Y 3':N	SUL	Db 75 lkslfntvavlycvhgrievkdtkdaldkieeigkkskgkt 115  ::  : : :  :  : :: :  :  :  :  :  :  :	Query Match 5.2%; Score 78; DB 1; Length 489; Best Local Similarity 22.0%; Pred. No. 1.29e+00; Matches 9; Conservative 18; Mismatches 11; Indels 3; Gaps 3;	DT 20-APR-1993  DE HIVVI57, GAG POLYPROTEIN  FT PEPT 1 >489  CC -i-5: Y 3':N  CC TRANSLATED USING PHASE 1  SQ SEQUENCE 489 AA; 54331 MW;	TOS
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RESULT
ID EN
AC M6
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Best Local
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L11767
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M60472
16-FEB-1989
 GAG$VI354
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L11777
20-APR-1993
HIVLBV23, GAG POLYPROTEIN
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TRANSLATED USING PHASE 1
SEQUENCE 242 AA; 26857 MW;
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HIVIC144, GAG
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                                                                                                                                                                                                                                                             102 IDTARKKY 109
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                                                                                       y Match 4.7%;
Local Similarity 19.0%;
hes 11; Conservative
                                         44 LNALAVIAISYLEKLDVTNIKEALETF-GGVKR-RFNETTIANQVIVDDYAHHPREISAT 101
                                                                                                                                                                                                                                                                                                                                             / Match 4.8%;
Local Similarity 30.9%;
les 21; Conservative
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Local Similarity 30.88;
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Similarity 27.8%;
10; Conservative
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AA; 54634
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 PRELIMINARY;
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MW;
                                                                                      Score 70; DB 1; Leg
Pred. No. 8.39e+00;
18; Mismatches 27;
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Pred. No. 4.26e+00;
14; Mismatches 9
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Pred. No. 4.26e+00;
10; Mismatches 8
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 PRT;
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Best Local S
Matches 1
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GAG$K124 PRELIMINAL
L11769
20-APR-1993
20-MPR-1993
1 >492
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Best Local :
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20-APR-1993
20-APR-1993
HIVC159, GAG POLYPROTEIN
1 >304
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                                                                     SEQUENCE
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TRANSLATED USING PHASE
SEQUENCE 489 AA; 54658
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L11762
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-1-5':Y 3':N 1 >264
TRANSLATED USING PHASE 1
SEQUENCE 264 AA; 29206 1
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20-APR-1993
HIVVI354, GAG POLYPROTEIN
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48 AVIAISYL-EKLDVTNIKEALETFGGVKRRFNETT 81
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Local Similarity 27.5%;
les 11; Conservative
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Local Similarity 22.0%;
les 11; Conservative
                      Match 4.7%;
Local Similarity 24.4%;
es 10; Conservative
                                                                 TRANSLATED USING PHASE QUENCE 492 AA; 54739
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Similarity 22.9%;
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Pred. No. 8.39e+00;
15; Mismatches 13
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Pred. No. 6.72e+00;
14; Mismatches 12
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GAG$DJ258
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M10608; M18039;
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VLVCG, POL POLYPROTEIN PRECURSOR
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SEQUENCE 1033 AA; 116942 MW;
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SEQUENCE 1045 AA; 119999 MW;
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71771310, GAG POLYPROTEIN
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Local Similarity 27.8%; Pred. No. 1.05e+01;
nes 10; Conservative 12; Mismatches 11; Indels
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56 EKLDVTNIKEALETFGGVKRRFNETT 81
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Local Similarity 26.9%; Pred. No. 1.05e-
hes 7; Conservative 11; Mismatches
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Pred. No. 8.39e+00; 
19; Mismatches 23; Indels
                        Score 69; DB 1; Length 1045, 
Pred. No. 1.05e+01; 
19; Mismatches 22; Indels
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L21492
09-SEP-1993
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SEQUENCE 91 AA; 10138 MW;
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44 LNAL-AVIAISY-L-EKLDYTNIKEALETF 70
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_tpn n.a. - n.a. Smith-Waterman search, using a protein query
which has been backtranslated into n.a. using IUPAC symbols

Run on: Sat Nov 27 10:18:25 1999; MasPar time 5.07 Seconds 378.625 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
N.A. Sequence: Title: >US-09-103-287-4 (1-215) from US09103287.pep 2663

Comp: 1 TTYAARGAYWSNGAYGAYAT......TNGGNATGAARAAYGCNTTY 645
AARTTYCTRWSNCTRCTRTA.....ANCCNTACTTYTTRCGNAAR

Scoring table: TABLE bktranslate2 Gap 30

Nmatch

STD:

Dbase 0; Query 0

Searched: 1052 seqs, 1486975 bases  $\times$  2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:H\_PRI 2:H\_UNA 3:H\_VIR

Statistics: Mean 71.740; Variance 150.863; scale 0.476

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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141 131 131 131 131 126 126 126 127 121 121 121 121 121 121 121 121 121	Score
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1480 303 309 1474 1459 1459 1459 1459 1492 1492 9706 9711 1459 9737 1459 1459 1459	Length
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HIVB2167 HIVP10S1 HIVP110S1 HIVPH136 HIVCAM1 HIVCAM1 HIVVI415 HIVVI415 HIVVI415 HIVVI57 HIVPH153 HIVVB1321 HIVVB02581 HIVSF2 HIVVJ2581 HIVVJ2581 HIVVJ3581 HIVVJ3581	ID
Human	Descr
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7.18e-03 7.83e-02 7.83e-02 7.83e-02 7.83e-02 2.42e-01 2.42e-01 5.15e-01 7.16e-01 7.1	Pred. No.

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BASE COUNT	source	FEATURES CDS	JOURNAL STANDARD COMMENT	TITLE	ORGANISM REFERENCE	LOCUS DEFINITION ACCESSION SOURCE	RESULT 1
/organism="Human immunodeficiency virus type 1" /isolate="BZ167" /cell_type="lymphocyte" /proviral /sequenced_mol="DNA" /tissue_type="blood" 281 c 369 g 286 t	/product="gag protein" /gene="gag" /gene="gag" /codon_start=1 /codon_start=1 /translation="MGARASYLSGGELDRWEKIRLRPGGKKKYRLKHYVWASRELERF /translation="MGARASYLSGGELDRWEKIRLRPGGKKKYRLKHYVWASRELERF AVNPGLLETAAGCRQILGQLQPSLQTGSEELRSLYNTVATLYCVHQKIDVRDTKEALE KVEERONKSKEKAQAQAAAADAGTSSQYSQNYDIVQNQQMVHQAISPRTLNAWVKVI EEKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKDTINEEAAEWDRLHP VHAGFIAPGOMREPRGSDIAGTTSTLOEQIGMRTNINPPIPVGKIYKRWIILGLUKIVR MYSPISIJDIRGGFKEEPFRDYVGNFRYKTLAEAGASQDVKNMATETLLVQNANDCKTI LKALGPAATLEEMMTACQGVGGPGHKARVLAEAMSQVPNSSATIMMQKGNFRNQRKIV KCFNGGKEGHIAKNCRAPRKKGCWKCGKEGHGMKDCSERQANFLGKIWPSYKGRPGNF LQRREEPTAPPEEIFRFGEETTTPSQKQETKDKELYPLASLKSX" 11480	Research Laboratory, 1500 East Gude Drive, ROCKVIIIe, MD 20850.  The BZ167 gag sequence clusters with HIV-1 B subtype gag sequences.  Location/Qualifiers 11480	TT TT	Sanders-Buell, E., Eddy, G., van der Groen, G., Fransen, K., Gershy-Damet, M., Deleys, R. and Burke, D.  Phylogenetic analysis of gag genes from seventy international HIV-1	Human immunodeficiency virus type 1 Human immunodeficiency virus type 1 Viridae; ss-RNA enveloped viruses; Positive strand RNA virus; Retroviridae; Lentivirinae. 1 (bases 1 to 1480) 1 (bases 1 T. McCutchan F. Brennan T. Deeters M. Brennan T.	HIVBZ167. 1480 bp ss-RNA VRL 20-APR-1993 Human immunodeficiency virus type 1, Brazilian isolate BZ167, gag region. L11752 Human immunodeficiency virus type 1 (HIV-1), Brazilian isolate RZ167 (Contitivation on PBMCs)	

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This sample has been taken from patient M, one of the seven

This sample has been taken from patient M, one of the seven

patients (A, M, L, F,C,V,R), in the study(1). All patients had acute,

patients (A, M, L, F,C,V,R), in the study(1). All patients had acute,

patients (A, M, L, F,C,V,R), in the study librarial patients of the virus to patient Viremia followed

by seroconversion. Patient M was a chronically infected male who

subsequently transmitted the virus to patient F. The authors

report that the sequences in this study are found to be uniformly

macrophage-tropic and non-syncytium-inducing. The sequence for

sample M clone 2, along with other patient M clones 1, 3-9, 11, and

12, is shown in alignment following the printed text entry. These

gag sequences cluster with HIV-1 B subtype sequences. See also L212

L21591 and L24161, L24462.
                                         gag cds, p17 region.
L21375
                                                                                Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhu.T., Mo.H., Wang.N., Nam.D.S., Cao.Y., Genotypic and phenotypic characterization with primary infection Science 261, 1179-1181 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1 (HIV-1), clone 2, ADC sam Human immunodeficiency virus type 1 Viridae; ss-RNA enveloped viruses; Positive strand RNA virus; Retroviridae; Lentivirinae.
Human immunodeficiency virus type 1 (HIV-1), clone 10, ADC sample F
                                                                                                     HIVF10S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIVM2S1 303 bp ss-RNA VRL Human immunodeficiency virus type 1, clone gag cds, p17 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 5.3%;
Similarity 43.1%;
31; Conservative
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                                                                            0S1 309 bp ss-RNA immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     downstream from beginning of gag cds
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Human immunodeficiency virus type
/sequenced_mol="RNA"
61 c 62 g 55 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="myristylated gag protein
/gene="gag"
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                                                                                                                                                                                                                                                                                                                                                               Score 131; DB 3; Pred. No. 7.83e-02;
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Pred. No. 7.18e-03;
14; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                              type
                                                                              1,
                                                                                clone
                                                                                                                                                                                                                                                                                                                                                                                Length 303;
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                                                                                10,
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                                                                              sample
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AUTHORS
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full staff review

This sample has been taken from patient F, one of the seven
patients (A,M,L,F,C,VR), in the study(1). All patients had acute,
patients (A,M,L,F,C,VR), in the study(1). All patients had acute,
self-limited symptomatic illness with measurable viremia followed
by seroconversion. Patient F was infected by patient M via sexual
transmission. The authors report that the sequences in this study
are found to be uniformly macrophage-tropic and nonsyncytium-
inducing. The sequence for sample F clone 10, along with other
patient F clones 1-9, 11, and 12, is shown in alignment following the
printed text entry. These gag sequences cluster with HIV-1 B subtype
sequences. See also L12124-L21591 and L24161, L24162.
                                                                                                                                                      Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. The PH136 gag sequence clusters with HIV-1 B subtype sequences.
                                                                                                                                                                                                                                                              1 (bases 1 to 1474)
Louwagie, J. J., McCutchan, F., Brennan, T., Peeters, M., Brennan, T.,
Sanders-Buell, E., Eddy, G., van der Groen, G., Fransen, K.,
Gershy-Damet, M., Deleys, R. and Burke, D.
Phylogenetic analysis of gag genes from seventy international HIV-1
isolates provides evidence for multiple genotypes
AIDS 7, 769-780 (1993)
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Human immunodeficiency virus type 1, Philippines isolate PH136, gag
region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
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Zhu,T., Mo;H., Wang,N., Nam,D.S., Cao,Y.,
Genotypic and phenotypic characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
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Science 261, 1179-1181 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retroviridae; Lentivirinae.
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Similarity 41.78;
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/sequenced_mol="RNA"
64 c 62 g 55 t
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QNKSKKKAQQATAAADTANSSQVSQNYPIVQNIQGQMVHQPISPRTLNAWVKVVEEKA
translation="MGARASVLSGGELDRWERIRLRPGGKKKYKLKHIVWASRELERF"
                                               /product="gag protein"
/gene="gag"
                                                                                                                             Location/Qualifiers
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Pred. No. 7.83e-02;
14; Mismatches 28
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WRERQRHIRAISNWILSTHLGRPAEPVPLQLPPLERLTLDCSKDGTSGTQGVGSPQI LVESPAVLESGTKE"  LTR 2455  misc_signal 351360  misc_signal 365374  CC_signal 36539  GC_signal 390399  GC_signal 428433 LTR 456553		JOURNAL Immunodelicelency virus type 1  JOURNAL Thesis (1991) Cambridge University, U.K.  STANDARD full staff_entry  COMMENT Kindly provided in computer-readable form by Dr. Alison McIntosh, Sir William Dunn School of Pathology, University of Oxford, South Parks Rd., Oxford OX1 3RE, United Kingdom. CAM-1 sequences cluster  with B subtype sequences.  FEATURES  Location/Qualifiers	itive strand RNA vii	RESULT 5 LOCUS HIVCAM1 9591 bp ss-RNA VRL 09-JUL-1991 LOCUS HUMAN immunodeficiency virus type 1, isolate CAM1 from Cambrige, England, complete genome. ACCESSION D10112 D00917 SOURCE Human immunodeficiency virus type 1 (HIV-1), isolate CAM1 from	269 aaaagatagatgi  :  :  :  :  167 ARAARVINGAYGI 329 aaagtaagaaaa 329 aaagtaagaaaa	y Match Local Similar hes 30; Co	source 1.1474 /organisme"Human immunodeficiency virus type 1" /isolate="pHi36" /cell_type="lymphocyte" /proviral /sequenced_mol="DNA" /tissue_type="blood" BASE COUNT 551 a 278 c 365 g 280 t	AVNPGLLETSGGCRQILEQLQPALQTGSEELKSLHNTVATLYCVHQKIDVKDTKEALE KIEEEQNKSKKKAQQAAADTGNKSQVSQNYPIVQKLQGQNVHQALSPRTLNAWVKVVE EKAFSPEVIPWFSALSEGATPODLNTMLNTVGGHQAAMOMLKETINEEAAEMDRLHPV HAGPVAPGQMREPRGSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKKWIIMGLNKIVEN YSPTSILDIKOGPKEPFRBYVDRFYKTLRAEQASQEVKNWMTETLLVQNANPDCKTIL KALGPAATLEEMMTACQGVGGPSHKARTVLAEBAMSQVTNSATAMMQBGNFRNQRKIVEC FNCGKEGHIAKNCRAPRKKGCWKCGRECHQMKDCTERQANFLGKIWPSHKGRPGNFLQ SRPEPTAPPEESFRFGEETTTPSQKQEPIDKELYPLASLKSX"
	exon 58326046 /number=1 /product="tat protein" /partial exon 59716054 /number=1 /product="rev protein" /partial "partial" /partial 506	ADQLIHLYYDDCFSEARLVYTTYWGLHTGERDWHLGQGVSIEWRTKGYNTQVDPDL ADQLIHLYYDDCFSEAIRKAIVGRLVSPRCEYQAGHNKVGSLQYLALTALIAPKKIK PPLPSVRKLTEDRWNKPQKTKGHRGSHTMNGH"  CDS 55615851  /product="vpr polyprotein" /codon_start=1 /translation="MEQTPEDQGPQRQPYNEWTLELLEELKSEAVRHFPRPWLLALGQ HIYETYGDTWPGVEALIRSLQQLLFTHFRIGCRHSRIGIIQORRSRNGASRS"	PYNPOSOGVVESMINELKKIIGQVEDQAEHLKTAYQMAVFIHNFKRKGGIGGYSAGER IIDIIATDIQTKELQKQITKIQNFRVYYRDSRDPLWKGPAKLLWKGEGAVVIQDNSDI KVVPRRKAKIIRDVGKQMAGDDCVASRQDED"  50435621 Cproduct="vif polyprotein" /codon_start=1 /translation="MENRWQVMIVWQVDRMRIRTWKSLVKHHMYISGKAKKWSYRHHY	IYOYMDLYYGSDLEIGOHRYK IEELROHLLRWGLITPDKKHOKEPPTLWGYELHPD KWTYQPIMLPEKSWTYNDIOKLUGK LINASOI KAKI KVKQLCKLLRGTKALTEVVPL TEEAELELAENREILKEPVHGYYYDPSKDLLAELQKOGQGWTYQIYQEPFKNLKTGK YAKWRGTHTMDVKOLTEAVQKIATESIYINGKT PKEKLPJOKETWDAWMIDYWQATWI PEWEFWNITPPLYKLMYQLEKEPIYGAETFYYDGAANKETRLGKAGYYTDRGRQKVVPL TDTTMOKTELQAIYLAAQDSGLEVNIYDTSGYALGIIQAQPDKSESELVSQIIEELIK KEKYYLAWWPAHKGIGONEOVDKLVSAGIRKVLFLDGIDKAQEEHEKYHSMWRAMASD FNLPPVVAKEIVASCDKQLKGEAMHGQVDCSPGIWQLDCTHLEGKVILVAVHVASGY IEAEWIPASCDKQLKGEAMHGQVDCSPGIWQLDCTHLEGKVILVAVHVASGY IEAEWIPASCDKGOLKGEAMHGVDTSGTIVKAACWWAGIKQEFGII		CDS CORP."start codon missing. it starts right after TAA."  /product="pol polyprotein"		LTR 554636 /note="5'LTR R region" /note="5'LTR US region" misc_signal 638655 /note="PBS related site" RBS 744747 CDS 7922294 /product="gag polyprotein"

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FEATURES
CDS
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AUTHORS
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ORIGIN
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                                                                                                                                                                                                                           Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. This sequence contains a premature stop codon at position 913. The CI59 gag sequence clusters with HIV-1 A subtype sequences.
                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1459)
Louwagie, J.J., McCutchan, F., Brennan, T., Peeters, M., Brennan, T.,
Sanders-Buell, E., Eddy, G., van der Groen, G., Fransen, K.,
Gershy-Damet, M., Deleys, R. and Burke, D.
Phylogenetic analysis of gag genes from seventy international HIV-1 isolates provides evidence for multiple genotypes
AIDS 7, 769-780 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1 (HIV-1), Abidjan, Ivory Coast isolate CI59 (cocultivation on PBMCs).

Human immunodeficiency virus type 1

Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;

Retroviridae; Lentivirinae.
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Human immunodeficiency virus type 1, isolate CI59
IVory Coast, gag region.
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Similarity 41.78;
30; Conservati
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ALNPGLLETADGCQQLMEQLQSALRTGSEELKSLFNAIAVLWCVHQRIDIKDTKEALD
KLEEVQNKSKQKTQQAAAATGSGSQNYPIVQNAQGQMTHQPMSPRTLNAWVKVIEEKA
FSPEVIPMFTALSEGATPQDLNMMLNIVGGHQAAMQMLKDTINEEAAEWDRVHPVQAG
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GAITSSNTAATNADCAWLEAQEEEEVGFPVRPQVPLRPMTYKAALDISHFLKEKGGLE
GIIYSQRRQDILDLWIYHTQGYFPDWQNYTPGPGIRYPLTFGWCFKLVPVEPEQVEEA
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STKWANTIKOIVTKLKEOFGRKTIIINOSSGGDEEIVMHSFNOGGEFFYCNTTOLFNT
TWLFNGTWNDTEGLNNTERNITLPCRIKOIINRWQEVGKAMAPPITGTISCSSNITG
LLLTROGGGGGERETETFERFGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQRE
KRAVGAIGALFLGFLGAAGSTMGAVALTLTVQUTRQLLSGIVQOONNLLRAIEAQQHLL
OLTVNGIKQLQARVLAVERYLKDQQLLGIWGCSGKLICTTAVBASWSNSLDKIWN
NYTWMEWEREIDNYTNLIYTLLESQNQOEKNEKDLLEDTWASUMWFDITNWLWYI
KIFKMIIGGLIGLRIVFTLLSLUNRVRQGYSPLSFQTRFPVFRGPDRFEGIEEEGGGR
DRDTSGRLVTGFLALIWDDLRSLCLFSYHRLRDLLLIVARIVELLGRRGWEALKYWWN
LLQYWSQELRNSAVSLFDTIAIAVAEGTDRVIEVVQRACRAILHIPRRIRQGLERLLL
                                                                                                                                           /note="premature termination at 913"
/product="gag protein"
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                                                                                   translation="MGARASVLSGGKLDAWEKIRLRPGGKKKYRLKHLVWASRELERF/
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Pred. No. 7.83e-02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNTTYAAYGARACNAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. The LBV23-10 gag sequence clusters with HIV-1 A subtype sequences. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Louwagie, J.J., McCutchan, F., Brennan, T., Peeters, M., Brennan, T., Sanders-Buell, E., Eddy, G., van der Groen, G., Fransen, K., Gershy-Damet, M., Deleys, R. and Burke, D. Phylogenetic analysis of gag genes from seventy international HIV-1 isolates provides evidence for multiple genotypes AIDS 7, 769-780 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1
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Human immunodeficiency virus type 1, isolate LBV23-10 taken
Gabonese national residing in Libreville, gag region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Retroviridae: Lentivirinae.
1 (bases 1 to 1459)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolate LBV23-10
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Similarity 42.18;
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GPAATLEEMMTACQGVGGPGHKARVLAEAMSQVQQTNIMMQRGNFRGQRTIKCFNCGK
EGHLARNCKAPRKRGCMKCGKEGHQMKDCTERQANFLGKIWPSSKGRPGNFPQSRPEP
                                                                                                                                                                                                                                                            /translation="MGARASVLSGGKLDSWEKIRLRPGGKKKYRLKHLVWASRELERF ALNPGLLETAEGCQOLMEQLOSALRTGSEELKSLENTIATLWCYHQRIDYKDTKEALD KLEEIONKSKOKTQQAAAATGSSQNYPIVQNAGQQMTQPMSPRTLNAWYKYIEEKA FSPEVIPMFSALSEGATPQDLNMMLNIVGGHQAAMQMLKDTINEEAAEMDRVHPVHAG FSPEVIPMFSALSEGATPGDLNMMLNIVGGHQAAMQMLKDTINEEAAEMDRVHPVHAG FSPEVIPMFSALSEGATPGDLNMMLNIVGGHQAAMQMLKDTINEEAAEMDRVHPVHAG FSPEVIPMFSALSEGATPGDLLNMMLNIVGGHQAAMQMLKDTINEEAAEMDRVHPVHAG FSPEVIPMFSALSEGATPGDLAWMTSNPPIPVGEIYKRWIVLGLNKIVRMYSP
/sequenced_mol="DNA"
/tissue_type="blood"
                                                                                            /organism="Human immunodeficiency virus type 1"
/isolate="LBV23-10"
                                                                                                                                                                  TAPPAESFGMGEEITSSPKQEPRDKGLYPPLTSLKSX"
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VSILDIRQGPKEPFRDYVDRFFKTLRAE"
                                                                     /cell_type~"lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                             /product="gag protein"
/gene="gag"
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/product="gag protein"
/gene="gag"
                                                 /provira
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/isolate="CI59"
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Pred. No. 2.42e-01;
13; Mismatches 31
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Best Local
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  GNTTYAAYGARACNAC 242
                                 agaacaagcaaaagac 344
                                                                                                  agaggatagatgtaaaagacaccaaagaagctttagataaaatagaggaaataaaaaaata 328
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                                                                             ARAARYINGAYGINACNAAYAIHAARGARGCNYINGARACNIIYGGNGGNGINAARMGNM 226
                                                                                                                                                                                                                                         gag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. The VI415 gag sequence clusters with HIV-1 A subtype sequences. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1 (HIV-1), Rwandan isolate VI415 Human immunodeficiency virus type 1
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                                                                                                                                                        h 4.7%;
Similarity 42.1%;
32; Conservative
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Similarity 42.1%;
32; Conservative
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ALNPGLLETAEGCQOILEQLQPALKTGTEEIKSLYMTVATLYCVHQRIDVKDTKEALD
KIEEIKNKKOKOTQQAAAGTGNSSWYSQNYPIOTONAGOMIHQAISPRTLNAWKVIE
EKAFSPEVIPMESALSEGATPQDLNMMLNIVGGHQAAMOMLKDTINEEAAEWDKUHPV
HAGPIPPGQMREPRGSDIAGTTSTTQEQIAMMTGNPPNPVGDIYKRWIILGLNKIVRM
                                                                                                                                                                                                                                                                                                                                                                                                                                         RALGTGATLEEMMTACQGVGGPGHKARVLAEAMSQVQHTNIMMQRGNFKGQRRIKCFN
CGKEGHLARNCRAPRKKGCWKCGKEGHQMKDCTERQANFLGKIWSSSKGRPGNFPQSR
                                                                                                                                                                                                                                                          /tissue_type="blood"
278 c 366 g
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/gene="gag"
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                                                                                                                                                                                                                                                                                                                                                                /organism="Human immunodeficiency virus type 1"
/isolate="VI415"
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                                                                                                                                                                                                                                                                                                                                         /cell_type="lymphocyte"
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                                                                                                                                                                                                                                                                                                    /sequenced_mol="DNA"
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Pred. No. 2.42e-01
13; Mismatches 3
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Pred. No. 2.42e-01
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                                           Louwagie, J.J., McCutchan, F., Brennan, T., Peeters, M., Brennan, T., Sanders-Buell, E., Eddy, G., van der Groen, G., Fransen, K., Gershy-Damet, M., Deleys, R. and Ber, D. Phylogenetic analysis of gag genes from seventy international HI isolates provides evidence for multiple genotypes AIDS 7, 769-780 (1993)
                                                                                                                                                                                              Human immunodeficiency virus type 1 Viridae; ss-RNA enveloped viruses; Retroviridae; Lentivirinae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. The authors group the outlying VI557 gag sequence with VI525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Louwagie, J.J., McCutchan, F., Brennan, T., Peeters, M., Brennan, T., Sanders-Buell, E., Eddy, G., van der Groen, G., Fransen, K., Seleys, R. and Burke, D. Phylogenetic analysis of gag genes from seventy international HIV-1 isolates provides evidence for multiple genotypes AIDS 7, 769-780 (1993)
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  Kindly
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Similarity 46.68;
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Alnpdildtaegclqlieqlqpalkyggteelqslevllativgvhqridykdyreale
klkeaqnksqurtqqatgdkgngnkisqnypiquaggqpyhqaisptilheraaewdrypye
exafsyebyipwesalsegatpodlamkinivgghqamqmlkotineraaewdrypye
Hagpippgqmreprgsdiagtistlqeqiawmtsnppipygdiykrwiilglnkivrm
yspysildirgspkepprdyvdrefralfaegatqevgwmtdyllvynanpcktil
Ralgogasieemmtacogyggpghkakvalraegatqevgwmtdyllvynanpckriikc
Ralgogasieemmtacogyggpghkakvalraegaydvynamydkgnfkggrriikc
enggkeehlarwcaaprkkgcwkcgkbghglkdcterqanflckiwspwkgrpghriikc
enggkeehlarwcaaprkkgcwkcgkbghglkdcterqanflckiwspwkgrpghriikc
srpeptappaesfgfgeemtpppkqerkdaespltslksx"
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Pred. No. 5.78e-01;
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                                                                                                                                                                                                                      Genetic variants of HIV-1 in Thailand AIDS Res. Hum. Retroviruses (1992) In press full staff_entry
                                                                                                                                                         Kindly provided prior to publication by Henry M. Jackson Foundation and the Walter Reed Army Institute of Research, Rockville, MD 20850 The 132 sequence clusters with HIV-1 B subtype gag sequences.
                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1492)
McCutchan, F.E., Hegerich, P.A., Brennan, T.P., Phanuphak, P.,
Singhara, P., Jugsudee, A., Berman, P.W., Gray, A.M., Fowler,
                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1 (HIV-1), Bangkok, Thailand sample BK132, PCR amplified and cloned after coculture on PBMCS than immunodeficiency virus type 1 Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
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Human immunodeficiency virus
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The PH153 gag sequence clusters with HIV-1
Location/Qualifiers
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    Similarity 30; Conser
                                                                                                                                                                                                                                                                                                                                                                     Retroviridae; Lentivirinae.
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Similarity 41.7%;
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295 c 357 g
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FNCGKEGHIARNCKAPRKKGCWKCGREGHQMKDCTERQANFLGKIWPSHKGRPGNFLQ
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/isolate="PH153"
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Score 121; DB 3; Length 1492; Pred. No. 7.15e-01; 13; Mismatches 29; Indels
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362 g 285
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Pred. No. 7.15e-01;
13; Mismatches 29;
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B subtype sequences.
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                                                                                                                                                                                                                                                                                                                                      167 ARAARYINGAYGINACNAAYAIHAARGARGCNYINGARACNITYGGNGGNGINAARMGNM 226
                                                                                                                                                                                                                                                                                                                                                       605 aaatgatagatgtaaaagacaccaaggaagctttagagaagatagaggaagagcacaaaca 664
                                                                                                                                                                                                                                                               227 GNTTYAAYGARA 238
                                                                                                                                                                                                                                                                                                665 acagtaagaaaa 676
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t (bases 7005
Li,Y., Karr
                                                   macrophage-tropic clone.
Human immunodeficiency virus type 1
Viridae, ss-RNA enveloped viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chimpanzee lymphocytes virology 194, 858-864 (1993) full staff_review full staff_review full staff_review full staff_review full staff_review funding provided in computer-readable form by Dr. Beatrice Hahn, CFAR, University of Alabama at Birmingham, Birmingham AL. This represents one of the most cytopathic variants that the authors of [1] have encountered. The BC virus is cytopathic in both human and chimp lymphocytes. This sequence clusters with HIV-1 subtype B sequences. SG3 is T-cell tropic as opposed to mono-
                                                                                                                               genomic sequence.
M93258 M89974
                                                                                                                                                                    Human immunodeficiency virus type 1 brain clone YU2; complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hahn, B.H. and Shaw, G.M.
A molecular clone of HIV-1 tropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone.SG3.
                                      Retroviridae; Lentivirinae.
                                                                                                              Human immunodeficiency virus type 1 brain clone YU2; infectious
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llarity 40.3%;
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g of R region of the
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competent plasmid clone pSG3.1"
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 Conway, J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                            Score 121; DB 3; L
Pred. No. 7.15e-01;
14; Mismatches 29;
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     Price, R.W.,
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     Shaw, G.M.
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simple staff_entry
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Kindly provided prior to publication by Shaw and Hahn, University
of Alabama. YUZ clusters with HIV-1 B subtype sequences. Four
full-length genomes were cloned from uncultured brain [1] and
compared [2]. YUZ, unlike three of the minimally defective clones
(see HIVYUIO>), was found to be replication competent and macro-
phage tropic. 10 nonsynonymous nucleotide differences are found
hatween YUZ and YUIO, 7 of which are seen in the env cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete nucleotide sequence, genome organization, and biological properties of HIV-1 in vivo: Evidence for limited defectiveness and
Shaw, G.M.
Complete nucleotide
                                                                                                       Molecular characterization of HIV-1 cloned directly from uncultured human brain: Identification or replication competent and defective
                                                                                                                                                   Viridae; ss-RNA enveloped viruses;
Retroviridae; Lentivirinae.
1 (bases 7007 to 7516)
Li.Y., Kappes,J.C., Conway,J.A., Pr
                                                                                                                                                                                                                                                                  proviral genome.
M93259 M89974
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Similarity 41.7%;
30; Conservative
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                             Hui,H.,
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                           Burgess, C.J., Price, R.W., Sharp, P.M., Hahn, B.H.
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                                                                                                                                                      Price, R.W.,
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organization,
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and biological
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FEATURES

Location/Qualifiers

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occurs at position 332 in 7A and 9B; occurs at position 420 in 7A and 9B; occurs at position 4233 in 8A; "g" occurs at position 4677 in 8A; "c" occurs at position 6215 in 7D; "g" occurs at position 6215 in 7D; "g" occurs

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                                                                                                                                                                                                                                                                                                                                                                                  ARAARYINGAYGINACNAAYAIHAARGARGCNYINGARACNIIYGGNGGNGINAARMGNM 226
                                                                                                                                         Human immunodeficiency virus type 1 (HIV-1), isolate ARV-2, integrated proviral DNA and circular unintegrated DNA from cells; clones lambda-[7A,7D,8A,8B,9B]. Infectious clone.
                                                                                                                                                                                                                          HIVSF2 9737 bp ss-RNA VRL 01-MAR-1989 Human immunodeficiency virus type 1, isolate ARV-2/SF2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compared [2] YULO and two other clones were found to be defective, whereas YU2 <HIYYU2> is replication competent. Pairwise transfections with the defective genomes led to replication competent and transmissible virions. The authors of [2] argue that complementation among minimally defective genomes is "readily attainable" in vivo. 10 nonsynonymous nucleotide substitutions separate YULO and YU2, 7 of which are seen in the env cds. YULO has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   simple staff_entry
Kindly provided prior to publication by Shaw and Hahn, U
findly provided prior to publication by Shaw and Hahn, U
for Alabama. The YU viruses cluster with HIV-1 B subtype
Four full length genomes were cloned from uncultured bra
                                                                                             Sanchez-Pescador,R., Power,M.D., Barr,P.J.,
Stempien,M.M., Brown-Shimer,S.L., Gee,W.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a 1bp deletion in the pol cds relative to YU2. There is a premature stop codon at base pair 2955 and a reading frameshift to reading frame 3 circa posision 2952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    properties of HIV-1 in vivo: Evidence for limited defectiveness and complementation
             full staff_review
                                                                             Stempien, M.M., Brown-Shimer, S.L., Levy, J.A., Dina, D. and Luciw, P.A.
                                                                                                                                                                                                              complete proviral genome.
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                           Science 227, 484-492 (1985)
                                                            Nucleotide sequence and expression
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13; Mismatches 29;
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pol polyprotein (premature
vif protein
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/note="nef protein"
/codon_start=8802
9103..9736
/note="3' LTR"
9555..9652
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637..654
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454..551
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/note="rev protein,
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/note="tat protein, exon 3 (AA at 8385)"
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389..398
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'codon_start=6071
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'codon_start=791
                                                                                                                                      note="envelope polyprotein" codon_start=6233
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note="rev cds intron 2"
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32..332
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pin(5840..6054,8384..8474)
pote="tat protein"
                                                                                                                                                                                                                                                                                                                                ote="rev protein, exon 2 (first expressed exon)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           odon_start=5840
in(5979..6054,8384..8658)
ote="rev protein"
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                                                                                                                                                                                                                                                                                                                                                             te="tat protein, exon 2 (first expressed exon)"
                                                                                                                                                                                                                                     ..6187
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                                                                                  exon 3 (AA at 8386)"
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BASE COUNT
ORIGIN
                                                      misc_signal
/note="mRNA polyadenylation signal" 3445 a 1738 c 2377 g 2177 t 5' terminus of LTR-U3.
                                                      /note="R repeat 3' copy"
9628..9633
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В Query Match 4.5%; Best Local Similarity 40.3%; Matches 29; Conservative Score 121; DB 3; Length 9737; Pred. No. 7.15e-01; 14; Mismatches 29; Indels Gaps

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V74703 V80065 V99650 V53479 X13717 V27381 V52194 V43027	MRIES	Variance of results qual to the sis of the	part2 3:part. part9 10:part. 15:part15 16 20:part20 21 20:part25 26 30:part35 36 40:part40 41 45:part45 46 50:part50 51 55:part55 56 60:part60	Match 0% first 45 summaries	s, 107135622 bases	Query 0	bktranslate2	103-287-4 from US09103287.pep TTYAARGAYWSNGAYGAYAT. AARTTYCTRWSNCTRCTRTA.	10:20:03 1999;	Smith-Waterman search, n backtranslated into	LO.	
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2.78e+01	3:		. 7	.70e+0	.70e+0	.70e+0	.70e+0	.70e+0	.70e+0	.70e+0	3.70e+0	3.70e+0	2.78e+0	2.78e+0	3.21e+0	1.81e+0	2.41e+0	2.41e+0	1.35e+0	1.56e+0	1.01e+0	1.17e+0	.17e+0	.30e+0	.98e+0	57e-0	.57e-0	576-0	.57e-0	.57e-0	.57e-0	.57e-0	.08e-0	. 48e	486-0	

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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic spock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating computer readable medium.

Sequence 2424 BP; 839 A; 302 C; 462 G; 759 T;
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Best Local S
Matches 38
MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC pol bacterial; infection; H. pylori; cancer; ulcer; gastritis;
                        Partial nucleotide sequence of the MurC
                                    V80065 standard;
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                                                                                                                                                                                                                                                                                         ttacaaaatgcatatttagataaattaggcatgaaaaatgcgttt 1937
                                                                                                                                                                                                                                                                                                                                       gtattagaacaatttgataatgctgttattttatttatgggtgcaggtgatattcaaaaa 1892
                                                                                                                                                                                                             TYAARGAYWSNGAYGAYATHTAYGCNCARATHTYCARATHACNGAYAARGGNACNGCN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tttaaagattcggatgacatttatgctcaaaatattcaaattacggataaaggtactgct 1352
                                                                                                       YTNCARAAYGCNTAYYTNGAYAARYTNGGNATGAARAAYGCNTTY
                                                                                                                                                   GTNYTNGARCARTTYGAYAAYGCNGTNGTNYTNTTYATGGGNGCNGGNGAYATHCARAAR
                                                                                                                                                                                                                                              GAYMGNGTNTTYYTNTGYGARATHTTYGGNWSNATHMGNGARAAYACNGGNGCNYTNACN 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                             acaaatattaaagaagcattagaaacgtttggtggtgttaaacgtcgtttcaatgaaact 1532
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                                                                                                                                                                                                 ATHCARGAYYTNATHGAYAARATHGARGGNGCNWSNYTNATHAAYGARGAYWSNATHAAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384;
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                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.6%;
59.5%;
                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2573; DB 58;
Pred. No. 3.53e-212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 103;
                        gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2424;
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                                                                                                       645
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Claim 2: Pages 4-5; 39pp; English.

CC The invention relates to a UDP-N-acetylmuramate:L-alanine ligase

CC (Murc polypeptide) encoded by the S. aureus Murc gene. Host cells

CC containing an expression system comprising the Murc gene can be used for

CC the recombinant production of the polypeptide. Agonists or the Murc

CC polypeptide are used to treat conditions requiring increased activity or

CC competitive polypeptide are useful for inhibiting the polypeptide e.g.

CC competitive polypeptide are useful for inhibiting the polypeptide e.g.

CC competitive polypeptide are useful for inhibiting the polypeptide e.g.

CC competitive polypeptide are useful for inhibiting the polypeptide e.g.

CC competitive polypeptide are useful for inhibiting the polypeptide e.g.

CC competitive polypeptide are useful for treat in dwelling devices for

CC competitive polypeptide are useful to treat in dwelling devices for

CC antibacterial agents are useful to treat in dwelling devices for

CC infection prevention or generally as wound treatments to prevent adhesion

CC diagnosing or prognosing a (susceptibility to) disease, for raising

CC antibodies; to identify modulators or specific receptors; in rational

CC antibodies; to identify modulators or specific receptors; in rational

CC antibodies; to identify modulators or specific receptors; in rational

CC antibodies; to identify modulators or specific receptors; in rational

CC antibodies; to determine bacterial serotype; and for gene;

CC for chromosomal mapping; to determine bacterial serotype; and for gene;

CC for chromosomal mapping; to determine bacterial serotype; and for genetic

CC sequence (Murc ORF) of the Murc gene

Sequence (Murc ORF) of the Murc gene

Sequence 660.Bp; 233 A; 83 C; 120 G; 224 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Key
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM (SMIK ) SMITHKLINE BEECHAM Burnham MKR, Wallis NG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; W89199
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gatcgtgtattcttatgtgaaatttttggctcaattagagaaaaattctggcgcattaacg
                                                               CAYACNTTYWSNMGNACNCARGCNTTYYTNAAYGARTTYGCNGARWSNYTNWSNAARGCN
                                                                                                                                                                                                                                                                                                        CAYACNGTNYTNAAYGCNYTNGCNGTNATHGCNATHWSNTAYYTNGARAARYTNGAYGTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.0%; Score 2557; DB 60; larity 59.4%; Pred. No. 9.99e-211; Conservative 157; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305064.
US∹052720
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  밁
                                                                                                                                                                                                                                                                                                                                             The present sequence represents a MurC gene encoding a Staphylococcus aureus UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide). Host cell containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. competitive polypeptide are useful for inhibiting the polypeptide e.g. competitive polypeptide are useful for inhibiting the polypeptide e.g. competitive polypeptide are useful to treat in-dwelling devices for the antibacter pylori infections and related cancers, ulcers and gastritis. The Helicobacter pylori infections are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The MurC polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to identify modulators or specific receptors; in rational cuseful in antisense/riozyme therapeutics; to detect mutant MurC gene:
                                                                                                                                                              Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM (SMIK ) SMITHKLINE BEECHAM Burnham MKR, Wallis NG; WPI; 99-062655/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Pages 3-4; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated MurC polypeptide from Staphylococcus aureus and nucleic acid - useful in diagnosis, treatment and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP-889123-A2.
07-JAN-1999.
26-JUN-1998; 305064.
03-JUL-1997; US-052720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UDP-N-acetylmuramate: I-alanine ligase (MurC polypeptide) encoding MurC gene; UDP-N-acetylmuramate: I-alanine ligase; MurC polypeptide bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine immunogen; drug; genetic immunisation; ds.
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V99650;
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                                                                                                                                                                                                                                                                                                                         chromosomal mapping;
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tttgatgtgtatgtggatggtgagttttatgatcacttcctgtctccacaatatggtgac
                                                                                                                                                              l Similarity
383; Conse
                                                                                                                                                                                                                                                                         1351 BP;
                                                                                                                                                              96.0%;
larity 59.4%;
Conservative 1
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/gene= "MurC"
/product= "UDD-N-acetylmuramate:L-alanine ligase
/product= (MurC polypeptide)"
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157;
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                                                                                                                                                           Score 2557; DB 60;
Pred. No. 9.99e-211;
157; Mismatches 105;
                                                                                                                                                                                                                                                                         166 C;
                                                                                                                                                                                                                                                                         260 G;
                                                                                                                                                                                                              Length 1351;
                                                                                                                                                              Indels
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respiratory tract and central nervous system Claim 1; Page 146; 390pp; English.

This sequence encodes a Staphylococcus aureus protein of unknown function, and represents a DNA Sequence of the invention.

The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to
                                                                                                                                                                                                                                                                                                                                                        DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; cardiac infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
                                                                                                                                                                                                                                                                                                              Staphylococcus aureus. EP-841394-A2.
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V53479;
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                                                                                                                         New nucleic acid sequences from Staphylococcus aureus WCHU29 useful in vaccines and for treatment of bacterial infections
                                                                                                                                                          P-PSDB; W77686
                                                                                                                                                                                       Ward JM;
                                                                                                                                                                                                       Lonetto MA,
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24-SEP-1996; US-027032.
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                                                                                                                                                                                                       Nicholas
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Reichard RW,
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Best Local
                                                                     vaccine; attenuation; computer Enterococcus faecalis.
W09850555-A2.
12-NOV-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-044655.
(HUMA-) HUMAN GENOME SCI INC.
BATASH SC, Dillon PJ, Kunsch CJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   x13717
                                                                                                                                                                                                                                                                                            Enterococcus faecalls; contig; detection Enterococcus faecalls; computer readable
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                         Barash SC, Dillon WPI; 99-045171/04. New isolated Enter
                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1999
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isolated Enterococcus faecalis
sed to develop products for the
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Pred. No. 4.65e-190;
143; Mismatches 97;
                                                                                CA;
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polynucleotides and polypeptides detection of Enterococcus and fo
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WO9818930-A2.
07-MAY-1998.
30-OCT-1997; U19422.
31-OCT-1996; US-029960
                                                                                                                                                                                         727381 standard;
V27381;
                                                                                                                     Streptococcus pneumoniae
                                                                                                                                      Streptococcus pneumoniae; detection; pneumonia; oti:
                                                                                                                                                          02-OCT-1998 (first entry)
Streptococcus pneumoniae SP0070 nucleotide.
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                                                   /product= "SP0070"
/note= "no stop com
                                                                                                           Location/Qualifiers
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                                                                                                                                                   vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis Claim 1; Page 72; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
Choi GH, Hromockyj A, Johnson
WPI: 98-272224/24.
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                                                                                                        RYTNCARAAYGCNT
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                                                                                                                                                                            YGTNYTNGARCARTTYGAYAAYGCNGTNGTNYTNTTYATGGGNGCNGGNGAYATHCARAA
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1267 BP; 365 A; 269 C;
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Pred. No. 6.67e-49;
102; Mismatches 217; Indels 6
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V52194 standard; DNA; 11864 V52194; 23-OCT-1998 (first entry)

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Sequence 1864 BP; 3440 A; 2668 C; 2183 G; 3573 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
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Barash SC, Choi GH, Dillon
Kunsch CA, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae genome fragment SEQ ID NO:61.
Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds. streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded on it, or a representative fragment or a sequence at least 95% identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-1996;
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  TNACYTGRTTNGCDATNGTNGTYTCRTTRAANCKNCKYTTNACNCCNCCRAANGTYTCNA
                          TNCKNGCNGTRTCDATNGTNGCNSWDATYTCNCKNGGRTGRTGNGCRTARTCRTCNACDA
                                                                                                         ggtctaggagtggagaaacattttcaacagtaatcacttggtgtttttttgttgattttgt 587
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                                                                                                                                                                        GNGTNCKNSWRAANGTRTGNGGYTGRAANACNGCNACNACYTCYTTRTGNGGRTAYTTYT
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Similarity 41.2%;
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Dillon PJ, Dougherty BA, Fannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 749; DB 47;
Pred. No. 6.67e-49;
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                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis claim 1; Page 151-152; 181pp; English.

The sequence is that of a Streptococcal polypeptide coding region. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially Sp infection. It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid. Sequence 1825 BP; 550 A; 385 C; 366 G; 524 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae polypeptide coding region. Polypeptide: ORF; open reading frame; infection; basteremia; diagnosis; prophylaxis;
                               1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Reid RH, Zarfos PN; WPI; 98-322654/28.
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24-NOV-1997; U21976.
27-NOV-1996; US-031879.
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V43027;
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                                                                                                                                                                                                                                                                                                                       Local
GNGTNCKNSWRAANGTRTGNGGYTGRAANA-CNGCNACNACYTCYTTRTGNGGRTAYTTY
                  CRCANARRAANACNCKRTCNGCYTTNSWNARNSWYTCNGCRAAYTCRTTNARRAANGCYT
                                                                           CDATNARRTCYTGDATNGTNARNGCNCCNGTRT-T--YTCNCKDATNSWNCCRAADATYT
                                                                                                                                                                                 AYTGYTCNARNACRTTDATNSWRTCYTCRTTDATNARN-SWNGCNCCYTCD--ATYTTRT
                                                                                                                                                                                               tggctaggtcttctaccttaacgtcaccatgatctacttcacgagccgagccataaattt
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1 Similarity 40.7%;
226; Conservati
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complement (731..868)
/*tag= b
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                                                                                                                                                                                                                                                                                                         Pred.
103; 1
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                                                                       PS Claim 1; Page 77; 235pp; English.

CC This sequence encodes an H. pylori cytoplasmic protein involved in CC outer membrane or cell wall blosynthesis. This sequence showed CC homology to N-acetylmuramate-Alanine ligase.

CC duodenal ulcer disease. The nucleic acid sequences of the invention CC duodenal ulcer disease. The nucleic acid sequences of the invention CC are used to evaluate compounds, especially activators or inhibitors of CC bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequences, and corresponding proteins, are CC sequence. The nucleic acid sequences and corresponding proteins, are CC sequence in detecting the presence of Helicobacter species in CC also useful for generating vaccines for immunising subjects against H. CC pylori or for use in detecting the presence of Helicobacter species in CC asample. Antisense nucleic acid sequences of these sequences are CC used to inhibit expression of a gene from Helicobacter species. H. CC pylori whole genomic DNA was isolated and nebulised to a median size of C2 2000 bp. Purified DNA fragments were blint-ended and ligated to unique CC Sequence adapters in 100-1000 fold molar excess. These linkers are cc complementary to the BstXI-cut pMPX vectors, while the overhang is not CC sequenced.

CC will the cut vector re-ligate itself easily. The linker-adapter inserts construct a series of CC sequenced.

CC sequenced libraries. The purified DNA samples were then
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Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisense; inhibition; ds.
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from the related specification, WO9640893. Sequence 861 BP; 291 A; 130 C;
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15-NOV-1996; U18542.
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                                      The ORF/protein reference number for this sequence was obtained
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(pos:397..399, aa:Xaa)
(pos:496..498, aa:Xaa)
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Best Local Similarity
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                                                                                                                                                                                                                                                    prolypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter

SC Claim 9; Page -; 1481pp; English.

CC This sequence encodes a H. pylori cytoplasmic protein involved in conter membrane or cell wall biosynthesis.

CC The protein may be used in a vaccine to prevent or treat H. pylori conter infection or to identify H. pylori polypeptide binding compounds, cuseful as potential H. pylori life cycle activators or inhibitors.

CC The genomic sequence of H. pylori (ATCC 55679) was determined from coverlapping contigs generated by mechanically shearing the bacterial may be sequences were analysed for ORF of at least 180 nucleotides, cand the predicted coding regions defined by computer evaluation. To comply the sequences were analysed for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant conditions of the pylori antigens for vaccine development, the amino conditions of the pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.

CC Note: This DNA sequence is not reproduced in the specification and cc has been derived from the related specification, wo3719098.
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Helicobacter pylori nucleic acid sequences and related related receives to treat or previous to treat or previous treat o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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Cytoplasmic; vaccine; prevention; treatment; identification; binding compound; bacterium; bacteria; inhibitor; duodenal ulcer disease;
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diagnosis; ds.
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275 CNCAYCAYCCNMGNGARATHWSNGCNACNATHGAYACNGCNMGNA
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Pred. No. 2.48e-05;
34; Mismatches 71;
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                                                                                                                                                                   Вb
                                                                                                                                                                                                                                                                                            PT Helicobacter pylori nucleic acid sequences and related PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori PT infection, and to detect Helicobacter PS Claim 9; Page 752; 1481pp; English.

CC Inim 9; Page 752; 1481pp; English.

CC The present sequence encodes a Helicobacter pylori cytoplasmic CC protein involved outer membrane or cell wall biosynthesis.

CC The protein may be used in a vaccine to prevent or treat H. pylori CC infection or to identify H. pylori polypeptide binding compounds, CC useful as potential H. pylori life cycle activators or inhibitors.

CC The genomic sequence of H. pylori (ATCC 55679) was determined from CC overlapping contigs generated by mechanically shearing the CC nucleotides, and the predicted coding regions defined by computer CC evaluation. To identify likely H. pylori antigens for vaccine CC development, the amino acid sequences predicted from various ORE CC were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences CC of interest, particular regions can be isolated from H. pylori by the computation for recombinant polypeptide production, e.g. in
                                                                                                                                                                                                                   Query Match
Best Local
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Helicobacter pylori.
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Vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnos cytoplasmic; outer membrane; cell wall; biosynthesis; ds.
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07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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P-PSDB; W20606.
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19-DEC-1996.
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                                                                  GNGTNAARMGNMTTYAAYGARACNACNATHGCNAAYCARGTNATHGTNGAYGAYTAYG
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e 1365
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Similarity 36.4%;
60; Conservative
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/note= "no stop codon
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Pred. No. 7.08e-04;
32; Mismatches 73;
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Best Local Similarity
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detection; pneumonia; otil
                                                                                                                                                                                    Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present protection is the sequence of commercial importance, or expression modulating the present of the S. pneumoniae genome.
                                                                                                                                                                                                          02-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae genome fragment SEQ ID NO:356. Streptococcus pneumoniae; S. pneumoniae; genome; diagno computer readable medium; vaccine; pharmaceutical compo streptococcus pneumoniae.
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Claim 1; Pa
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Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon
Kunsch CA, Rosen CA;
WPI: 98-272225/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 12
V52489 standard;
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31-OCT-1996; US-029960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes a computer readable medium which h nucleotide sequences SEQ ID NO:1 to 391 (VS2134 to VS5524) recit, or a representative fragment or a sequence at least 95% ide SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ II (VS2134 to VS2524) are genomic fragments from Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                        atcacgaagcttggctacagcaatagtcgcaagggcattttccacattgtgg
                                                                                                                                                                                                                                                                                                                YTTYTCNARRTANSWDATNGCDATNACNGCNARNGCRTTNARNACNGTRTGR
                                                                                                                                                                                                                                                                                                                                                                                     RAANCKNCKYTTNACNCCNCCRAANGTYTCNARNGCYTCYTTDATRTTNGTNACRTCNAR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Page 1370-1371; 1409pp; English.
                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                  pneumonia; otitis
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                               pneumoniae Sp0067 nucleotide.
pneumoniae; antigen; vaccine; info
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                  pneumoniae.
/product= "SP0067"
/transl_except= (pos:1,aa:Gly)
/note= "this codon has an apparent 2 nucleotide deletion
which alters the reading frame; no stop codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                          DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 183; DB 47;
Pred. No. 1.57e-02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                 infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 843;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                composition;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and pharmaceutical
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                    28-OCT-1997.
18-JUN-1996;
18-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.

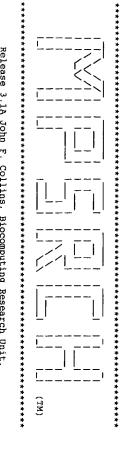
Sequence 1003 BP; 282 A; 211 C; 243 G; 267 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9818930-A2.
07-MAY-1998.
30-OCT-1997; U
Example 1; Columns 1-4; 13pp; English.

The present sequence represents DNA encoding Streptococcus pneumoniae MurD protein (uridine-diphosphate-N-acetylnuramyl-L-alanyl-D-isoglutamate ligase). The murD protein is useful in a method for identifying compounds that inhibit Streptococcus pneumoniae murD activity. Compounds identified are potentially useful as antibacterial agents. Sequence 1350 BP; 384 A; 272 C; 328 G; 366 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Choi GH,
WPI; 98-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MurD gene; antibacterial agent; drug screening; uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                             Streptococcus pneumoniae
                                                                                                                                                                                                                                                                           P-PSDB; W29454.
                                                                                                                                                                                                                                                                                                18-JUN-1996; US-665435.
(ELIL ) LILLY & CO ELI.
Hoskins JA, Peery RB,
WPI; 97-535046/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T89154 standard; T89154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis Claim 1; Page 71-72; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484 ccacaatgtggaaaatgcccttgcgactattgctgtagccaagcttcgtgatgtggacaa 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMA-) HUMAN GENOME
                                                                                                                                                                                                                  screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YCAYACNGTNYTNAAYGCNYTNGCNGTNATHGCNATHWSNTAYYTNGARAARYTNGAYGT 179
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US-029960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= MurD protein
/note= "no stop codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 1.57e-02;
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                                                                                                                                                                                                                                             protein - useful for antibacterial
                                                                                                                                                                                                                                                                                                                                 PL,
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Search completed: Sat Nov 27 10:22:50 1999
Job time: 167 secs.
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Best Local Similarity 29.5%;
Matches 33; Conservative
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Best Local Similarity 40.2%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligase. The nucleic acid can be used for the production of recombinant Murb protein and the implementation of large scale screens to identify new antibacterial compounds targeted at the stem peptide biosynthetic pathway involved in the synthesis of the bacterial cell wall. Structural analysis of the Murb protein will enable structure-based drug design to develop novel compounds for the treatment of antibiotic content is the synthesis of the synthesis o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Column 22-24; 14pp; English.
This sequence represents the mRNA for the Streptococcus pneumoniae murD biosynthesis protein. The murD gene encodes the enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae mur D biosynthetic gene - which encodes uridine-diphosphate-N-acetylnuramyl-L-alanyl-D-isoglutamate ligase,. ...
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14-APR-1997; 843309.
14-APR-1996; US-665435.
14-APR-1997; US-843309.
(ELIL ) LILLY & CO ELI.
HOSKINS JA, Peery RB, Skatrud PL, Wu CE;
WPI; 99-008720/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. pneumoniae MurD mRNA sequence.
Biosynthesis; recombinant; antibacterial; bacterial cell wall;
uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligase;
drug design; resistance; microorganism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug design to the resistant microorganisms.
1350 Bp; 384 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for identifying antibacterial compounds Claim 1; Column 22-24; 14pp; English.
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V33971 standard; mRNA; 1350 BP.
                                                                                                                                                                                                                                                                                                                                                                                         891 ucaaaccaucaaggaaacucuuucagccuucgguggugucaaacaccgucuc 942
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                                                                                                                                                                                                    180 NACNAAYATHAARGARGCNYINGARACNTIYGGNGGNGINAARMGNMGNTIY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 183; DB 52; Length 1350;
Pred. No. 1.57e-02;
32; Mismatches 47; Indels 0
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Pred. No. 1.57e-02;
20; Mismatches 47; Indels
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Mon Nov 29 10:17:04 1999



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MPsrch\_tpn n.a. - n.a. Smith-Waterman search, using a protein query which has been backtranslated into n.a. using IUPAC symbols

Tabular output not generated. Run on: Sat Nov 27 10:18:50 1999; MasPar time 49.83 Seconds 1119.486 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: >US-09-103-287-4 (1-215) from US09103287.pep 2663

1 TIYAARGAYWSNGAYGAYAT......TNGGNATGAARAAYGCNTTY 645
AARTTYCTRWSNCTRCTRTA.....ANCCNTACTTYTTRCGNAAR

Scoring table: TABLE bktranslate2 Gap 30

Nmatch STD: 165359 seqs, 43243793 bases x 2 Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-issued 1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1

Statistics: Mean 47.980; Variance 191.666; scale 0.250

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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	ce 14, Application US/08232463 ce 14, Application US/08232463 NO. 5670367 AL INFORMATION: LICANT: DORNER, F. LICANT: SCHEIFLINGER, F. LICANT: FALKNER, F. G. LICANT: FOLEVERIENT FOWLPOWERS BER OF SEQUENCES: 52 RESPONDENCE ADDRESS: DORESSEE: Foley & Lardner TREET: 1800 Diagonal Road, Suite 50 TIY: Alexandria TANE: VA UNTRY: USA DUNTRY: USA	LT 1 US-08-232-463-14 STANDARD: DNA: UNC: 7218 BP

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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293
                                MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          APPLICANT: APPLICANT:
                                                                            ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             TITLE OF INVENTION: Biosynthetic Gene MurD of Streptococcus
                                                                                                                                                                                                                 APPLICANT: Hoskins, Joann
APPLICANT: Wu, Chyun-Yeh Earnest
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CLASSIFICATION: 435
           APPLICATION NUMBER: FILING DATE:
                                                                                                              COUNTRY:
                                                                                                                           STATE:
                                                                                                                                                ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center
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Similarity 7.4%;
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                      US/08/665,435A
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                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1350 base pair
                                                                                                                                                                                                                                                                                                                           APPLICANT: Skatrud, Paul
APPLICANT: Peery, Robert
APPLICANT: Hoskins, Joann
APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: pneumoniae
NUMBER OF SEQUENCES: 3
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                                                         REFERENCE/DOCKET NUMBER: X-TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3334
                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                  STREET: Lilly Corp. CITY: Indianapolis STATE: Indiana
                                                                                          NAME: Webster, Thomas D
REGISTRATION NUMBER: 39,872
                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                              TELEFAX:
                                                                                                                                            FILING DATE:
                                                                                                                                                         APPLICATION NUMBER:
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Lilly Corporate Center
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VENTION: Biosynthetic Gene MurD of Streptococcus
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Pred. No. 2.60e-04,
32; Mismatches 4:
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Best Local :
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LOCATION: 1..1350
SEQUENCE 1350 BP; 384 A; 272 C; 328 G; 366 T; 0 OTHER
                                    SEQUENCE 1350
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                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Local Similarity 40.2%;
hes 45; Conservative
                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                     REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: Biosynthetic Gene Mur D of Streptococcus
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                                                       MOLECULE TYPE:
HYPOTHETICAL:
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                               TOPOLOGY:
                                                                                                                                                                                          NAME: Webster, Thomas D
REGISTRATION NUMBER: 39,872
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                                                                                                                                                                                                                                                   US/08/843,309
  Score 183; DB 3;
Pred. No. 2.60e-04;
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Pred. No. 2.60e-04;
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                                   328 G; 0 T; 366 OTHER
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Best Local 9
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                                                                                                                                 LOCATION: 1..1353
SEQUENCE 1353 BP; 386 A; 272 C; 328 G; 367 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08843309 Sequence 1, Application US/08843309
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 180
                      891
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                                                               831 CCACAATGTGGAAAATGCCCTTGCGACTATTGCTGTAGCCAAGCTTCGTGATGTGGACAA 890
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                                                                                                 Match 6.9%;
Local Similarity 40.2%;
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APPLICANT: F
APPLICANT: F
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NAME: Webster, Thomas D
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: X-TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                     FEATURE:
                                                                                                                                                                              ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: . Skatrud,
NACNAAYATHAARGARGCNYTNGARACNTTYGGNGGNGTNAARMGNMGNTTY
                   TCAAACCATCAAGGAAACTCTTTCAGCCTTCGGTGGTGTCAAACACCGTCTC 942
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                                          YCAYACNGTNYTNAAYGCNYTNGCNGTNATHGCNATHWSNTAYYTNGARARYTNGAYGT
                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Lilly Corporate CITY: Indianapolis
                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                LENGTH:
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Lilly Corporate Center
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                                                                                                                                                                                                               linear
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                                                                                      Mismatches
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                                                                                                  No. 2.60e-04;
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                                                                                                           DB 3;
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Best Local (
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SEQUENCE CHARACTERISTICS:
LENGTH: 2588 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
                                          Sequence 1, Application US/07725083
Sequence 1, Application US/07725083
Patent No. 5407821
GENERAL INFORMATION:
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                                                                                                                          US-07-725-083-1 STANDARD; DNA; UNC; 2608 BP
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                                                                                                                                                                                                                                                            2046 AGAGGTTCCTGGTGAGCTCATGCAGGAAGACCTGGCAACGGATGACGTCATGCTTCTGGA 2105
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                                                                                                                                                                                                                                                                                5.2%;
Local Similarity 36.8%;
les 32; Conservation
APPLICANT: Breakefield, Xandra O.
APPLICANT: Ozelius, Laurie J.
TITLE OF INVENTION: Genetic Diagnosis of Torsion Dystonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B144CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 715-0630
TELEFAX: (212) 715-0634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,368
FILING DATE: 04-MAY-1990
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: STOSSEL, THOMAS P.
TITLE OF INVENTION: MULTIMERIC GELSOLIN FUSION CONSTRUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                   WNARNSWYTCNGCRAAYTCRTTNARRAANGCYTGNGTNCKNSWRAANGTRTGNGGYTGRA 353
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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STATE: New York
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PC/TUS9102954
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Pred. No. 1.00e+00;
19; Mismatches 36; Indels
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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                                                                                                                                                                                                                                                          US-08-413-118-118 STANDARD; DNA; UNC; 1760
                                                                                                          GENERAL INFORMATION:
APPLICANT: ...PAOLETII, ENZO
APPLICANT: .L.PAOLETII, ENZO
APPLICANT: LLPBACH, KEITH J.
TITLE OF INVENTION: UUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CAMINE HERPESVIRUS 9B, 9C, AND 9D AND 1
                                                                                                                                                                                                                                                                                                                                                                           412 WNARNSWYTCNGCRAAYTCRTTNARRAANGCYTGNGTNCKNSWRAANGTRTGNGGYTGRA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/353,43
EILING DATE: 18 MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609
TREFERENCE/TOKET NUMBER: 0609
TREFERENCE/TOKET NUMBER: 07004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: \(202\) 371-2540 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                     352 ANACNGCNACNACYTCYTTRTGNGGRT 326
                                                                                  NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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ZIP:
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             COUNTRY:
                            STATE:
                                                      STREET:
                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
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Similarity 36.8%;
32; Conservative
10036
                                           NEW YORK
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                            NEW YORK
                                                      E: CURTIS, MORRIS & SAFFORD, P.C. 530 FIFTH AVENUE, 25TH FLOOR
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             UNITED STATES
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Pred. No. 1.00e+00;
19; Mismatches 36;
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Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443 ATYTCRCANARRAANACNCKRTCNGCYTTNSWNARNSWYT 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562 CRTTRTCRAAYTGYTCNARNACRTTDATNSWRTCYTCRTTDATNARNSWNGCNCCYTCDA 503
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INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 1760 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               756 ATATTACTAAAAAATAATCCATATGTTTAGTTGGTCATT 795
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 25,506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
CURRENT APPLICATION DATA:
                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                      APPLICANT: KOTHS, K: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 29-MA
                                                                                                                                        ADDRESSEE: CHIRON CORPORATION STREET: Intellectual Property - R440, P.O. Box 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                 COUNTRY:
                                                                                                                STATE: California
                                                                                                                                CITY: Emveryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                     94662-8097
                                                                                                                                                                                                                                                                                                                                  Application 5643563
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                                                                                                                                                                                                                                            LADNER, MARTHA B.
NOBLE, JANELLE A.
MARTIN, GEORGE A.
KAWASAKI, ERNEST S.
COYNE, MAZIE YEE
                                                                                                                                                                                                     KOTHS, KIRSTON E. VENTION: NEW FORMS OF
                                                                                                 U.S.A.
                                                                                                                                                                                                                                HALENBECK, ROBERT F.
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.19e+00;
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Best Local :
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Sequence 3, Application US/08401013
Patent No. 5681719
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                                                                                                                                                                                                                                                                                                                                                                                                        US-08-401-013-3 STANDARD; DNA; UNC; 1642
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 NYTNGARCARTTYGAYAAYGCNGTNGTNYTNTTY 576
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Local Similarity 34.0%;
                                                                                                                                                                                                                                            APPLICANT: LADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST:
APPLICANT: COYNE, MAZIE YEE
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                      APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
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                                                                                                                                                                       CORRESPONDENCE ADDRESS
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CURRENT APPLICATION DATA:
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       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McGarrigle Jr., Phili
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 21-AP CLASSIFICATION: 43
                                                                                   ZIP:
                                                                                               COUNTRY:
                                                                                                              STATE: California
                                                                                                                               CITY:
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                                                                                                                                            STREET:
                                                                                                                                                          ADDRESSEE: CHIRON CORPORATION
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                                                                                   94662-8097
                                                                                                                             Emveryville
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Pred. No. 2.82e+00;
25: Mismatches 37;
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Best Local S
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US-08-354-456A-3 STANDARD; DNA; UNC; 1642 BP
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OTHER INFORMATION:
SEQUENCE 1642 BP; 356 A:
                                                                                                                                                                                                                                       Sequence 3, Application US/08354456A Sequence 3, Application US/08354456A
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LENGTH: 1642 base pairs
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les 32; Consei
                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                          APPLICANT: Larrick, James W.
TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: McGarrigle Jr., Phili, REGISTON NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/999,280 FILING DATE: 28-DEC-1992 ATTORNEY/AGENT INFORMATION:
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                                                                                STREET: Intellectu
CITY: Emveryville
STATE: California
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                          HCARGAYYTNATHGAYAARATHGARGGNGCNWSNYTNATHAAYGARGAYWSNATHAAYGT 542
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                                                                    COUNTRY: U.S.A.
                                                                                                                 ADDRESSEE:
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                                                                                                     Intellectual Property - R440, P.O. Box 8097
                                                                                                                                                                                Martin, George
Piatek, Michael
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08-MAR-1995
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480 C; 403 G; 403 T; 0 C
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Pred. No. 2.82e+00;
25; Mismatches 37
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Best Local Similarity 34.0%;
Matches 32; Conservative
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NAME/KEY:

NAME/KEY:

LOCATION: 340

OTHER INFORMATION: /

SEQUENCE 1642 BP; 356 A; 4
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                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LADNER, MARTHA B.
APPLICANT: MOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
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INFORMATION FOR SEQ ID NO:
                                           ATTORNEY/AGENT INFORMATION:
NAME: MCGAIRIGLE JT., Phillip
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 750
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                             APPLICANT: COYNE, MAZIE YEE APPLICANT: HALENBECK, ROBERT F. APPLICANT: KOTHS, KIRSTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 21-DEC-1992
                                                                                                                                    ADDRESSEE: CHIRON CC
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COMPUTER READABLE FORM
                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                            TITLE OF INVENTION:
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                     COUNTRY: U.S.A. ZIP: 94662-8097
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                                                                                                       E: CHIRON CORPORATION
Intellectual Property - R440, P.O. Box 8097
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179..946
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275..946
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480 C; 403 G; 403 T; 0 OTHER
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Pred. No. 2.82e+00;
25; Mismatches 37;
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                                                                                                                                                                                                             Sequence 3, App. Sequence 3, App. 5672
                                                                                                                                                                                                                         Sequence 3, Application US/08426279 Sequence 3, Application US/08426279
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                                                                                                                                                                                                  Patent No. 5672343
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        US-08-426-279-3 STANDARD; DNA; UNC; 1642 BP
                                                                                                                                                                                                                                                                                                                       543 NYTHGARCARTTYGAYAAYGCNGTHYTHTTY 576
                                                                                                                                                                                                                                                                                                                                                                      483 HCARGAYYTNATHGAYAARATHGARGGNGCNWSNYTNATHAAYGARGAYWSNATHAAYGT 542
                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 5.0%;
Local Similarity 34.0%;
hes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/999,280A FILING DATE: 28-DEC-1992
                                                                                                                           APPLICANT: LADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
                                                                                                 TITLE OF INVENTION: NEW FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
COMPUTER READABLE FORM
                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1642 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                 CITY: Emveryville
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: McGarrigle Jr., Philip L. REGISTRATION NUMBER: 31,395
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COMPUTER: I
                                                          STREET:
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                     COUNTRY:
                                                                    ADDRESSEE:
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            94662-8097
                                                        Intellectual Property - R440, P.O. Box 809
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                                                                                                      NEW FORMS OF
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Matches 3
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APPLICANT: ZENNO, Shuhei
APPLICANT: SHIRAISHI, Shinji
APPLICANT: SHOUYE, Satoshi
APPLICANT: SAIGO, Kaoru

APPLICANT: TNVENTION: FIREFLY LUCIFERASE GENE
                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08231729B Sequence 2, Application US/08231729B Patent No. 5618722
                                                                                                                                                                                                                                                                                                                          1113 ATTTGTGCAGATTAAGATTGCATTAGTTTTTTTC 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 340
OTHER INFORMATION:
SEQUENCE 1642 BP; 356 A;
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                                                                                                                                                                                                                                                         US-08-231-729B-2 STANDARD; DNA; UNC; 1659
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SEQUENCE CHARACTERISTICS:
LENGTH: 1642 base pairs
TYPE: nucleic acid
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Local Similarity 34.0%;
nes 32; Conservative
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER
STREET: 700 Thirteenth Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY:
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REGISTRATION NUMBER: 31,395
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COMPUTER: I
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COMPUTER: IBM PC OPERATING SYSTEM:
                                                     COUNTRY:
                                                                          CITY: Washington
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                                                                D.C.
                                                       USA
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275..946
          IBM PC compatible
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 PC-DOS/MS-DOS
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480 C; 403 G; 403 T; 0 OTHER
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Pred. No. 2.82e+00;
25; Mismatches 37;
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Sequence 1, Application US/08231729B
Patent No. 5618722
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  US-08-231-729B-1 STANDARD; DNA; UNC; 1659
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                                                                                                                                                                               APPLICANT: ZENNO, Shuhei
APPLICANT: SHIRAISHI, Shinji
APPLICANT: INUYE, Satoshi
APPLICANT: SAIGO, Kaoru
TITLE OF INVENTION: FIREFLY LUCIFERASE GE
NUMBER OF SEQUENCES: B
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,729B
FILING DATE: 20-APR-1994
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                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: ROSE, Herbert C.
REGISTRATION NUMBER: 29846
REFERENCE/DOCKET NUMBER: 50130/No. 5618722aka
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-6770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 119050/1993
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
NAME/KEY: CDS
LOCATION: 1.1659
LOCATION: 1.1659
LOCATION: 1.1659
LOCATION: 1.1659
For codons 28, 32, 112, 130, 142, 190, 212, 2011
OTHER INFORMATION: 217, 222, 266, 329, 336, 386, 436, 512, and 532, if the OTHER INFORMATION: nucleotide is T or C, then the 5' nucleotide is C; and i OTHER INFORMATION: nucleotide is A, then the 3' nucleotide is A or G JENCE 1659 BP; 321 A; 193 C; 268 G; 265 T; 612 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYWSNGAYGAYATHTAYGCNCARATHTTYCARATHACNGAYAARGGNACNGCNGTNGAYG 67
                                                                                                                                                     STREET: 700 Thirteenth Street, N.W., CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                          TNTAYGTNGAYGGNGARTTY 87
                                                                                                                              COUNTRY:
                                                                                                                                         STATE: D.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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Similarity 20.0%;
16; Conservative
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Best Local Similarity 20.0%;
                              1636 TCNAARTCNAARGCNAARYT 1655
                                                                                      1576 ACNGGNAARATHGAYACNMGNAARATHAARGARATHYTNATHAARGCNCARAARGGNAAR 1635
                                                                                                                                                                     NAME/KEY: CDS

LOCATION: 1..1659

LOCATION: "Xaa" at codon 409 is either Glu or Asp;
OTHER INFORMATION: "Xaa" at codons 28, 32, 112, 130, 142, 190, 212, 217, 30THER INFORMATION: "Xaa" at codons 28, 32, 112, 130, 142, 190, 212, 217, 30THER INFORMATION: 329, 336, 386, 436, 512, and 532 is either Arg, Ser or SEQUENCE 1659 BP; 321 A; 193 C; 268 G; 265 T; 612 OTHER.
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-737-6776
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-6770
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Rose, Herbert C.
REGISTRATION NUMBER: 298
                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA
   TNTAYGTNGAYGGNGARTTY
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-737-6776
                                                           AYWSNGAYGAYATHTAYGCNCARATHTTYCARATHACNGAYAARGGNACNGCNGTNGAYG 67
                                                                                                                                                                                                                                                                                             TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 1 FILING DATE: 21-APR-1993
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                                                                                                                    Conservative
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   87
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                                                                                                                 Score 132; DB 1;
Pred. No. 2.82e+00;
30; Mismatches 34
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                                                                                                                   34;
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Search completed: Sat Nov 27 10:19:43 1999 Job time : 53 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed Nov 24 00:48:01 1999; MasPar time 11.00 Seconds 783.051 Million cell updates/sec

Description: Perfect Score:

Sequence: >US-09-103-287-4
(1-215) from US09103287.pep
1495
1 FKDSDDIYAQIFQITDKGTA.....GDIQKLQNAYLDKLGMKNAF 215

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

ACCESSIONS REFERENCE #authors

ORGANISM DATE

RESULT ENTRY TITLE

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 47.121; Variance 120.640; scale 0.391

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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104	109	114	118	127	128	130	132	150	185	193	232	235	239	259	264	283	291	293	341	343	356	863	Score	
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hypothetical protein	molybdenum cofactor b	UDP-N-acetylmuramoyla	hypothetical protein	RESA-H3 antigen PFB09	UDP-N-acetylmuramyl t	<pre>UDP-N-acetylmuramoyla</pre>	UDP-N-acetylmuramoyla	3	hypothetical protein	hypothetical 48.5K pr	<pre>UDP-N-acetylmuramate-</pre>	<pre>UDP-N-acetylmuramate-</pre>	udp-n-acetylmuramate-	probable murC protein		UDP-N-acetylmuramate-	<pre>UDP-N-acetylmuramate-</pre>	probable muramate-Ala	UDP-N-acetylmuramate-	UDP-N-acetylmuramoyla	<pre>UDP-n-acetylmuramate-</pre>	UDP-N-acetylmuramate-	Description	
4.19e+00	1.31e+00	3.94e-01	1.48e-01	1.52e-02	1.17e-02	6.98e-03	4.14e-03	3.20e-05	1.32e-09	.20e-	6.83e-16	2.64e-16	7.40e-17	.19e-1	2.35e-20	4.65e-23	3.31e-24	1.70e-24	.68e-3	8.51e-32	1.01e-33	4.56e-113	Pred. No.	

#journal #title

The complete genome sequence of the  $\operatorname{Gram-positive}$  bacterium  $\operatorname{Bacillus}$  subtilis

24 104 7.0 447 2 D71812 UDP-MurNac-tripeptide 25 103 6.9 447 2 F64706 UDP-MurNac-tripeptide 26 103 6.9 881 2 S37895 LHS1 protein precurso 27 102 6.8 452 2 JC6561 UDP-N-acetylmuramoyla 28 102 6.8 477 2 A4937 50k outer membrane process 29 101 6.8 591 2 S70524 guanine nucleotide-bi 101 6.8 1092 1 S37676 glutamate dehydrogena 32 100 6.7 420 2 S75514 sensory transduction 27 532 2 D71267 probable membrane process 31 100 6.7 532 2 D71267 probable membrane process 31 100 6.7 532 2 D71267 probable membrane process 31 100 6.7 532 2 S7049 probable membrane process 20 57030 conserved hypothetical protein 37 100 6.7 591 2 S43506 hypothetical protein 38 98 6.6 185 1 RWZ22 DNA-directed DNA poly 39 6.6 445 2 G70371 UDP-MURNAC-pentapepti 41 98 6.6 589 2 A46459 macrophage-activation 42 99 6.6 1235 2 C71210 probable DNA-directed RNA poly 39 6.5 185 2 R46459 macrophage-activation 44 97 6.5 914 2 JC5574 inter-alpha-trypsin 1
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udp-n-acety/nuramyi-t UDP-MurNac-tripeptide LHS1 protein precurso UDp-N-acety/nuramoyla 50k outer membrane pr guanine nucleotide-bi preprotein translocas glutamate dehydrogena sensory transduction probable UDP-N-acetyl probable UDP-N-acetyl probable UDP-N-acetyl probable Membrane pro conserved hypothetica hypothetical protein DNA-directed RNA poly UDP-MURNAC-pentapepti UDP-N-acety/nuramoyla macrophage-activation probable DNA-directed DNA-directed RNA poly conserved hypothetica inter-alpha-trypsin i

V.; Ponl, T.M.; Portetelle, D.; Porwoilk, S.; Prescott, A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takenaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Winters, P.; Wipat, A.; Yamamoto, H.; Weitzenegger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.	Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood, C.R.; Hennaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,	C69662 #type complete  UDP-N-acetylmuramatealanine ligase (EC 6.3.2.8) murC - Bacillus Subtilis  #formal_name Bacillus subtilis 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-1999 C69662; S71002 A69580  Kunst, F:; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Boriss, R.; Boursler, L.; Brans A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
.M.; Portetelle, D.; Porwolik, S.; Prescott, ccan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; ynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; ynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Skinceter, R.; Scoffone, F.; Sekiguchi, J.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo, A.; Tacconi, E.; Takaqi, T.; Takahashi, H.; Tamakoshi, A.; Tarachi, M.; Tamakoshi, A.; Tanaka, T.; Yognoni, A.; Tosato, V.; Uchiyama, S.; Wanier, F.; Vassarotti, A.; Viari, A.; Wedler, E.; Wedler, H.; Weitzenegger, T.; Wedler, A.; Yamamoto, H.; Yamane, K.; Yasumoto, Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.; H.; Danchin, A.	Entian, K.D.; Errington, J.; Fr, D.; Fritz, C.; Fujita, Zi, A.; Galleron, N.; Ghim, Golightly, E.J.; Grandi, G.; K.; Haiech, J.; Harwood, Holsappel, S.; Hosono, S.; L.; Joris, B.; Karamata, D.; M.; Klein, C.; Kobayashi, J.; Krogh, S.; Kumano, M.; Dis, S.; Lauber, J.; e, A.; Liu, H.; Masuda, S.; e, A.; Liu, H.; Masuda, S.; e, A.; Liu, H.; Masuda, S.; e, A.; Liu, J.; e, A.; Liu, P.; O'Reilly, Grank, S.H.; Parro,	<pre>ine ligase (EC 6.3.2.8) murC - ilis sion 05-Dec-1997 #text_change sion 05-Dec-1997 #text_change  Moszer, I.; Albertini, A.M.; Bertero, M.G.; Bessieres, P.; Bertero, R.; Boursier, L.; Brans, S.C.; Bron, S.; Brouillet, S.; B.; Capuano, V.; Carter, N.M.; ; Connerton, I.F.; Cummings, N.J.; ; Devine, K.M.; Duesterhoeft, A.;</pre>

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KEYWORDS
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#journal
#title
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#cross-references_MUID:96310371
#accession S71002
                                                                                                                                                                                                                                                           #authors
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#accession C69662
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                           ##cross-references
                                                             ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 IKHALKSFGGVKRRFNEKQLGDQVLIDDYAHHPTEIKVTIEAARQKYPDREIVAVFQPHT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 85-432 ##label VAR
##cross-references EMBL:L31845; NID:g556013; PID:g556014
##experimental_source strain 168, substrain Marburg
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                                                                                                                         C71679
                                                                                                                                           Nature (1998) 396:133-140
The genome sequence of Rickettsia of mitochondria.
                                                                                                                                                                                                                 Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.C.M.; Podowski, R.M.; Naeslund, A.K.; Eriksson, A.S.; Winkler, H.H.; Kurland,
                                                                                                                                                                                                                                                                                                                                   Rickettsia prowazekii
#formal_name Rickettsia prowazekii
21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change
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ATP binding; cell division; cell wall; ligase; peptidoglycan
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UDP-n-acetylmuramate--alanine ligase (murC) RP247
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1-495 ##label AND
ices GB:AJ235271; GB
PID:g3860809
                                                                                                                                         mitochondria.
                                                                               preliminary; nucleic acid translation not shown
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32; M
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                     GB:AJ235269; NID:g3860788; PID:e1342553;
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Best Local Similarity 43.8%;
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#title Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
                                                                                                                                                                                                                                                 #start_codon
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                                                              322 GDHNISNALÄAVAVGRLLGLDFPVIAQAIASFNGAKRFFECKGYCNGITFIDDYAHHPSE 381
                                                                                                                                                                                                                                                                                                           ##cross-references EMBL.D90916; GB:AB001339; NID:g1653715; PID:d1019367;
##note the nucleotide sequence was submitted to the EMBL Data
Library, June 1996
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382 LLATLAAAKQKVTHGKYERVVAIFQPHRYSRTHTFMAEFATAFKDADLVVLTDIYSAGEQ 441
                                                                                                                                                                                                                                                                                                                                                                                                     ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              ##status
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                                            39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FKDSDDIYAQIFQITDKGTAVDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISY-LEKLD 59
                                        GDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNETTIANQV-IVDDYAHHPRE
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Similarity 31.5%;
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S74322
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protein slr1423
#formal_name Synechocystis
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#length 495
                                                                                                                                                                                                           #length 505 #molecular-weight 54513 #checksum
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murC - Synechocystis sp. (strain PCC 6803)
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                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               1-505 ##label KAN
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                                                                                                                                               Score 343; DB 2;
Pred. No. 8.51e-32;
                                                                                                                            29; Mismatches 40;
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Pred. No. 1.01e-33;
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                                                                                                                                                                  Length 505;
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ISATIDTARKKYPH-K-E-VVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRE 154

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ACCESSIONS
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Best Local :
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                                                                                                       #cross-references MUID:99000809
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                          ##molecule_type DNA
##residnes
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##cross-references GB:AE000736; NID:g2983763;
##experimental_source strain VF5
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            ##cross-references
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYGVSAEELARKSGAVFAKDKEEVFEKVREVHDEGDVILFLGAGSISKWCEEFLKEVNL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REISATIDTARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIREN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEIKAVINSLRDMYPDKNLLVVFQPHRYSRTYYLFEDFVKVLKDIDKLIVTDIYPASENN 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDHTVLNALAVIAISYLEKLDVT-N-IKEALETFGGVKRRFNETTI-ANQVIVDDYAHHP 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 61; Conser
                                                                                                                      Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov, R.L.; Zhao, Q.; Koonin, E.V.; Davis, R.W. Science (1998) 282:754-759
Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, G.J.; Swanson, R.V.
Nature (1998) 392:353-358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UDP-N-acetylmuramate-alanine ligase - Aquifex aeolicus
#formal_name Aquifex aeolicus
08-May-1998 #sequence_revision 08-May-1998 #text_change
                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis (serotype D, strain UW3/Cx) #formal_name Chlamydia trachomatis 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change
                                                                                                                                                                                                                                                                                                                                        A71475 #type complete probable muramate-Ala ligase and D-Ala-D-Ala ligase Chlamydia trachomatis (serotype D, strain UW3/Cx)
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#length 454 #molecular-weight 50893 #checksum 2346
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1-803 ##label ARN
:es GB:AE001348; GB:AE001273; NID:g3329216;
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Pred. No. 1.68e-31;
48; Mismatches 62
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                     349
                                                                                       289 GKHNALNATAALAVAKEEGIANEAILEALADFQGAGRRFDQLGEFIRPNGKVRLVDDYGH 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-475 ##label TIGR
##cross-references GB:U32794; GB:L42023; NID:g1574694;
TIGR:HI1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
##residues 1-4
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                 HPTEVGVTIKAAREGWGDKRIVMIFQPHRYSRTRDLFDDFVQVLSQVDALIMLDVYAAGE 408
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Similarity 34.6%;
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Similarity 32.6%;
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"langth 803
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Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
Science (1995) 269:496-512
                                                                                                                                                                                                                                                                                                                                                                                             one of the ligases responsible for the synthesis of UPD-N-acetylmuramyl pentapeptide, an intermediate
                                                                                                                                                                                                                                                                                                            peptidoglycan biosynthesis
#superfamily UDP-N-acetylmuramate--alanine ligase
ATP; cell division; cell wall; ligase; P-loop; pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
                                                                                                                                                                                                                             #region nucleotide-binding motif A (P-loop)
#length 475 #molecular-weight 51994 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E64185 #type complete
UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)
Haemophilus influenzae (strain Rd KW20)
#formal_name Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
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                                                                                                                                                                                                                                                                                          biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                cell-wall biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid sequence not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 293; DB 2; Le
Pred. No. 1.70e-24;
42; Mismatches 49;
                                                                                                                                                                Score 291; DB 2;
Pred. No. 3.31e-24;
                                                                                                                                              48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shown; translation not shown
                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 803;
                                                                                                                                                                                   Length 475;
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                                                                                                                                              Indels 18;
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                                                                                                                                                                                                                                                                                                                peptidoglycan
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                                                             93
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RESULT
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                 #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *cross-references_MUID:98065943
                                                                                                                                                                                                                                                                                                                                                                                                                   177
                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 VKDSINFIKSLLISGDLFITMGAGNNFILHD-FL 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-468 ##label KLE ##cross-references GB:AE001180; GB:AE000783; NID:g2688755; PID:g2688761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##experimental_source strain B31
Y #length 468 #molecul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 18.9%;
Local Similarity 38.3%;
hes 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TESRTQAFLNEFAESLSKADRVFLCEIFGSIREN--TGALTIQD-L-IDKIEGAS-LINE
                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFTRTKEFFADFVEVLSAADILILHNIYLSNRENFNPDELSVKLFLNIKKINKNTYFFKD 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKEALETFGGVKRRFNETTIANQVI-VDDYAHHPREISATIDTARKKYPHKEVVAVFQPH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-IR-ENTGAL--TIQDLIDKIEGASLINEDS-I-NVLEQF--DNAVVLFMGAGDIQKL 201
                                                                                                                                                                                                                                                                                                                                                                                                            --DSINVLEQFDNAVVLF--MGAGDIQKLQNAYL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKRIAKNYSGIKRRVEVVKEENGVIYMDDYAHHPREIKNTLFGIKNFYKNKRIILDFMPH 375
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         Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.;
Sutton, G.G.; Dodson, R.; Gwinn, M.; Hickey, E.K.; Clayto
R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod,
M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson,
D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clayton, R.; Lathigra, R.; Mile, O.; Ketchum, K.A.;
Codson, R.; Lathigra, R.; Mile, O.; Ketchum, K.A.;
Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb,
J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.;
Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
Yugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman,
J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.;
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst,
K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C.
Nature (1997) 390:580-586
Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                             syphilis spirochete
24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change
17-Mar-1999
                                                                                                                                                                                                                                               #formal_name Treponema pallidum subsp. pallidum #common_name
                                                                                                                                                                                                                                                                     probable UDP-N-acetylmuramate--alanine ligase (murC) -
syphilis spirochete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H70201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #formal_name Borrelia burgdorferi #common_name Lyme disease
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Artiach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ranslation
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                                                                                                                                                                                                                                                                                                                      #type complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #molecular-weight 53480 #checksum
P.; Bowman, C.; Cotton, M.D.; Fujii,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 283; DB 2; Le
Pred. No. 4.65e-23;
33; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not shown
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.; McDonald,
i, C.;
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                                                                                     Clayton,
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DATE
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ENTRY
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                                                                                                             SUMMARY
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#authors
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                              #journal #title
                                                                                                                                                                                                                                                                                                                    #title Deciphering the biology of Mycobacterium tuberculosis the complete genome sequence.
#cross-references MUID:98295987
#accession D70579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
##residues 1-494 ##label COL
##cross-references GB:255388; GB:AL123456;
##cross-references PID:92104326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 DRVFLCEIFGSIRE-NTGALTIQDLID 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 DVVILHEIYASAREVYQGEVNGEHLFE 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 EVRGILEMDDYGHHPTAIKKTLRGLKTEFFPERRIVVDFMSHTYSRTAALLTEFAESFQDA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues : 1-481 ##label COL
##cross-references GB:AE001213; GB:AE000520; NID:g3322606; PID:g3322616
##experimental_source strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 GEFYVALPGEHSVLNATGALALALSLVKKQYGEVTVEHLTALRKVLALFQGCRRRSEVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 TIANQVIVDDYAHHPREISATIDTARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 GEFYDHFLSPQYG-DHT-VLN-ALAVIAISYLE-KLD-VTNIKEALETFGGVKRRFNE-T 80
       60;
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
50; Conser
                                                                                                                                                                                                                                                                                                                                                                                                          Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churc, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, Chillingworth, T.; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D70579 #type complete probable murC protein - Mycobacterium tuberculosis (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garland, S.; Hatch, B.; Horst, K.; Rot
L.; Weidman, J.; Smith, H.O.; Venter,
Science (1998) 281:375-388
                                                                                     #length 494 #molecular-weight 51176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                    preliminary; nucleic acid sequence
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                     17.3%;
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Score 259; DB 2;
Pred. No. 1.19e-19;
44; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 264; DB 2;
Pred. No. 2.35e-20;
35; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid sequence n not shown
                                                                                                                                                                                                         NID:g3261759;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K.; Basham, D.; Brown,
                                               Length 494;
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                                                                                            #checksum
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    15;
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Best Local Similarity 29.9%;
Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #title Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.
#cross-references MUID:99120557
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                                                                                                                                                                                                                              119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##experimental_source strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-449 ##label ARN 1-449 ##label ARN 1-449 ##cross-references GB:AE001489; GB:AE001439; NID:g4155102; PID:g4155106
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                                                                                                                                                                                                                                                                  352 QAHKYSRLMDNLEEFKKCFLEHCDRLIILPVYSA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##status
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"#molecule_type DNA
#residues
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                                                                                                                                                                                                                                                                                                                                                                                          DSDDIYAQIFQITDKGTAVDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTN 62
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                                                                                                                                                                                                                            QPHTFSRTQAFLNEFAES-LSKADRVFLCEIFGS
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G.F.; Trust, T.J.

Nature (1999) 397:176-180
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A71800
                                      #formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
10-Oct-1997
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12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
12-Feb-1999
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Pred. No. 7.40e-17;
40; Mismatches 60
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**residues 1-491 ##label IKE
##cross-references EMBL:X52644; NI
REFERENCE $40531
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Best Local Similarity 29.9%;
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  #journal
#title
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                                                                                                                                                                                                                                                                                                                                                                    #journal Nucleic Acids Res. (1990) 18:4014
#title Nucleotide sequence involving murG and murC
cluster region of Escherichia coli.
#cross-references MUID:90326550
#accession JQ0545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #title The complete genome sequence Helicobacter pylori. #cross-references_MUID:97394467
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                                                                                                             ##cross-references EMBL:D10483; NID:g216434; PID:d1001828; PID:g216505
                                                                                                                                     ##molecule_type DNA
##residues 1-491 ##label YUR
                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
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                                                                                                                                                                                                     Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, Fujita, N.; Isono, K.; Mizobuchi, K.; Nakata, A. submitted to the EMBL Data Library, December 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UDP-N-acetylmuramoyl-L-alanine synthetase
#formal_name Escherichia coli
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    Escherichia coli
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Nature (1997) 388:539-547
Over-production,
                       Eur. J. Biochem. (1995) 230:80-87
                                                                  Liger, D.; Masson, A.; Blanot, D.;
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                                             Parquet,
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Pred. No. 2.64e-16;
  purification and
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properties of
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#authors Burland, V.; Plunkett III, G.; Sofia, H.J.; Dani
Blattner, F.R.
#journal Nucleic Acids Res. (1995) 23:2105-2119
#title Analysis of the Escherichia coli genome VI: DNA.
#cross-references MUID:95334362
#accession S56459
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#accession S65354
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Similarity 38.8%;
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2 min
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#superfamily UDP-N-acetylmuramate--alanine ligase
ATP; cell division; cell wall; ligase; P-loop; peptidoglycan
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hypothetical 48.5K protein (fbp-pmba intergenic region) -
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#length 491 #molecular-weight 53626 #checksum
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Pred. No. 6.83e-16;
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Rirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;

Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;

FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;

Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;

Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.; #journal Science (1995) 269:496-512

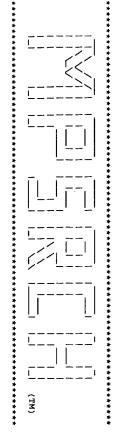
#title influenzae Rd.

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                                                                      ##residues 1-453 ##label TIGR
##cross-references GB:U32698; GB:L'
TIGR:HI0121
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##note the nucleotide sequence was submitted to the EMBL Data
Library, August 1994
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Blurland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
                                             #length 453
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Pred. No. 1.20e-10;
29; Mismatches 41
Score 185;
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                                                                      573 QDLRGK 578
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Complete genome sequence of Methanobacterium
thermoautotrophicum Delta H: functional analysis and
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Pred. No. 3.20e-05;
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Search completed: Wed Nov 24 00:49:00 1999 Job time: 59 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed Nov 24 00:44:36 1999; MasPar time 7.74 Seconds 785.202 Million cell updates/sec

Description: Perfect Score:

>US-09-103-287-4
(1-215) from US09103287.pep
1 FKDSDDIYAQIFQITDKGTA......GDIQKLQNAYLDKLGMKNAF 215

Scoring table: PAM 150 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 48.359; Variance 105.436; scale 0.459

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

23 23 24 44 45 45 46 47 47 47 47 47 47 47 47 47 47 47 47 47	Result No.
1454 865 343 343 303 303 291 259 243 225 132 132 133 1185 1130 1130 1130 1131 1131 1131 1131 113	Score
577 3 222.9 2 22.9 3 20.1 3 119.5 3 117.3 3 117.3 3 117.3 3 117.3 3 115.5 5 8.8 4 8.8 4 8.8 6 6.8 6 6.8 6 8.8 6	Query
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DNA-DIRECTED RNA POLYM	DNA MISMATCH REPAIR PR	P74 PROTEIN.	UDP-N-ACETYLMURAMOYLAL	HYPOTHETICAL 43.4 KD P	HYPOTHETICAL PROTEIN M	INTER-ALPHA-TRYPSIN IN	PHOSPHOGLYCERATE KINAS	PHOSPHOGLYCERATE KINAS	ENOLASE (EC 4.2.1.11)	N-ACETYL-GAMMA-GLUTAMY	DNA-DIRECTED RNA POLYM	DNA POLYMERASE (EC 2.7	BETA-GALACTOSIDASE PRE	INTERFERON-INDUCED GUA	UDP-N-ACETYLMURAMOYLAL	TYPE II RESTRICTION EN	DNA-DIRECTED RNA POLYM	DNA POLYMERASE (EC 2.7	UDP-N-ACETYLMURAMOYLAL	NAD-SPECIFIC GLUTAMATE	PREPROTEIN TRANSLOCASE
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1 FKDSDDIYAQIFQITDKGTAVDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDV 60	223 FKDSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDV 282	Query Match 97.3%; Score 1454; DB 1; Length 437; Best Local Similarity 97.7%; Pred. No. 1.39e-245; Matches 210; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	NP_BIND 108 114 ATP (POTENTIAL). SEQUENCE 437 AA; 49176 MW; 64D68582 CRC32;	EMBL; AF034076; G2642659; PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE; ATP-BINDING.	or send an email to licenseelsb-sib.cn).	modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/		between the Swiss Institute of Bioinformatics and the EMBL outstation -		-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.		ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.		-1- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).	LOWE A.M., DERESIEWICZ R.L.; SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.	SEQUENCE FROM N.A.		BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;	STAPHYLOCOCCUS AUREUS.	MIDO	UDP-N-ACETYLMURAMATEALANINE LIGASE (EC 6.3.2.8) (UDP-N-		36,	1998 (REL.		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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P40778;
01-FEB-1995
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   SUBTILIST; BG10973; MURC. PEPTIDOGLYCAN SYNTHESIS;
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF008220; G22932;
EMBL; L31845; G556014;
SUBTILIST; BG10973; MUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: CELL WALL FORMATION.
-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
-!- RATHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
-!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (REL. 31, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.
ACETYLMURANOYL-L-ALANINE SYNTHETASE).
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                                                                                                 DSDDIYAQIFQITDKGTAVDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTN 62
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                                                                                                                                                                                                   l Similarity
120; Conser
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432 ‡
                                                                                                                                                                                                 57.7%;
larity 59.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                          CELL WALL; CELL DIVISION;
                                                                                                                                                                                                                                                                                                     WW;
                                                                                                                                                                                                 Score 863; DB 1; I
Pred. No. 1.20e-132;
32; Mismatches 51;
                                                                                                                                                                                                                                                                                                                         ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                     163166CB
                                                                                                                                                                                                                                                                                                  (POTENTIAL).
63166CB CRC32;
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Bacillus subtilis
                                                                                                                                                                                                                                               Length 432;
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transcription
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Best Local Similarity 43.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA RES. 3:109-136(1996).
-!- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE.
-!- PATHWAY: PRETIDOGLYCAN BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MURC_SYN
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HOSOUCHI T., MATSUNO A., MURAKI A., NI
SHIMPO S., TAKEUCHI C., WADA T., WATAI
TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANOTATION UPDAT
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D90916; G1653723; -.
PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 97061201.
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                  155
                                                                                                                                                                                           382 LLATLAAAKQKVTHGKYERVVAIFQPHRYSRTHTFMAEFATAFKDADLVVLTDIYSAGEQ 441
                                                                                                                                                                                                                                                                                           322 GDHNISNALAAVAVGRLLGLDFPVIAQAIASFNGAKRRFECKGYCNGITFIDDYAHHPSE
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                                                                                                                                      86
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                                                                                                                                                                                                                                                      GDHTVLNALAVIAISYLEKLDYTNIKEALETFGGVKRRENETTIANQV-IVDDYAHHPRE 97
NTGALTIQUL
                                                                       NPYNIRGEDL 451
                                                                                                                                      ISATIDTARKKYPH-K-E-VVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRE 154
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505 AA;
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               164
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                                                                                                                                                                                                                                                                                                                                                                          Score 343; DB 1;
Pred. No. 1.62e-37
29; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (POTENTIAL).
; B3D7FC7C CRC32;
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(EC 6.3.2.8) (UDP-N-
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ASUDA M.,
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Best Local
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KIRZNER S., KAPLAN A.;
SUBMITTED (JAN-1997) TO
-i- FUNCTION: CELL WALL
-i- CATALYTIC ACTIVITY:
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-!- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
-!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
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15-DEC-1998
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=381;
ANSAI T.;
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15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDAT
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                     BACTERIA;
                                                                                                                                                                              SYNECHOCOCCUS
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MICROBIOLOGY 141:2047-2052(1995).
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                                                                                                                                                  CYANOBACTERIA; C
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BACTEROIDACEAE; PORPHYROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 327; DB 1; Pred. No. 9.15e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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(EC 6.3.2.8)
(FRAGMENT).
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P45066;
01-NOV-1995
01-NOV-1995
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                               FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M. MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C. FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                 -!- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-!- CATALYIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANINE.
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
-!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and influenzae Rd."; SCIENCE 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-RD / KW20;
MEDLINE; 95350630.
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAEMOPHILUS INFLUENZAE.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE -I- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS. -I- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE). -I- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
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051757;
15-DEC-1998
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LATHICRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M.,
DOUGHERTY B., TOMB J.-F., FLEISCHAANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.,
VAN VUGT R., PALMER N., ADAMS M.D., GOCAXNE J.D., WEIDMAN J.,
UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
SMITH H.O., VENTER J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
burgdorferi";
                                                                         modified and this statement is not remo
entities requires a license agreement (
or send an email to license@isb-sib.ch)
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BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)

""""""" SPIROCHAETALES; SPIROCHAETACEAE; BOF
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15-DEC-1998 (REL. 37, LAST SEQUENCE UI
15-DEC-1998 (REL. 37, LAST ANNOTATION
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (
ACETYLMURANOYL-L-ALANINE SYNTHETASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                             <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NATURE 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U32794; G1574695; -. TIGR; HI1139; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289
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                                                                                                                                                                                                                                                                                                        FUNCTION: CELL WALL FORMATION (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

PATHWAY: PEPFILOGLYCAN BIOSYNTHESIS.

SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).

SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                 sWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restruction by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPREISATIDTARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIF--G- 150
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                       AE001180; G2688761;
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475 AA;
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51994 MW;
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                                                                                        is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
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; DE40C270 CRC32;
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(EC 6.3.2.
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. 1.17e-28;
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                                                                                                                                                                 There are no restrictions ong as its content is in
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                                                                                                                                                                                                                            a collaboration -
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Best Local :
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O83361;

15-DEC-1998 (REL. 3

15-DEC-1998 (REL. 3

15-DEC-1998 (REL. 3
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15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDD-N-ACETYLMURAMOYL-L-ALANINE SYNTHETASE).
                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND 121
SEQUENCE 468 AA;
SEQUENCE
                                                                             EMBL; AE001213; G3322616;
                                                                                                           entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        -i- FUNCTION: CELL WALL FORMATION.
-i- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
-ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
-i- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                                                                                                                                                                       spirochete.";
SCIENCE 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                       KHALAK H., RICHARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J., KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T., MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S., HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDOGLYCAN ATP-BINDING.
                               ATP-BINDING.
                                             PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION;
                                                                                                                                                                                                                                                                                                                                                                                           VENTER J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DODSON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRASER C.M., NORRIS S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-NICHOLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIA; SPIROCHAETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TREPONEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MURC OR TP0341
                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                         'Complete genome sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --DSINVLEQFDNAVVLF--MGAGDIQKLQNAYL
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59; Conser
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481 AA;
                122
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larity 38.3%;
Conservative
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128 /
53762 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EY E.K., CLAYTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPIROCHAETACEAE; TREPONEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 283; DB 1;
Pred. No. 2.56e-27
33; Mismatches 5:
                                                                                                                                                                                                                                                                                                                                                                       Treponema
ATP (POTENTIAL).
9F643678 CRC32;
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Similarity 50; Conser

Conservative

Score Pred. 35; M

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Length 481;

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Gaps

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOMYCETALES; CORYNEBACTERINEAE; MY
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MURC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;
                                                                                                                          151
                                                                                                                                                                                       415
                                                                                                                                                                                                                                                                                                           355
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                                                                                                                                                                                                                                                 94
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les 60; Consei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CELL WALL FORMATION (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
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                                                                                                                          SIRENT-GALTIQDLIDKIEGA-SLINE-DSIN--VLEQFD-NAVVLFMGAGDIQKLQNA 204
                                                                                                                                                                                    A-REQPLAGVSGASVAEHVTVPMRYVPDFSAVAQQVAAAAASPGDVIVTMGAGDVTLLGPE
                                                                                                                                                                                                                                                                                     HPTEISATLAAARMVLEQGDGGRCMVVFQPHLYSRTKAFAAEFGRALNAADEVFVLDVYG 414
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   YLDKLGMK
                                                             ILTALRVR
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31.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51176 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 259; DB 1;
Pred. No. 2.40e-23;
44; Mismatches 69
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051926;
15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                    025340;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDAT
UDP-N-ACCTYLMURAMATE--ALANINE LIGASE (EC 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of ftsZ, the cell diviaphidicola (endosymbiont of aphids) and CURR. MICROBIOL. 36:85-89(1998).
                                                                            HELICOBACTER PYLORI (CAMP)
BACTERIA; PROTEOBACTERIA;
     SEQUENCE
                                                        HELICOBACTER.
                                                                                                                                       MURC OR HP0623
                                                                                                                                                             ACETYLMURANOYL-L-ALANINE SYNTHETASE)
                                                                                                                                                                                                                                                                                                                           MURC_HELPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF012886; G2738586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE - i - PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAUMANN L., BAUMANN P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                         201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LQN 203
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FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483
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                                                                            PYLORI (CAMPYLOBACTER PYLORI).
OTEOBACTERIA; EPSILON SUBDIVISION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
  N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AΑ;
                                                                                                                                                                                                                                                                                                                              STANDARD;
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54852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL WALL; CELL DIVISION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAMMA SUBDIVISION; BUCHNERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 243; DB 1;
Pred. No. 9.72e-21;
49; Mismatches 56
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; 23E8697B CRC32;
                                                                                                                                                                                                                                                                                                                              PRT;
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(EC 6.3.2.
                                                                                                                                                                                                                                                                                                                              449 AA
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8)
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                                                                                 HELICOBACTER GROUP;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MURC_ECOLI STANDARD; PRT; 491 AA. P17952; 007099; 01-NOV-1990 (REL. 16, CREATED) 01-NUG-1991 (REL. 19, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOMB J. F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.
NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,
MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.
COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WAITHEY L., WALLIN
HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
"Nucleotide sequence involving murG a region of Escherichia coli."; NUCLEIC ACIDS RES. 18:4014-4014(1990)
                                                                                                                                                                         MEDLINE; 90326550
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                               ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                              ESCHERICHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACETYLMURANOYL-L-ALANINE
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                                                                                                                               IKEDA M., WACHI M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=26695 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VENTER J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352
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CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE). SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
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97394467.
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29.9%;
                                                                                                                               JUNG H.K.,
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Pred. No. 1.89e-19;
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                                                                                    murG and murC in the mra
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                                                                                                                                                                                                                                                                                                                                                                                 SUBDIVISION;
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                                                                                         gene
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SEQUENCE FROM N
STRAIN-K12;
MEDLINE; 92334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss institute. There are no item the European Bioinformatics Institute. There are no item is use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement agreement (See http://www.isb-sib.
                                                                                                                                  NP_BIND
                                                                                                                                                                                                                                                                                                                                                          EMBL; X52644; G42056; -. EMBL; X55034; G40859; -. EMBL; D10483; G216505; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 92334977.

YURA T., MORI H., NAGAI H., NAGATA T., ISHIHAMA A., FUJITA N., ISONO K., MIZOBUCHI K., NAKATA A.;

"Systematic sequencing of the Escherichia coli genome: analysi."

"Systematic sequencing,";
                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                          EMBL; AE000118; G178627
EMBL; U67892; G2177094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
-!- PATHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
-!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   poly-gamma-glutamate ligases: identification of a ligase
superfamily."; .
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EVELAND S.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12 / MG1655;

MEDLINE; 97426617.

BLATTMER F.R., PUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V

RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
                                                                                                                                                                                  ATP-BINDING.
                                                                                                                                                                                                     PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 95324553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAU B., SHAO Y.;
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S40601; S40601.
ENE; EG10619; MURC
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     Similarity
47; Conse
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491 AA;
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  Conservative
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                                                                                                     132 A
344 G
; 53626 MW;
                             15.5%;
38.8%;
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Pred.
28; M
                             Score 232; DB 1;
Pred. No. 5.72e-19;
                                                                                                  ATP (POTENTIAL).
G->D: IN MURC3.
; C68ED87D CRC32;
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     Mismatches
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     36;
                                                  Length 491
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                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                              MENGIN-LECREUIX D., VAN HEIJENOORT J., PARK J.T.;

"Identification of the mp1 gene encoding UDP-N-acetylmuramate:
L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase in Escherichia
coli and its role in recycling of cell wall peptidoglycan.";
J. BACTERIOL. 178:5347-5352(1996).
-!- FUNCTION: INVOLVED IN CELL WALL FORMATION. REUTILIZES THE INTACT
TRIPEPTIDE L-ALANYL-GAMMA-D-GLUTAMYL-MESO-DIAMINOPIMELATE.
-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                    EMBL; AE000494; G1790680; -.
EMBL; X12545; -; NOT_ANNOTATED_CDS
                                                                                                              EMBL; U14003; G537075;
                                                                                                                                         entities re
or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMILTON W.D.O., HARRISON D.A., DYER T.A.; "Sequence of the Escherichia coli fructose NUCLEIC ACIDS RES. 16:8707-8707(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-64 FROM N.A. MEDLINE; 88335617.
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NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 95334362.
BURLAND V.D., PLUNKETT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE:L-ALANYL-GAMMA-D-GLUTAMYL-MESO-DIAMINOPIMELATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1994 (REL.
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P37773; P76804;
                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                bacterial genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
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                                 ATP-BINDING
                                              PEPTIDOGLYCAN SYNTHESIS;
                                                            HSSP; P14900;
                                                                        ECOGENE; EG12440; MPL.
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"Intrinsic and extrinsic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                   NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION
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                                                                                                                                         requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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110
457
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/ MG1655;
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       AA;
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       116
49874
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                   ATP
                                            DIVISION; CELL WALL;
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       A2BF8001
                   (POTENTIAL)
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       CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPL_HAEIN P43948;
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15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE:L-ALANYL-GAMMA-D-GLUTAMYL-MESO-DIAMINOPIMELATE
                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: INVOLVED IN CELL WALL FORMATION. REUTILIZES THE TRIPEPTIDE L-ALANYL-GAMMA-D-GLUTAMYL-MESO-DIAMINOPIMELATE.
-i- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      influenzae Rd.";
SCIENCE 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPL OR HI0121.
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                                                                                                                                                                                                                                         PEPTIDOGLYCAN SYNTHESIS; CELL DIVISION; CELL WALL;
                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whole-genome random sequencing and assembly of Haemophilus
                               312
                                                                                               252
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                                                                                                                                            Local
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VKRRFNETTIANQVIV-DDYAHHPREISATIDTARKKYPHKE-VVAVFQPHTFS-RTQAF 129
                              AKRRLEVKGEVNSITVYDDFAHHPEAILATLTALRDKVGGGVRILAVLEPRSNTMKMGVH
                                                               QITDKGTAVDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGG
                                                                                             RITNDASHFAVFHHGEKVAEVKWNVVGQHNMHNALMAIAAAHHTGVAIEDACKALGSFVN 311
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                                                                                                                           Similarity 29.4%; 40; Conservative
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453 AA;
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32, LAST SEQ
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50074 MW;
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                                                                                                                                            12.4%;
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                                                                                                                           Score 185; DB 1;
Pred. No. 1.16e-11
33; Mismatches 6
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Pred. No. 7.16e-13;
                                                                                                                                                                                                           ATP (POTENTIAL)
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                                                                                                                                                                                            CRC32;
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                                                                                                                                                         Length 453;
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Matches 3
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EMBL; Z25865; G397896; -.
EMBL; Z99111; E1185108; -.
PIR; S23914; S23914
PIR; B47691; B47691.
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Q1-QCT-1993 (REL. 27, CREATED)

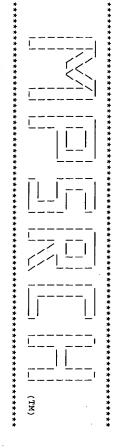
Q1-QCT-1993 (REL. 27, LAST SEQUENCE UPDATE)

15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE

(EC 6.3.2.13) (UDP-N-ACETYLMURAMYL-TRIPEPTIDE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DANIEL R.A., ERRINGTON J.;
"DNA sequence of the murE-murD region of Bacillus subtilis 168.";
J. GEN. MICROBIOL. 139:361-370(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBTILIST; BG10223; MURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DANIEL R.A., DRAKE S., BUCHANAN C.E., SCHOLLE R., ERRINGTON J.;
"The Bacillus subtilis spovD gene encodes a mother-cell-specific
penicillin-binding protein required for spore morphogenesis.";
J. MOL. BIOL. 235:209-220(1994).
J. MOL. BIOL. CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME.
I-- FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME.
I-- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANYL-D-
GLUTAMATE + MESO-2,6-DIAMINOHEPTANEDIOATE - ADP + ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-168
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BACTERIA; FIRMICUTES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 94118264.
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                                                             321 EIITEAVEELHGVRGRFELVNQQQEFPVIVDYAHTPDSLENVLETCRDMTEGKLFVVV 378
                                                                                                                                                                                                      262 IKNDADVMAKNISITAQGTSFDL-VTNKGTKHITMSLVGQFNVYNVLAAVATCIAAGIPF 320
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                                                                                                                                                                                                                                                                           y Match 8.8%;
Local Similarity 28.8%;
hes 34; Conservative
61 TNIKEALETFGGVKRRFNETTIANQV-IVDDYAHHPREISATIDTARKKYPHKEVVAV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIAMINOHEPTANEDIOATE
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                                                                                                                                     FKDSDDIYAQIFQITDKGTAVDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDV 60
                                                                                                                                                                                                                                                                                                                                                                                                                 109 115 ATP (POTENTIAL).
494 AA; 54325 MW; BCC9A893 CRC32;
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                                                                                                                                                                                                                                                                                                           Score 132; DB 1; Length 494; Pred. No. 3.76e-04;
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                                                                                                                                                                                                                                                                               60;
                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                       Gaps
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Search completed: Wed Nov 24 00:45:09 1999 Job time: 33 secs.



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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Nov 24 00:45:25 1999; MasPar time 15.38 Seconds 762.986 Million cell updates/sec

Tabular output not generated.

Title: >US-09-103-287-4 (1-215) from US09103287.pep 1495

Description: Perfect Score:

Sequence: 1 FKDSDDIYAQIFQITDKGTA......GDIQKLQNAYLDKLGMKNAF 215

Scoring table: PAM 150 Gap 11

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 46.142; Variance 99.559; scale 0.463

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

20 20 20 20 20 20 20 20 20 20 20 20 20 2	Result No.
341 150 1150 1118 1119 1111 1111 1111 1111 1111 111	Score
192 8 10.00 10.00 7.59 7.44 7.00 7.00 7.00 7.00 7.00 86.88	ch ch
454 803 598 517 517 517 113 647 1116 1116 1116 1119 1119 1119 1119 111	1.5
505000000000000000000000000000000000000	DB
084767 026630 0584767 026630 069847681 0007681 0026283 0026283 0062890 0062890 0069277 018883 0468388	ID
UDP-N-ACETYLMURAMATE-A UDP-N-ACETYLMURAMYL TR 598AA LONG HYPOTHETICA UDP-N-ACETYLMURAMYL TR 598AA LONG HYPOTHETICA UDP-N-ACETYLMURAMOVLAL TRANSCRIPTIONAL ACTIVA MOLVEDENUM COPACTOR BI FE-HYDROGENASE ALPHA S MURC (UDP-N-ACETYLMURA UDP-N-ACETYLMURAMOVLAL BETA-GALACTOSIDASE (EC NONTOXIC-NONHAEMAGGLUT NTNHA. NTNHA. NTNHA. NONTOXIC-NONHAEMAGGLUT UDP-MURNAC-TRIPEPTIDE ZK1010.9 PROTEIN (FRAG URIDINE DIPHOSPHATE N- ZK520.1 PROTEIN.	Description
8.59e-30 7.36e-07 1.71e-02 9.79e-01 1.30e-01 1.30e-01 4.03e-01 7.01e-01 7.01e-01 7.01e-01 7.02e-01 9.22e-01 9.22e-01 9.22e-01 9.22e-01 9.22e-01 9.22e-01 1.59e+00 1.59e+00	Pred. No.

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HYPOTHETICAL 171.1 KD SODIUM CHANNEL.	ORGANELLE-TYPE CALCIUM	z	FRAGM		PHOSPHOGLYCERATE KINAS	379AA LONG HYPOTHETICA	HYPOTHETICAL 33.1 KD P	CONSERVED HYPOTHETICAL	ORF5.		HOMOLOG OF VACCINIA VI	MAL3P6.20 PROTEIN.	HYPOTHETICAL 245.6 KD	멅	BETA-GALACTOSIDASE (EC	SWAP-70.	RESPONSE REGULATOR SPD	UDP-MURNAC-PENTAPEPTID	RNA POLYMERASE 22 KD S	67	HYPOTHETICAL 68.4 KD P	CHROMOSOME XV READING	SENSORY TRANSDUCTION H
1.01e+01 1.01e+01					7.78e+00	7.78e+00	1.01e+01	1.01e+0	6.00e+00		6.00e+00		3.55e+00		3.55e+00				•	2.72e+00	•	2.72e+00	2.72e+00

## ALIGNMENTS

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394 VYGVSAEELARKSGAVFAKDKEEVFEKVREVHDEGDVILFLGAGSISKWCEEFLKEVNL 452	96 REISATIDTARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIREN 155	RDMYPDKNLLVVFQPHRYSRTY	39 GDHTVLNALAVIAISYLEKLDVT-N-IKEALETFGGVKRRENETTI-ANQVIVDDYAHHP 95	NTGVA-LE-LGVSFEVIKKSLEEFRNAERRLELKGYYKNSPVY	Query Match 22.8%; Score 341; DB 2; Length 454; Best Local Similarity 34.1%; Pred. No. 4.03e-38; Matches 61; Conservative 48; Mismatches 62; Indels 8; Gaps 8;	SEQUENCE 454 AA; 50893 MW; 1207F9CE CRC32;	EMBL; AEUUU/36; G2983/64; LIGASE.	/GE	OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M.,	DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,	SEQUENCE FROM N.A. STRAIN-VF5;	[2]	NATURE 392:353-358(1998).	Or one of per circumopinate o passociation	"The complete genome of the hyperthermophilic bacterium Aquifex	OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M.,	DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,	MEDLINE; 98196666.	STRAIN-VF5;	SEQUENCE FROM N.A.	[1]	NOTITE TO YOU'S E.	MORC.	UDP-N-ACETYLMURAMATE-ALANINE LIGASE.	(TREMBLREL. 08, LAST ANNOTATION)	(TREMBLREL. 07,	01-AUG-1998 (TREMBLREL 07, CREATED)	067373; FRELIMINARI; FRI; 454 AA.	1

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TGALTIQDLIDKIEGA-SLINEDSIN-VLEQFDNA-VVLFMGAGDIQKLQNAYLDKLGM

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SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBO ALDREDGE T., BASHLRZADEH R., BLAKELY D., COOK R., GILBERY K., HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D., SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R., JUNANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR MCDOUGALL S., SHEMER G., GOYAL A., PIETROVSKI S., CHURCH G.M., DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
                                                                                                                                                                                                                                         STRAIN-DELTA H;
MEDLINE; 98037514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAVIS R.W.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ
EMBL; AE001348; G3329224; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  METHANOBACTERIUM THERMOAUTOTROPHICUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UDP-N-ACETYLMURAMYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            026630;
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MITCHELL W.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHLAMYDIA TRACHOMATIS. BACTERIA; CHLAMYDIALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               METHANOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                   ARCHAEA; EURYARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-D/UW-3/CX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCIENCE 0:0-0(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=D/UW-3/CX;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TREMBLREL. 05, CREATED)
(TREMBLREL. 05, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
LMURAMYL TRIPEPTIDE SYNTHETASE RELATED P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
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08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
""THE LIGASE AND D-ALA-D-ALA
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                                                                                                                                                                                                                                                                                                                                                                                                               METHANOBACTERIALES; METHANOBACTERIACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 293; DB 2;
Pred. No. 8.59e-30;
42; Mismatches 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.L., ZHAO Q., KOONI
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                                                                                                                                                                                                                                                                                                                                                                                     069556 PRELIMINARY; PRT; 517 AA.
069556; 01-AUG-1998 (TREMBLREL 07, CREATED)
01-AUG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE)
01-NUC-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
UDP-N-ACCTYLMURAMOYLALANYL-D-GLUTAMYL
   SEQUENCE
PARKHILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
J. BACTERIOL. 179:7135-7155(1997).

EMBL; AE000836; G2621664;
SEQUENCE 682 AA; 73795 MW; 67377BFE CRC32;
                                                                                           SEQUENCE FROM N.A. BROWN D., CHURCHER SUBMITTED (APR-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAMARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y., YAMAWOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAWA A., NAGAI Y., SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y., FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hyper-thermophilic Arc
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                                                                                                                                                                                                                            CTINOMYCETALES;
                                                                                                                                                                                                                                                                                                                                                             2,6-DIAMINOPIMELATE--D-ALANYL-D-ALANYL LIGASE
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
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"Use of an ordered cosmid library to deduce the genomic organization
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                                                                    TRAAI-LLR--FINLKIVDISERLFYDSQQTFTREF 93
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ISATIDTARKKYPHKEVVAVFQPHTFSRTQAFLNEF
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272 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 AA; 52874 MW;
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32359 MW;
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                                                                                                                                                                                                                                                                                    Score 111; DB 2; Length 272; Pred. No. 1.30e-01; 27; Mismatches 37; Indels
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Pred. No. 9.79e-02;
13; Mismatches 26;
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of the major structural
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01-JUG-1-998 (TREMBLREL
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01-AUG-1-998 (TREMBLREL
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01-JAN-1998 (TREMBLRI
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MOLYBDENUM COFACTOR I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRALN-DSM 3109;
O'ROURKE T.W., VERHAGEN M.F.J.M., ADAMS M. SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ EMBL; AF044577; G2865517; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-DELTA H;
MEDLINE; 98037514.

SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DU
SMITH D.R., DOUCETTE-STAMM L.A., BLAKELY D., COOK R., GILBERT K.,
ALDREDGE T., BASHIRJADEH R., BLAKELY D., COOK R., GILBERT K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00198; 4FE4S_FERREDOXIN; 2. IRON-SULFUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                         306 YPQYLQNLSSVKSPQQALGTVIKKIYARKLGVPEEKIFLVSFMPCTAKKFEAEREEHEGI 365
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                                                                     366 VD-IVLITRELAQLI----KM-SRIDINRV-EPQPFDRPYGVSSQAGLGFGKAGGVFSC- 417
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3 (TREMBLREL. 07, L.
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REL. 05, LAST SEQUENCE UPDATE)
REL. 07, LAST ANNOTATION UPDATE)
BIOSYNTHESIS PROTEIN MOAE.
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06, LAST
07, LAST
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pred. No. 2.30e-01;
24; Mismatches 45
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Pred. No. 4.03e-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.W.W
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                                                                                                                                                                                                                                                                                                                                                                        Length 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                  14;
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Best Local
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069290;
069290;
01-AUG-1998 (TREMBLREL. 0
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P94335;
01-MAY-1997
01-NOV-1998
01-NOV-1998
                                                                                                                                                STRAIN-NCTC 11168;
GRIFFITHS P.L., CONNERTON
SUBMITTED (MAR-1998) TO EN
                                                                                                                                                                                                                                                                                                                                                                                                                                       MURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TREMBLREL. 03, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MURC (UDP-N-ACETYLMURAMATE--ALANINE LIGASE) (EC 6.3.2.8
(UDP-N-ACETYLMURAMOYL-L-ALANINE SYNTHETASE) (FRAGMENT).
              SEQUENCE
                                                                                                                       EMBL;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              CAMPYLOBACTER JEJUNI.
BACTERIA; PROTEOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MARCOS P.H., GIL J.A.;
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-:- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE -
+ PHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
EMBL; AB003132; D1022538; -.
                                                  NON_TER
                                                                                      LIGASE
                                                                                                                                                                                                                                                                                                                                 CAMPYLOBACTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coryneform bacteria.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 97382442.
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ACTINOMYCETALES; CORYNEBACTERINEAE; CORYNEBACTERIACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 4-90 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORYNEBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning, sequencing, and characterization of the coryneform bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YUKAWA H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOBAYASHI M., ASAI Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129
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                                                                                                                Y16882; E1266307;
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31; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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              350
38656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMUN.
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                                                                                                                                             EMBL/GENBANK/DDBJ DATA BANKS
              WW.
                                                                                                                                                                                            I.F.;
                                                                                                                                                                                                                                                                                                                                                                  EPSILON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 105; DB 2
Pred. No. 7.01e:
18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                              SUBDIVISION; CAMPYLOBACTER GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350
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.01e-01;
              CRC32;
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Best Local Similarity
Watches 31; Conserv
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Best Local
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62800 PRELIMINARY;
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61-AUG-1998 (TREMBLREL. 0
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101-AUG-1998 (TREMBLREL. 0
101-AUG-1998 (TREMBLREL 0
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ACT_SITE
SEQUENCE
                                   RODRIQUEZ JOVITA M., COLLINS M.D., CURR. MICROBIOL. 36:226-231(1998).
                                                                                                                                                                                                                                                                                             CLOSTRIDIUM BOTULINUM. BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF PROSITE;
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EUKARYOTA; METAAOA; CHORDATA; VERTEBRATA; MAMMALIA;
CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.
[1]
                                                                                                                                                                                                                                                                   CLOSTRIDIUM.
                                                                                                                           EQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 FGPGANI-TAAFQIQRKSEPKGPLVNSEFYTGWLD-HWGQPHSTVRT-EVVASSLHDILA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 FE 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -HGANVNLYMFIGGTNFAYWNGANMPYQAQPTSYDYDAP-LSEAGDLTEKYFALREVIRK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FQ 119
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Similarity 24.6%;
30; Conservati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183<sup>,</sup>
662 AA;
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larity 28.7%;
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1, 74394 MW;
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                                                                                                                                                                                                                                                                                                  BACILLUS/CLOSTRIDIUM GROUP;
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. 07, LAST SEQUENCE UPDATE)

. 07, LAST ANNOTATION UPDATE)

3.2.1.23) (LACTASE) (FRAGMENT).
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LAST SEQUENCE ANNOTED ANNOTED ANNOTED AND ADDRESS AND ADD
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Pred. No. 7.
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25; M
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929FDD75 CRC32;
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d. No. 9.22e-01;
Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE UPDATE)
ANNOTATION UPDATE)
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01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 13
Q45891
                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96210012.
HUTSON R.A., ZHOU Y.,
SUGIYAMA H.;
                                                                                                                                                                                                                                                                                                "Genetic characterization of Clostridium botulinum silent type B neurotoxin gene sequences.";
J. BIOL. CHEM. 271:10786-10792(1996).
EMBL; X87848; E183922; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLOSTRIDIUM BOTULINUM. BACTERIA; FIRMICUTES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTNH PROTEIN
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SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; Y14238; E1288018; -.
SEQUENCE 1161 AA; 135221 MW; 98FF7CF2 CRC32;
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                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-667AB;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLOSTRIDIUM.
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                                                                                                                                                                                               611 FKDLSENLFN-IFS-KNNSYFEKIYYD--FLDQWWTQYYSQYFDLICMAKRSVLAQESLI 666
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Local Similarity 18.9%;
es 37; Conservation
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Local Similarity 18.9%;
es 37; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKIIQKKLSYLIGNSNISSDNLALMNLTTTNTLRDISNESQIAMNNV-NNFLNNVAICVF 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLKSL--FNSETGLLI 797
 SINVLEQFONAVVLFM 193
                          NLKSL - - FNSETGLLI
                                                      QPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTG-ALTIQDLIDKIEGASLINED
                                                                               QTNIYPKFISFMEQCINNINKNTREFI-QKCTNITENEKLQLINQNIFSSLDFDFL-NIE 783
                                                                                                            VTNIKEALE-TFGGVKRRFNETTIANQVIVDDYAHHPREISATIDTARKKYPHKEVVAVF
                                                                                                                                       KKIIQKKLSYLIGNSNISSDNLALMNLTTTNTLRDISNESQIAMNNV-NNFLNNVAICVF 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTG-ALTIQDLIDKIEGASLINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTNIKEALE-TFGGVKRRFNETTIANQVIVDDYAHHPREISATIDTARKKYPHKEVVAVF 118
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                                                                                                                                                                   FKD-SDDIYAQIFQITDKGTAVDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLD
                                                                                                                                                                                                                                                                                    1161 AA;
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                                                                                                                                                                                                                                                                                  135353 MW; 1D555D62 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                     COLLINS M.D., JOHNSON E.A.,
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08,
                                                                                                                                                                                                                        Score 104; DB 2;
Pred. No. 9.22e-01;
60; Mismatches 87
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LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                           Mismatches 87;
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No. 9.22e-01;
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Q1-NOV-1998
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EMBL; L42537; G840641; -.
SEQUENCE 1193 AA; 138200 MW; 6B4A51F7 CRC32;
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HUTSON R.A., ZHOU Y.,
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# ALIGNMENTS

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FEATURES	TITLE JOURNAL COMMENT	ORGANISM ORGANISM REFERENCE AUTHORS	RESULT 1 LOCUS DEFINITION ACCESSION NID VERSION KEYMORDS
Tel: 215-898-9384  Fax: 215-898-8780  Email: jecker@atgenome.bio.upenn.edu  Seq primer: T7  Class: BAC ends  High quality sequence start: 113  High quality sequence stop: 777.  Location/Qualifiers	BAC End Sequences at ATGC Unpublished (1997) Other_GSSs: F21H10-Sp6 COntact: Ecker J. Arabidopsis Thaliana Genome Center University of Pennsylvania Dept. of Piology, University of Pennsylvania, Philadelphia, PA	Arabidopsis. thaliana Arabidopsis. thaliana Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Elkaryotae; mitochondrial eukaryotes; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; vascular plants; seed plants; Magnoliophyta; Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.  1 (bases 1 to 1144) Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and Ecker, J.	B08906 1144 bp DNA GSS 13-MAY-1997 F21H10-T7 IGF Arabidopsis thaliana genomic clone F21H10, genomic survey sequence. B08906 g2090036 G2090036 GSS.

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JOURNAL COMMENT
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Best Local Similarity 34.6%;
 1544
                                                                1484 WKRRKGRRKRMTGMYKRMYRAMMAMCAMMACWWYYWKMRGMKKCWKYRKYKKYTSTYYK 1543
                                                                                                                                                                                                                                                                                               source
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                                                                                                                   Local Similarity 12.2%;
SWS-RWYWYTTYTYWYCWCCTSMKSASCAMMRWMGYMGSRSSRSYWGYWGSMSGCYGMTK 1602
                                YTCRTTRAANCKNCKYTTNACNCCNCCRAANGTYTCNARNGCYTCYTTDATRTTNGTNAC 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 2275)
Tripodis, N. and Ragoussis, J.
Generation of a transcription map in the region immediately
centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                  Guys Hospital
7th floor, Gu
                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tripodis, Nikos Division of Medical and
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
On Jan 19, 1998 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF034173 Human mRNA (Tripodis and F clone ntcon2 contig, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                      18;
                                                                                                                                                                                                                                                                                                                              floor, Guy's Tower, London
l: nikos@nki.nl.
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/clone_lib="IGF"
/sex="hermaphrodite"
165 C 141 g
                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: BeloBACII; Site_1: EcoRI; Site_2:
Produced by Thomas Altmann"
/db_xref="faxon:3702"
/clone="F21H10"

    . 1144
/organism="Arabidopsis thaliana"
/strain="Columbia"

                                                                                                                                                                                /clone="ntcon2 contig"
/clone_llb="Human mRNA (Tripodis and Ragoussis)"
619 c 470 g 599 t 149 others
                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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                                                                                                  Score 162; DB 20;
Pred. No. 1.36e-08;
73; Mismatches 55
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31; M
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sapiens cDNA
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   Fugu rubripes
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1 (bases 1 to 398)

Hillier;L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jos: Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin;J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA486130 398 bp mRNA EST 06-MAR-1998 ab14b03:r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840749 5' similar to gb:X04412 GELSOLIN PRECURSOR, PLASMA
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                    FR0029201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Sep 12, 1996 this sequence version replaced
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larity 34.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                           " /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                              /dev_stage="72 years"
/lab_host="SOLR cells
101 c 122 g
                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:840749"
                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Stratagene lung (#937210)"
/sex="male"
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   576
GSS
 bp DNA sequence,
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Pred. No. 1.01e-07;
25; Mismatches 51
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     clone
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93 t
GSS
9 038C04aE2,
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   genomic survey
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HS_2190_A2_C03_T7 CIT
sapiens genomic clone
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Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
Reopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
                                                                                                                                                                                    Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Furlong,J., Shaker,R., Schmidt,S., Traicoff,R. and Hood,L.E.
Construction of a Characterized Clone Resource for Genomic
                                                                                Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                       Unpublished (1998)
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Elgar,G., Clark,M., Smith,S., Meek,S.,
Williams,G. and Brenner,S.
Direct Submission
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1 (bases 1 to 468)
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Sequence Tagged Connector
                                                                  401 Queen Anne Avenue North,
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(206) 616-3887
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larity 43.0%;
Conservative
                jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="cosmid 038C04"
/clone="038C04aE2"
120 c 124 g 157
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/db_xref="taxon:31033"
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Pred. No. 2.71e-07;
18; Mismatches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 TACATCTAACTCATTTGAGAGAAGCGTTTTAATTCTTT 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 ATTGTGACCATACTTTATTTCATTTGCAATTTGCTGTATATAATACATAGGTTGAGAAAC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA110915 605 bp mRNA EST 04-FEB-1 mm02c04.r1 Stratagene mouse kidney (#937315) Mus musculus clone IMAGE:520326 5' similar to gb:J04953 Mouse gelsolin
                                                                                                                                                                                Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 375.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 605)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop:
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Apr 14, 1993 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                      This clone is available royalty-free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston,R.
                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA110915.1
                                                                                                                                                                                                                                                                IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
              /note="Organ: kidney; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: sperm;
E-Coli DH10B"
                                                                                                                  /organism="Mus musculus"
/strain="C57/B16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
/db_xref="taxon:10090"
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37.8%;
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Pred. No. 1.17e-06;
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v) for further
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 419)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                             WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W29681 419 bp mRNA EST 11-SEP-1996 mc07e04.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:347838 5' similar to gb:J04953 Mouse gelsolin gene, complete
                                                                                                                                                                                                                                                                                                                          MGI:219638
                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996
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W29681.1 GI:1309830
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Similarity 39.18;
34; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Apr 14, 1993 this sequence version
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/dev_stage="4 weeks"
/lab_host="SOLR (kanamycin resistant)"
161 c 144 g 146 t 1 othe
                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex-"females"
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/clone="IMAGE:520326"
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Pred. No. 1.91e-06;
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Apr 14, 1993 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA423163 455 bp mRNA EST 16-OCT-
ve36b02.rl Soares mouse mammary gland NbMMG Mus musculus of
IMAGE:820203 5' similar to gb:J04953 Mouse gelsolin gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; ThacE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
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1 (bases 1 to 455)
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h quality sequence stop: 165.
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llarity 37.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouseest@watson.wustl.edu
                                                                          T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                       _/clone="IMAGE:347838"
_/clone="15="Soares mouse p3NMF19.5"
_/dev_stage="19.5 dpc total fetus"
_/lab_host="DH10B (ampicillin resistant)"
a 112 c 122 g 91 t
                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
                                           /db_xref="taxon:10090"
/clone_lib="Soares mouse mammary gland NbMMG
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Local Similarity 37.9%;
nes 33; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 45)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
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Location/Qualifiers
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/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                     Dr. Minoru Ko (Wayne State University)."
/db_xref="taxon:10090"
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/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
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1 (bases 1 to 505)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
On Sep 12, 1996 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cds (MOUSE);, mRNA sequence.
AA097556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mo02c08.rl Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:552398 5' similar to gb:J04953 Mouse gelsolin gene, complete
                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                   mouseest@watson.wustl.edu
                                                                                                                                       /lab_host="DH10B (ampicillin resistant)"
123 c 130 g 102 t
               /tissue_type="lung"
/dev_stage="68 month old"
/lab_host="SOLR (kanamycin resistant)"
133 c 147 g 111 t 1 othe
                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6 x CBA"
                                                                                                       /clone_lib="Stratagene mouse
                                                                                        /sex="temale"
                                                                                                                          /clone="IMAGE:552398"
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37.9%;
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Query Match

5.6%;

Score 148;

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36;

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                                                                                                                                                                                                                                                                                                                                                                                                                                             WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
On Jan 19, 1998 this sequence version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 515)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                            T37]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                        /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                            /clone_lib="Soares mouse mammary gland NbMMG"
                                                                                                                               clone="IMAGE:1247254"
                                                                                                                                                                    /db_xref="taxon:10090"
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19; N
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                      107 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eukheria; Redentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 522)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, Gelsel; S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 328.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:898110
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Fax: 314 286 1810
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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On Jan 17, 1998 this sequence version replaced gi:2044964.
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  113
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Llarity 37.9%;
Conservative
                                                                                                                                                                                                                   T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                  /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:1364890"
                                                                                               'sex="male"
                                                                                                                         /clone_lib="Soares mouse mammary
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Pred. No. 1.29e-05;
19; Mismatches 35
153 g
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Mus musculus cDNA clone
gelsolin gene, complete
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370 AGAGGTTCCTGGCGAGCTTATGCAGGAAGACCTGGCTACTGATGACGTCATGCTCCTGGA 429
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                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA240493 539 bp mRNA EST 12-MAR-1997 mv33a01.rl GuayWoodford Beier mouse kidney day 0 Mus musculus cDNA clone IMAGE:656808 5' similar to gb:J04953 Mouse gelsolin gene, complete cds (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGI:402656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to 539)
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                         Similarity 33; Conser
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                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouseest@watson.wustl.edu
                                                                                                                                                                                                                                               /clone_lib="GuayWoodford Beier mouse kidney day 0"
/tissue_type="kidney"
/dev_stage="newborn (day 0)"
/lab_host="SOLR (kanamycin resistant)"
/ 148 c 166 g 107 t
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
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                                                       e 148; DB 10; L
. No. 1.29e-05;
Mismatches 35;
                                                         Mismatches
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206 AGAGGTTCCTGGCGAGCTTATGCAGGAAGACCTGGCTACTGATGACGTCATGCTCCTGGA 265
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubo Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA547287 542 bp mRNA EST 05-AUG-1997 vk27hil.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE:947877 5' similar to gb:X04412 GELSOLIN PRECURSOR, PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
On Sep 12, 1996 th
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The WashU-HHMI Mouse EST Project
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
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Similarity 37.9%;
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                                                                                                                                                                                                                                                                                                                                                                         constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                              /lab_
                                                                                                                                                                                                              /tissue_type="mammary gland"
/dev_stage="4 weeks"
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/clone="IMAGE:947877"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                              /sex="male"
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                                                                                                                                                                        host="DH10B"
                                                             Score 148; DB 14; 1
Pred. No. 1.29e-05;
19; Mismatches 35;
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                                                                              Query Match 5.6%;
Best Local Similarity 39.1%;
Matches 34; Conservative
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412 WNARNSWYTCNGCRAAYTCRTTNARRAANGCYTGNGTNCKNSWRAANGTRTGNGGYTGRA 353
                                     382 AGAGGTTCCTGGCGAGCTTATGCAGAAAGACCTGGCTACTGATGACGTCATGCTCGTTGA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 ANACHGCNACNACYTCYTTRTGNGGRT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 CACCIGGGACCAGGICITIGICIGGGI 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 547)
1 (bases 1 to 547)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M35762 547 bp mRNA EST 12-SEP-1996 mC14b03.r1 Soares mous p3NMF19.5 Mus musculus cDNA clone IMAGE:348461 5' similar to gb:X04412 GELSOLIN PRECURSOR, PLASMA (HUMAN); gb:J04953 Mouse gelsolin gene, complete cds (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g1317664
W35762.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality 
Seq primer: -28M13 rev2 from Amersham 
High quality sequence stop: 1. 
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On May 8, 1995 this sequence vers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                         125
                                                                                                                                                                                                                                                                                         GI:1317664
                                                                                                                                                                                     /clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH1OB (ampicillin resistant)"
143 c 168 g 111 t
                                                                                                                                                                                                                                                                        /clone="IMAGE:348461"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1995 this sequence version replaced gi:801502
                                                                              Score 148; DB 34; Length 547; Pred. No. 1.29e-05; 18; Mismatches 35; Indels
                                                                              0;
                                                                              Gaps
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Db 442 CTACTGCGACGAGGTCTTTGTGAGT 468
|| || || || || ||:||:|| ||:|
Cp 352 ANACNGCNACNACYTCYTTRTGNGGRT 326
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Search completed: Sat Nov 27 10:18:06 1999 Job time: 1149 secs;

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W40/12 R91247 W19520 W19513 R13895	7319167	W01669 W016713 W46713 R63794 R91240	00574451	W55716 W55594 R94358 W89964 P40615 W89981	92707
VIP2A(a) - VIP1A(a) proving VIP2A(a) - VIP1A(a) proving Maize optimised-B. ce B. cereus VIP1A(a)/VI ACV synthetase.	olyphosphate kinucleotide sequen IP1A(a) protein . cereus VIP1A(a . cereus VIP1A(a acillus cereus )	Human Factor Xa1. Influenza A/Beijing/3 80 kDa VIPIA(a) toxin Bacillus cereus 80 kD B. cereus VIP1 protei	human cadher ed precursor wo chain fact x. x (x). ri protein. ri protein.		. falciparum synthe equence of the P195 putrefaciens EPO iosynthetic enzyme
11111			4.81e+02 4.81e+02 4.81e+02 4.81e+02 4.81e+02 4.81e+02 4.81e+02 4.81e+02		2e+0 2e+0 2e+0 2e+0 2e+0

## ALIGNMENTS

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RESULT
ID
R43567; standard; Protein; 204 AA.
AC
R43567;
DT
19-UN-1994 (first entry)
DE Human cadherin-10.
KW
Antibodies; binding.
OS
Homo saptens.
PN
W0321302-A.
PD
28-CCT-1993; U03681.
PF
19-APR-1993; U03681.
PF
19-APR-1992; US-872643.
PA
RDDB; ODHENY EYE INST.
PI Suzuki S;
DR WPI; 93-351714/44.
DR N-PSDB; Q51225.
PT
DNA encoding cadherin 6,7,9 and 10 epr
and 10 - useful for modulating bind:
PT and 10 - useful for modulating bind:
CC cadherins
CL aim 14; Page 75; 99pp; English.
CC Full length cDNA sequences encoding
CC 4, 8; 11 and 13 and partial CDNAs er
CC cadherins 6 and 10 were isolated from the Cytoplasmic domain of mouse N-,
Sequence 204 AA;
Squence 204 AA;
     δÃ
                                                           유명
                                                                                                                                                                                                                                      OS Homo sapiens.

PN W09321302-A.

PN W09321302-A.

PD 28-OCT-1993; U03681.

PF 17-APR-1993; U03681.

PF 17-APR-1993; US-872643.

PA (DOHE-) DOHENY EYE INST.

PI SUZUKI S;

PI SUZUKI S;

PI SUZUKI S;

PI DNA encoding cadherin 6,7,9 and 10 antibodies to CH 5,6,7,9

PT DNA encoding cadherin for modulating binding and regulatory activities of cadherins

PT DNA encoding cadherins for modulating binding and regulatory activities of cadherins

CC Claim 14; Page 75; 99pp; English.

PS Claim 14; Page 75; 99pp; English.

CC 4, 8, 11 and 13 and partial cDNAs encoding human homologs of rat cadherins-

CC 4, 8, 11 and 13 and partial cDNAs encoding human foetal brain cDNA

CC 11brary using probes obtd. by amplifying human brain cDNA with

CC degenerate PCR primers designed from highly conserved segments in CC the cytoplasmic domain of mouse N-, E, and P cadherins.

SO Sequence 204 AA;
                                                                                                                                  Query Match 80.0%;
Best Local Similarity 52.9%;
Matches 9; Conservative
f i n e r
384 yttyathaaygarmgny 400
:||:||:||:||:||:
1 CTTCATTAATGAACGAT 17
                                                                                                                                  Score 76; DB 9; Length 204; Pred. No. 5.79e+01; 7; Mismatches 1; Indels
                                                                                                                                     0;
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                                                                                                                                                                                       US5646250-A.
08-JUL-1997.
17-APR-1992; 872643.
19-APR-1993; US-049460.
17-APR-1992; US-872643.
01-NOV-1994; US-332638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Columns 91-92; 59pp; English.

The present sequence is a partial human cadherin-10, which is a Ca2+ dependent cell adhesion protein. The human cadherin cDNA was isolated from a foetal brain cDNA library, using probes based on homologous rat cadherin cDNA.

Antibodies or fragments that specifically bind the human cadherin can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.

Sequence 241 AA;
                                                                                                             Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   superfamily;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cadherin: rat; calcium-dependent cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W25660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W25660 standard; Protein; 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibodies to cadherin proteins - useful as cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 97-108328/10.
N-PSDB; T61924.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-APR-1992; 872643.
17-APR-1992; US-872643.
19-APR-1993; US-049460.
26-JAN-1994; US-188228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Partial human
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W13133 standard; Protein; 241
                                                                                                                                                    (DOHE-) DOHENY EYE INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-1997.
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: CTTCATTAATGAACGAT
FINER
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                                          97-362997/33.
DB; T85435.
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n; human; antibody; purification; determination;
ue expression; binding antagonist; calcium ion; partial.
   and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
rat cadherin polypeptide(s) - mediate cell-cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Þ
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larity 52.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytoskeleton; eatenin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the specification of this sequence the specification 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                        one
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Encoded by TAA, this residue is
one reproduction of this sequence given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                         reproduction of this sequence given specification"
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Pred. No. 5.79e+01;
7; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        omitted
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in
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Combis sequence represents rat cadherin-10. The invention specifically comprovides details of human cadherin-5, -8, -11, -12 and -13, and rat cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell cadherin by -5, -11 and -13. Cadherins are calcium-dependent cell cadherin by -5, -11 and -13. Cadherins are calcium-dependent cell cadherin by -5, -11 and -13. Cadherins are calcium-dependent cell cadherin by -5, -11 and -13. Cadherins are calcium-dependent cell cadherin fictity, a hydrophobic membrane spanning region and a C-terminal composition of the cytosteleston conversed among members of the cytosteleston conversed among members of the conversed experimental conserved among members of the converse proteins and other cytoskeleton-associated proteins. The converse converse cadherin say be used in the analysis of the role of cadherins in various cancers. Sequence analysis of the cadherin of converse cadherin proteins may be isolated by using anti-cadherin conversed among members of cadherin conversed among the structure and function of cadherin. The cadherin proteins may be isolated by using anti-cadherin conversed among anti-cadherin conversed among the conversed among anti-cadherin conversed among among anti-cadherin conversed among among anti-cadherin conversed among among anti-cadher
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-APR-1992; 872643.
19-APR-1993; US-049460.
17-APR-1992; US-872643.
01-NOV-1994; US-332638.
(DOHE-) DOHENY EYE INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   w25657;
04-NOV-1997 (first entry)
04-NOV-1997 (first entry)
Rat cadherin-10;
Human; cadherin; rat; calcium-dependent cell adhesion protein;
superfamily; cytoskeleton; eatenin; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     through eatenins and other cytoskeleton-associated proteins. The novel cadherin proteins may be used in the analysis of the role of cadherins in various cancers. Sequence analysis of the cadherin proteins also allows investigation of the structure and function of cadherin. The cadherin proteins may be isolated by using anti-cadherin antibodies. These antibodies may also be used to modulate the activity of cadherin and to determine the tissue specific distribution of cadherin proteins. Each subclass of cadherins has a unique tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               provides details of human cadherin-5, -8, -11, -12 and -13, and rat cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell adhesion proteins. They are glycosylated integral membrane proteins that have an N-terminal extracellular domain that determines binding specificity, a hydrophobic membrane spanning region and a C-terminal cytoplasmic domain, which is highly conserved among members of the superfamily. The C-terminal domain interacts with the cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; T85432.

Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5646250-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2: Column 83-86; 56pp; English.
This sequence represents human cadherin-5. -8, -11, cadherin-8, -5, -11 and -13. Cadherins are ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W25657
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1 CTTCATTAATGAACGAT 17
F I N E R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                =
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larity 52.9%;
Conservative
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NY EYE INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              653
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Pred. No. 5.79e+01;
7; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention specifically 1, -12 and -13, and rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۳.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               f in er
1731 yttyathaaygarmgny 1747
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:TTTATTANTGAACGAT 17
F I N E R
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17-APR-1992; 872643.
17-APR-1992; US-872643.
19-APR-1993; US-049460.
26-JAN-1994; US-188228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Columns 61-64; 59pp; English.

The present sequence is full length rat cadherin-10, which is a Ca2+ dependent cell adhesion protein. The rat cadherin cDNA was isolated from a brain cDNA library using a labelled rat cadherin-10 extracellular domain PCR fragment as a probe. The rat cDNA was then used to isolate the cDNA encoding its full length human homologue from a human foetal brain cDNA library.

Antibodies or fragments that specifically bind the human cadherin can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.
             13-MAY-1998.
24-SEP-1997; 307485.
24-SEP-1996; US-027032.
(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1731 yttyathaaygarmgny 17.
:||:||:||:||:| :
1 CTTCATTAATGAACGAT 17
F I N E R
                                                                                                                                                                                                                                                                                      Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; cardiac infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ca2+ dependent; cell adhesion protein; foetal; cadherin; brain; human; antibody; purification; determination; tissue expression; binding antagonist; calcium ion.
                                                                                                                                                                                                                                       central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 97-108328/10.
N-PSDB; T61919.
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W13128 standard; Protein;
                                                                                                                                                           EP-841394-A2.
                                                                                                                                                                                     Staphylococcus aureus.
                                                                                                                                                                                                                   therapy
                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus protein of unknown function
                                                                                                                                                                                                                                                                                                                                                                                                                                                             W77686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies to cadherin proteins - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WS5597725-A.
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  Black MT,
                                                                                                                                                                                                                                                                                                                                                                                                     30-OCT-1998 (first entry)
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uence 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
Burnham MKR, Hodgson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%;
larity 52.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1747
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Pred. No. 5.79e+01;
7; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 5.79e+01; 7; Mismatches 1.
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  Knowles DJC
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Best Local S
Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae polynucleotides - useful for deve products for diagnosis, prevention and treatment of infect pneumonia, bacteremia, meningitis or endocarditis Claim 5; Page 32; 181pp; English.

The sequence is that of a Streptococcal polypeptide. The polypeptide can potentially be used for the diagnosis prevention of bacterial infections, especially SP infectio It may be used for the treatment of diseases such as othic conjunctivitis, pneumonia, bacteremia, meningitis, sinusit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a Staphylococcus aureus protein of unknown function, and is encoded by a DNA sequence of the invention. The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae polypeptide. Polypeptide; ORF; open reading frame; infection; k streptococcal; bacteremia; diagnosis; prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h r s l m A
4 caymgnwsnytnatgaar 21
||::|::|||||:|
|18 CATCGTTCATTAATGAAG 1
H R S L M K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ward JM;
WPI; 98-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas Reid RH, Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-1998.
24-NOV-1997; U21976.
27-NOV-1996; US-031879
                                                                                                                                                                                                                                                                                         empyema, endocarditis or infection of the cerebrospinal
Sequence 74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae.
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                   84 rcaytgywsnytnatgaar
:||:|::::|||||:
:|| GCATCGTTCATTAATGAAG
H R S L M K
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50.0%;
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                                                                                                                                                                               Score 71; D
Pred. No. 1.
7; Mismatc
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Pred. No.
6; Misma
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                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                          DB 34,
1.70e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monocot; P3 proteinase; NIa proteinase; RNA-dependent RNA polymerase; coat prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w79335-36 represent Staphylococcus aureus wCHU (NCIMB 40771) proteins that have homology to Bacillus subtilis histidine ammonia-lyase (histidase). The protein is used to generate antibodies and to screen for antimicrobials. The products are used to treat or prevent bacterial infections, particularly where caused by S. aureus but also against Helicobacter pylori. Particular applications are to treat subjects before surgery or insertion of an in-dwelling device (alternatively the device itself is impregnated before placement). The nucleic acid sequence is used as sources of antisense sequences (for therapeutic use) or regulatory elements for controlling expression of bacterial genes, and for antibacterial screening. The protein can be also used as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus histidine ammonia-lyase.
Bacillus subtilis; histidine ammonia-lyase; histidase; treatme prevention; bacterial infection; Helicobacter pylori; vaccine.
Staphylococcus aureus.
                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize dwarf mosaic virus polyprotein.
MDMV-B; viral resistance; disease resistance; transgenic plant;
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N-PSDB; V59883.
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25-NOV-1996; US-031469.
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Local Similarity 60.0%;
nes 9; Conservative
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Location/Qualifiers
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                                                                                                    /label= Cylindrical_inclusion_protein
/note= "claimed polypeptide (Claim 20
880..1010
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/note= "claimed
792..1430
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                                      1431..1483
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                                                                                                                                                                                                                                                                                                                                                                         "MDMV-B HC-Pro
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(CIBA) CIBA GEIGY AG.
Dietz JM, Law ...
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misc_difference 1346
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misc_difference 834
                                                                                                   Expression of the chimaeric gene inhibits infection of plants (pref. sorghum, sugarcane, esp. maize) by MDMV. The transgenic plants display an inheritable resistance trait.
                                                                                                                                                     The sequence of the polyprotein encoded by the polycistronic mRNA (T47073) of maize dwarf mosaic virus strain B (MDMV-B) is given in W10344. New chimaeric genes comprise a monocotyledonous plant promoter linked to a modified nucleic acid sequence derived from the MDMV-B genome. The modification is such that mRNA is translated to a truncated protein (pref. smaller than 200 amino acids), no translation of mRNA occurs or the transcribed mRNA lacks the
                                                                                                                                                                                                                                                N-PSDB; T47073.

Chimaeric gene for imparting viral resistance to plants - contains sequence modified to express non-translatable mRNA, or non-coat
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misc_difference 843
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misc_difference 829
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misc_difference 712
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Claim 20; Page 31-44; 64pp; English
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RNA_dependent replicases"
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Pred. No. 1.70e+02;
5; Mismatches 2
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RESULTING ACCORDANCE OF THE PROPERTY OF THE PR
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                                   30-OCT-1992; 118598.
31-OCT-1991; US-784234.
(THOM ) THOMAE GMBH KARL.
Augustin J. Engelke G. Entian K.
Kellner R. Kupke T. Rosenstein R
WPI; 93-168917/21.
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R39343
R39343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus
EP-543195-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Epidermin; derivatives; lantibiotic. Staphylococcus epidermis.
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Claim 1; Fig 1; 39pp;
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17-JUL-1997; US-895522.
(INCY-) INCYTE PHARM INC.
COrley NC, Hillman JL, Sh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 99-119878/10.
N-PSDB; V82520.
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09-APR-1998.

02-OCT-1997; E05441.

02-OCT-1996; DE-040817.

(BUJA/) BUJARD H.

BUJARD H. PAN W, Tolle R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W54145 stand
W54145;
23-SEP-1998
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N-PSDB; 051128.

Gene coding for eicosa-penta:enoic acid synthetase - is isolated from Pseudomonas, Alteromonas or Shewanella and used for recombinant prodn. of eicosa-penta:enoic acid Claim 6; Page 52-63; 106pp; Japanese.

EPA is useful as a drug, having anticoagulant, hypolipemic, antihypertensive and anticancer activity. It is a hypoglycemic, antihypertensive and anticancer activity is a company of the product of the 
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R42452;
R42452;
27-MAY-1994
reducing their AT content

Example 1; Fig 3c; 48pp; German.

This sequence represents a modified Plasmodium falciparum gp190/MSP-1

This sequence represents a modified Plasmodium falciparum gp190/MSP-1

(merozoite surface) protein. The gene encoding this protein has been stabilised by reducing the AT content of the nucleotide sequence. Sucle protein is useful in vaccines against malaria or for producing monocliprotein is useful in vaccines against malaria or for producing monocliprotein is useful in vaccines against malaria or for producing monocliprotein is useful in vaccines against malaria or for producing monocliprotein is useful in vaccines against malaria or for producing monocliprotein is useful in vaccines against malaria or for producing monocliprotein is useful in vaccines against malaria or for producing monocliprotein is useful in vaccines against malaria or for producing monocliprotein is useful in vaccines against malaria or for producing monocliprotein is useful in vaccines against malaria or for producing monocliprotein is useful in vaccines against malaria or for producing monocliprotein is useful in vaccines against malaria or for producing monocliprotein is useful in vaccines against malaria or for producing monocliprotein malaria or for producing
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N-PSDB; V21451, V35363.

Recombinant production of complete gp190/MSP-1 Plasmodium protein - useful in anti-malaria vaccines, also stabilisi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monoclonal antibody; passive immunisation; Plasmodium falciparum.
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(SAGA) SAGAMI CHEM RES CENTRE.
Kato S, Kondo K, Yamada A, Y
WPI; 93-386577/48.
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14-MAY-1993; J00641.
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No. 3.92e+02;
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W37050;
03-JUL-1998 (first entry)
S. putrefaciens EPO biosynthesis gene cluster ORF6 product.
SCRC-2874; FERM BP-1625; elcosapentaenoic acid; EPA;
biosynthesis gene cluster; synthetase.
Shewanella putrefaciens.
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                    10-JUL-1996; JP-180845.
(SAGA) SAGAMI CHEM RES
Kato S, Kondo K, Yamada
WPI; 98-101060/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Fig 1; 51pp; English. The sequence encoding the P195 protein of Plasmodium falciparum (N50530) and a peptide comprising at least one of its epitopes (see P50777) are claimed. Also claimed is a vaccine for inducing immunity to malaria comprising the novel peptide or P195 or a peptide comprising at least one epitope when derived from the new DNA sequence, together with a carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be produced outside the parasite and has, at least over extended regions, the native pattern of folding. Larger amounts of the protein can be produced recombinantly than would be possible using the parasites as
                                                                                        15-JAN-1998.
09-JUL-1997; J02371.
10-JUL-1996; JP-1808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WELL ) WELLCOME FOUNDATION I Holder A, Sandhu J, Odink K, WPI; 85-224845/37.
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22-FEB-1984; GB-004692.
26-SEP-1984; GB-024340.
21-FEB-1985; GB-004429.
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EP-154454-A.
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(1) bases 8081-9441, 12314-13084 and 1389-32520;
(2) bases 8081-9441, 12314-13084, 1389-32520;
(3) bases 8081-9441, 9681-13084 and 13889-32520;
(4) bases 8081-9441, 9681-13084 and 13889-32520 and 34627-35564; and (5) bases 8081-9441, 9681-13084 and 13889-35504, are claimed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coli -containing an eicosapentaenoic acid synthetase gene derived from the marine microorganism Shewanella Example 1; Pages 53-73; 110pp; Japanese.
The present sequence is encoded by the Shewanella putrefaciens SCRC-2874 (FERM BP-1625) eicosapentaenoic acid (EPA) biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene cluster
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                                                                                                                                                                                                                                              Sequence
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_ntp n.a. - n.a. Smith-Waterman search, using a protein database which has been backtranslated into n.a. using IUPAC symbols

Tabular output not generated. Run on: Wed Nov 24 02:29:02 1999; MasPar time 3.03 Seconds 448.944 Million cell updates/sec

>US-09-103-287-5 (1-19) from US09103287.seq 95

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 CTTCATTAATGAACGATGC 19 GAAGTAATTACTTGCTACG

Scoring table: TABLE bktranslate2 Gap 40

Nmatch STD:

Searched: 122461 segs, 35738955 bases x 2

Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 28.081; Variance 92.387; scale 0.304

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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APPLICATION NUMBER: US 07/872,643  FILING DATE: 17 APR 1992  ATTORNEY/AGENT INFORMATION: NAME: NO. 5597725and, Greta E. REGISTRATION NUMBER: 35,302  REFERENCE/DOCKET NUMBER: 31340  TELECOMMUNICATION INFORMATION:	199	ATION NUMBER:	FILING DATE: CLASSIFICATION: 435	APPLICATION NUMBER: US/08/188,228	SOFTWARE: PatentIn Release #1.0, Version #1.25	OPERATING SYSTEM: PC-DOS/MS-DOS	. 12	COMPUTER READABLE FORM:	COUNTRI: USA		STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago	EE: Borun	ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &	CORRESPONDENCE ADDRESS:	0	APPLICANT: Suzuki, Shintaro	GENERAL INFORMATION:	Datent No sso772s		Sequence 56, Application US/08188228			XXXXXX	US-08-188-228-56 STANDARD; PRT; 241 AA.

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                                                  TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                               ATTORNEY/AGENT INFORMATION:

NAME: NO. 5646250and, Greta E
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 3134
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 17 APR 1992
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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LENGTH: 241 amino acid
                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: CADHERII
MOLECULE TYPE: protein
                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                          STREET: 6300 CITY: Chicago
           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun
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(312) 474-0448
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           linear
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Pred. No. 3.90e+01;
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Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki
384 YTTYATHAAYGARMGNY 400
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                                                                                                                                                TELEFAX: (312) 984-97
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                   REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 2786
REGISTRATION NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                  Local
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                 MOLECULE TYPE: protein FINCE 241 AA; 26701 MW; 300025 CN;
                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/332,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suzuki, Shintaro
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/872,643 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                           LENGTH: 241 amino acids
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Similarity 52.9%;
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                                       Score 76; DB 1; L
Pred. No. 3.90e+01;
7; Mismatches 1
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Pred. No. 3.90e+01;
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1 CTTCATTAATGAACGAT 17
F I N E R
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Patent No.
                                                                                                                                                                                                                            TELEFAX: (312) 474-04-
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872
APPLICATION NUMBER: US 07/872
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                   MOLECULE TYPE:
ENCE 653 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHNE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 19 APR 1993
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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72459 MW;
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Pred. No. 3.90e+01;
7; Mismatches 1
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Sequence 1, Application US/08895522
Patent No. 5858719
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 46, Application US/08332638
                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                            NAME: NO. 5646250and, Greta E REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 312
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
TELEX: 25-3856
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F I N E R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 17 APR 1992
                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ENCE 653 AA; 72459 MW;
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NUMBER OF SEQUENCES:
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STATE: :Illinois
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AL INFORMATION:
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Pred. No. 3.90e+01;
7; Mismatches 1
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                                                                                                   Patent No. 5837485
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                              APPLICANT:
                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/895,522
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CITY: Palo Alto
CTATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acid
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MEDIUM TYPE: Diskett
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LIBRARY: OVARN
CLONE: 545981
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PRIOR APPLICATION NUMBER:
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SOFTWARE: FastSE(
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                                                                                                                                                 20, Application US/08392625
                                                                                                                 20, Application 5. 5837485
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                       G tz, Friedrich
Schnell, No. 5837485bert
Augustin, Johannes
Engelke, Germar
Rosenstein, Ralf
Kaletta, Cortina
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                                                                                                                                                                                                                                                                                                                                                                                                   OVARNOT02
              Klein, Cora
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                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                              73.7%;
52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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HUMAN
                                                                                          Karl-Dieter
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                                                                                                                            US/08392625
                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                        Score 70;
                                                                                                                                                                                                                                                                                                                                                                               2890233 CN;
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PORT PROTEIN
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                                                                                                                                                                                                                                                                                                                                               No. 1.35e+02;
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                                                                                                                                                                                                                    990 AA
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                                                                                                                                                                                                                                                                                                                                                       Length 747;
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Best Local S
Matches
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                                                                                                                                                                     Sequence 20, Application US/08466961A
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                                                                                                                                                                                                                                        US-08-466-961A-20
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                 Sequence 20,
                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 990 amino acids
                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  7 ATCGTTCATTAATGAA 2
S F I N F
APPLICANT: Kick... Bernu
APPLICANT: Wieland, Bernu
APPLICANT: Kupke, Thomas
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kellner, Roland
TITLE OF INVENTION: Biosynthetic Process For The Preparation
TITLE OF INVENTION: Of Chemical Compounds
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0:
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                              APPLICANT:
                                                                    APPLICANT:
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RWSNTTYATHAAYGAR 2061
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RCE 990 AA; 117141 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                      ), Application US/08466961A 5843709
                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                               Augustin, Johan
Engelke, Germar
                                            Rosenstein, Ralf
Kaletta, Cortina
                                                                                       Schnell, No. 5843709bert
                                                                                                    G tz, Friedrich
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                                                                                                               Karl-Dieter
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                                                                               Johannes
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Pred. No. 2.46e+02;
7; Mismatches 1
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Best Local Similarity 50.0%;
Matches 8; Conservative
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2046 RWSNTTYATHAAXGAR 2061
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17 ATCGTTCATTAATGAA 2
S F I N E
                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                       Sequence 15, Application US/08645193B
                                                         Sequence 15, Appr...
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/466,961A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
CRASSIFICATION DATA:
APPLICATION NUMBER: US 08/392,625
FILING DATE: 22-FEB-1995
PRIOR APPLICATION NUMBER: US 07/876,791
APPLICATION NUMBER: US 07/876,791
FILING DATE: 30-APR-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/784,234
APPLICATION NUMBER: US 07/784,234
FILING DATE: 31-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 20:
                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 990 amino acids
                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TITLE OF INVENTION: Oxidative Decarboxylation of Peptides TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD
                 APPLICANT:
                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Biosynthetic Process for the Preparation TITLE OF INVENTION: Chemical Compounds
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                                                                                                                                                                                                                                                                   990 AA; 117141 MW; 5092259 CN;
                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                 Esmond, Robert W
                                                                     Application US/08645193B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jung, G nther
Kellner, Roland
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                        Gotz, Friedrich
Kempter, Christoph
                                           Kupke,
                  Jung, Gunther
                                                                                                                                                                                                                                                                           linear
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                                                                                                                                           STANDARD;
                                             Thomas
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Pred. No. 2.46e+02;
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                                                                                                                                                           Patent No.
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                                                                                                                                                  GENERAL INFORMATION:
COMPUTER RÉADABLE FORM:
MEDIUM TYPE: Floppy disk
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Query Match 70.5%;
Best Local Similarity 50.0%;
Matches 8; Conservative
2049 RWSNTTYATHAAYGAR 2064
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LENGTH: '990 amin '7900'
TYPE
                                                                                                                         MOLECULE TYPE: protein JENCE 990 AA; 117190 MW; 5093687
                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 13-MAY-19:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: not relevant
                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Sterne, Kessler, Goldstein & Fox P.L.L.C
1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAY-1996
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                                                                       Score 67; DB 2; I
Pred. No. 2.46e+02;
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                                                      Indels
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Sequence 11, Application US/08752929 APPLICANT: YAZAWA, Kazunagi APPLICANT: YAMADA, AKIKO APPLICANT: KANDO, Seishi APPLICANT: KONDO, KIYOSI TITLE OF INVENTION: Gene C TITLE OF INVENTION: Enzyme TITLE OF INVENTION: Acid NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS CITY: Washington l, Application US/08752929 5798259 E: Foley & Lardner 3000 K Street, N.W., YAZAWA, Kazunaga STANDARD; : Gene Coding : Enzymes and I Acid Suite 500 for Eicosapentaenoic Acid Synthesizing Process for Production of Eiscosapentaenoic 2756 AA

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Best Local Similarity
Matches 9; Conser
                                                                           GENERAL INFORMATION:
APPLICANT: YAZAWA, KKZUNAGA
APPLICANT: YAMADA, AKIKO
APPLICANT: KAMADA, AKIKO
APPLICANT: KONDO, Kiyosi
TITLE OF INVENTION: Gene Codi
TITLE OF INVENTION: Eiscosape
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                             Sequence 11, Application US/08375709
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INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
JENCE 2756 AA; 292671 MW; 37455677 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,709
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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A S F I N E
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GCNWSNYTNATHAAYGAR 1566
                             COUNTRY:
ZIP: 200
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amir
                                                  STREET: 3000 K St
CITY: Washington
                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20-NOV-1996
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                                                                                                                                                                     No.
                             20007-5109
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                                                             E: Foley & Lardner 3000 K Street, N.W., Suite 500
                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                         2756 amino acids
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                            70.5%;
                                                                                                                                                                                                                                                 STANDARD;
                                                                                               Gene Coding For Eicosapentaenoic Acid
Synthesizing Enzymes and Process for Production of
Eiscosapentaenoic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 08/178,251
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Pred. No. 2.46e+02;
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Best Local Similarity
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                                                                                                                                                                                                                              Sequence 123, Application US/08933402
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                           Patent No.
GENERAL IN
                                                                                                                                                                                                             Sequence 123, Application US/08933402
                                                        ZIP: 20007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                             APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptide
TITLE OF INVENTION: Constrainit
TITLE OF INVENTION: Site
                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
  PRIOR APPLICATION DATA:
                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                      A S L
                                                                                                    STREET: Suite 500
CITY: Washington
         APPLICATION NUMBER: US/08/933,402 FILING DATE: 19-SEPT-1997
                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                      COUNTRY: USA
                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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                                                                                                                                                                                            INFORMATION:
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                                                                                                              Suite 500, 3000 K Street
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                                                                                                                        Foley & Lardner
                                                            Floppy disk
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Polypeptides That Include Conformation-Constraining Groups Which Flank A Protein-Protein Inter

Version #1

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1549 GCNWSNYTNATHAAYGAR 1566
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SEQUENCE CHARACTERISTICS:
LENGTH: 2756 amino
                                                                                                                                                                                                      | | :: : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
JENCE 2756 AA; 292671 MW; 37455677 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 14-MAY-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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50.0%;
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STANDARD;
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Pred. No. 2.46e+02
6; Mismatches
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RESULT
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Best Local 9
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APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Constraining
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-934-222-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 123, Application US/08934222
                                                                                                                        COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
                                                                                                                                                                                                                                                                                                                                                                              Sequence 123, Application US/08934222
Patent No. 5928896
                             PRILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA: 08/532,818
APPLICATION UNMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA: 0.5. 08/143,
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 03-MAY-PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: SU
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ICE 17 AA;
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           APPLICATION NUMBER: U.S. FILING DATE: 23-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Isacson, John P. REGISTRATION NUMBER: 33,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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; 1885 MW; 1336 CN;
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52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                 Polypeptides That Include Conformation-Constraining Groups Which Flank A Protein-Protein
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                                                                                                                                                                                                                                                           Lardner
3000 K Street NW
                       U.S.
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Pred. No. 3.00e+02;
5; Mismatches 4
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                       08/051,741
                                                        08/143,364
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         Query Match
Best Local S
Matches
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Best Local Similarity
Matches 10; Conser
                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 26 AA; 2950 MW; :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-942-245-472
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                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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3 GCNYTNYTNATHAAYGARG :
| | | : | | | : | : | : |
| 9 GCATCGTTCATTAATGAAG |
                                                                                                                                     CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7860
TELEFAX: (202) 293-7860
TELEX: 6491103
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                               STATE: D.C
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TYPE: amino acid
TOPOLOGY: linear
NCE 17 AA; 1885 MW; 1336
                                                                                                                                                                                                APPLICATION NUMBER: US/0
FILING DATE: 09-SEP-1992
                                                                                                                                                                                                                                                                                                      COUNTRY:
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REFERENCE/DOCKET NUMBER: 04
123:
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         h 69.5%;
Similarity 50.0%;
9; Conservative
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2100 Pensylvania
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ROGUSKA,
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Anthony
Michael
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        Score 66; DB 1; I
Pred. No. 3.00e+02;
6; Mismatches 3
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Pred. No. 3.00e+02
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. Avenue,
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e, N.W.
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Search completed: Wed Nov 24 02:29:25 1999 Job time: 23 secs.
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                                                                                                                                                                             STATE: CALIFORNIA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
COMPUTER READABLE FOR COMPATIBLE
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CAPPLICATION NUMBER: US/08/766,982
CILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
CHARME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-441
REFERENCE/DOCKET NUMBER: A-441
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
CLENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 224 AA; 24114 MW; 262738 CN;
                                                                                                                               Query Match 69.5%;
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                   L I N E Q
85 YTNATHAAYGARCARTG 101
:| ||:||:||:||
2 TTCATTAATGAACGATG 18
F I N E R
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59 CNWSNTTYTYAAYGARG 76
| :: ||: |::|:|:|
18 CATCGTTCATTAATGAAG 1
S F I N E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08766982
Patent No. 5948892
GENERAL INFORMATION:
APPLICANT: Wahl, Robert C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Analogs of Macrophage Stimulating TITLE OF INVENTION: Protein NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                      I N E Q
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                                                                                                                             Score 66; DB 2; Length 224; Pred. No. 3.00e+02; 5; Mismatches 2; Indels
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		Mean 6.442; Variance 3.042; scale 2.118  No. 1s the number of results predicted by chance to have greater than or equal to the score of the result being derived by analysis of the total score distribution.  SUMMARIES  Query  Query  Query  Description	em_h _ph in1 7:gb	Nmatch STD: Dbase 0; Query 0  Searched: 646147 segs, 1385953633 bases x 2  Post-processing: Minimum Match 0% Listing first 45 summaries	ption: (1-19) from US09 t Score: 19 1 CTTCATTAA comp: GAAGTAATT g table: TABLE default Gap 10	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd  MPSrch_nn n.a n.a. database search, using Smith-Waterman algorithm Run on: Sat Nov 27 12:37:31 1999; MasPar time 90.60 Seconds Tabular output not generated.	
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## ALIGNMENTS

RESULT 1 LOCUS LOCUS DEFINITION ACCESSION NID VERSION KEYWORDS SOURCE SOURCE TORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	AF034076 1314 bp DNA BCT 26-NOV-1997 Staphylococcus aureus UDP-N-acetylmuramoyl-L-alanine synthetase (murC) gene, complete cds. AF034076 1 G1:2642658 AF034076.1 G1:2642658 . Staphylococcus aureus Staphylococcus aureus Eubacteria; Firmicutes; Low G+C gram-positive bacteria; Bacillaceae; Staphylococcus. 1 (bases 1 to 1314) Lowe,A.M. and Deresiewicz,R.L. Cloning and sequencing of Staphylococcus aureus murC, a gene involved, in cell wall biosynthesis Unpublished 2 (bases 1 to 1314) Lowe,A.M. and Deresiewicz,R.L. Direct Submission Submitted (11-NOV-1997) Channing Laboratory, Brigham and Women's Hospital and Harvard Medical School, 181 Longwood Ave, Boston, MA 02115, USA
JOURNAL	sequencing of Staphylococcus aureus murC, a cell wall biosynthesis
AUTHORS TITLE	Lowe, A.M. and Deresiewicz, R.L. Direct Submission
JOURNAL	Submitted (11-NOV-1997) Channing Laboratory, Brigham and Wo Hospital and Harvard Medical School, 181 Longwood Ave, Bost 02115, USA
FEATURES Source	Location/Qualifiers 11314
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gene	11314 . /gene="murc"
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	<pre>//codon_start=1 //transl_table=1 //product="UDP-N-acetylmuramoyl-L-alanine synthetase" /protein_id="AAB87090.1"</pre>

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Best Local Similarity 94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (28-SEP-1994) Terence R. Whitehead, National Center for Argicultural Utilization Research, ARS, USDA, 1815 N. University Street, Peoria, IL 61604, USA
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QPFGIVPQETPVSIEGNVFTTELEPTTFAVYKFTKK"
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NKGIKILPEDANNIKEDMVVIQGNAFASSHEEKARHQMKLDVVSYNDELGQIIDQYT 
SVAVTGAHGKTSTTGLLSHVMNGDKKTSFLIGGTGRAHQMKLDVVSYNDELGCEYRRHELS 
YKPDYALMTNLDEDHPDYFKDINDPDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPI 
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LEKLDVTNIKEALETFGGVKRRENETTIANQVIVDDYAHHPREISATIETARKKYPHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
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                                                                                          gene
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                                                      CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsia prowazekii.
Rickettsia.prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.

1 (bases 1 to 279110)
Andersson,S.G., Zomorodipour,A., Andersson,J.O.,
Sicheritz-Ponten,T., Alsmark,U.C., Podowski,R.M., Naslund,A.K.,
Eriksson,A.S., Winkler,H.H. and Kurland,C.G.
Eriksson,A.S., Winkler,H.H. and Kurland,C.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-NOV-1998) S.G.E. Andersson, Siv.Andersson@molbio.uu.se, Dept. of Molecular Biology, University of Uppsala, Husargatan 3, Uppsala, S-751 24, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 396 (6707), 133-140 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andersson, S.G.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99039499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ235272.1 GI:3861033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ235272 AJ235269
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Similarity 100.0%;
16; Conservative
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                                                                                            (TTG)"
                                                      .3091)
                                                                                                                      .1265)
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WVIYKTPFETLIIACSFTILGIPVYYGWYRLMNRIKL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (nifU)"
     Db 101063 GCATCGTTTATTAATGAA 101080
                                                                                                                                                                      Note: remainder of
                                                       Query Match 84.2%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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                                                                                                                                                                      annotations omitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(7931. .8125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEEARSSIRISLSHTNTISDIKAFIKAFEEIYEYKSSCNHCI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement
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7931.

.8125)

SdS gene CDS gene

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                                                                                                                                                                                                                                                                                                                                                   PROTEIN HOMOLOG (spl1)"
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SEIFKONEVILTPEIIKKYFADNLLYAPNLFIFFGTPVIILFWFVTFLLERSIIVLLV
YGLANLLTTKTSIQTSIRLVMFSSGIPIILQPVIIILIPELSILIQLLQMFTTFLVFV
AILQINKSLSHI"
                                                                                                                                                                                           complement(9681.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'protein_id="CAA14941.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (8277. .9143)
                                                                                                                                             .10349)
                                                                                                                                                                                           .10349)
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CDS gene

Score 16; DB 17; Pred. No. 3.46e+01;

Length 279110;

Mismatches

0;

Gaps

0;

CDS gene

Сþ

19

GCATCGTTCATTAATGAA

δÃ

1 CTTCATTAATGAACGAT 17

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BASE COUNT
ORIGIN
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AUTHORS
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ORGANISM
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                                               Query Match
Best Local S
Matches 1
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                                                                                                                                                               gene
                                                                                                                                                                                                                                               tRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intron
                 366 CTTCATTAATTAACGAT 382
                                             / Match 78.9%;
Local Similarity 94.1%;
nes 16; Conservative
S.pombe
M57699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe DNA.
Schizosaccharomyces pombe
Schizosaccharomyces pombe
Eukaryotes; Fungi; Ascomycota;
Archaeascomycetes; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence repeats
Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1306-1310 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clustered tRNA genes in Schizosaccharomyces pombe centromeric DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA-Val-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transfer RNA; transfer RNA-Ala; transfer RNA-Ile-I; transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M57699.1
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Ile-1,Ala-1
                                                                                                                                                                                                                              /gene="Ala-tRNA"
complement(1123.
/gene="Ile-tRNA"
                                                                                                                            /anticodon=(pos:1157...complement(1123..1196)
/gene="Ile-tRNA"
176 c 232 g 5
                                                                                                                                                                                                                                                                                                              /note="codon recognized: GCT"
/product="tRNA-Ala"
                                                                                                                                                                                              /note="codon recognized: CTT"
/product="tRNA-Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Schizosaccharomyces pombe"
/db_xref="taxon:4896"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:173497
                                                                                                                                                                                                                                                                                          anticodon=(pos:1010.
                                                                                                                                                                                                                                                                                                                                                                                                'gene="Val-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                             'note="does not fit consensus"
'cons_splice=(5'site:no,3'site:no)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="Val-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oin(233. .270,281.
gene="Val-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="Val-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="tRNA-Va.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="codon recognized: ATC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="Val-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /anticodon=(pos:267. .269,aa:Val)
|oin(233. .270,281. .315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="codon recognized: GTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="Val-tRNA"
                                                                                                                                                                                                                                                                                                                                               gene-"Ala-tRNA"
                                                                                                                                                                                                                                                                                                                                                                             number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="tRNA-Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nticodon=(pos:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clarke, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p DNA
and Val-1 tRNA genes.
                                             Score 15; DB 27;
Pred. No. 1.32e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Carbon, J.
                                                                                                                                                                                                                                               .1196)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .37, aa: Val)
                                                                                                                               540 t
                                                                                                                                                                                                                                                                                               .1012,aa:Ala)
                                                                                                                                                                               .1159,aa:Ile)
                                                                            Length 1489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-APR-1995
                                             0
                                             Gaps
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DEFINITION
ACCESSION
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AUTHORS
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                                                                                                               BASE COUNT
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                                           Query Match
Best Local Similarity
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MEDLINE
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1108 ATCGTTAATTAATGAAG 1124
                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1489)
Kuhn, R.M., Clarke, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 APR-199 Schizosaccharomyces pombe Ile-1, Ala-1 and Val-1 tRNA genes. M57698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Centromere cen2 tRNA cluster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91142161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaeascomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M57698.1
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                                                                                                               540
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A.
                                                                                                             /number=1
232 c
                                                                                                                                           /note="does not fit consensus"
/cons_splice=(5'site:no,3'site:
complement(1220. .1257)
/gene="Val-trna"
                                                                                                                                                                                                                                        /anticodon=(pos:1209. .1211,aa:Val)
complement(join(1175. .1210,1220. .1257))
/gene="Val-tRNA"
                                                                                                                                                                                                                                                                                                                                                                   /anticodon=(pos:35. .37
complement(1175. .1210)
/gene="Val-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(1175. .1210,1220.
/gene="Val-tRNA"
                                                                                                                                                                                                                                                                                                                        complement(1175. .1257)
/gene="Val-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="codon recognized: ATT"
/product="tRNA-Ile"
/anticodon=(pos:328. .330,aa:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Ala-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Ala-tRNA"
                                                                                                                                                                                                            ′gene≖"Val-tRNA"
                                                                                                                                                                                                                                                                                        /note="codon recognized: CGA"
/product="tRNA-Val"
                                                                                                                                                                                                                                                                                                                                                                                                                     /product="tRNA-Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="Ile-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:4896"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product="tRNA-Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="Ile-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anticodon=(pos:475.
omplement(441. .514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:173496
                                                                                                                                                                                                                                                                                                                                                                                                                                     note="codon recognized: CTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note≖"codon recognized: CAT'
                                              78.9%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1489 bp
                             Score 15; DB 27;
Pred. No. 1.32e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Carbon, J
                                                                                                          176 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B-repeat region 3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                    37,aa:Val)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .477,aa:Ala)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 (4),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .330,aa:Ile)
                                                                                                             541 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transfer RNA-Ile-I; transfer
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                                                             Length 1489;
                                                                                                                                                                           :no)
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1257))
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                             0;
                             Gaps
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17 ATCGTTCATTAATGAAG 1

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AUTHORS
TITLE
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LOCUS
DEFINITION
ACCESSION
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                                                        trna
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Kuhn,R.M., Clarke,L. and
Clustered tRNA genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transfer RNA; transfer RNA-Ala; transfer RNA-Glu-II; transfer RNA-IIe-I; transfer RNA-Lys-I; transfer RNA-Val-I. Schizosaccharomyces pombe DNA. Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSPTGIVAC 2303 bp
S.pombe Lys-1, Ile-1,
M57700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Centromere cen2 tRNA cluster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence repeats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Fungi; Ascomycota;
Archaeascomycetes; Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Natl. Acad. Sci. U.S.A.
               complement(join(1562. .1598,1608. .1645))
/gene="Val-tRNA"
/note="codon recognized: TAT"
                                                                                         /anticodon=(pos:1596...complement(1562...1598)
/gene="Val-trNA"
                                                                                                                                                                                                        /anticodon=(pos:863.
complement(829. .902)
/gene="Ala-tRNA"
                                                                                                                                                                                                                                                                                                   complement(829. .902)
/gene="Ala-tRNA"
                                                                                                                                               /note="codon recognized:
/product="tRNA-Val"
                                                                                                                                                                                      complement (1562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cons_splice=(5'site:no,3'site:no)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:173498
   /product="tRNA-Val'
                                                                                                                                                                                                                                                                /note="codon recognized: CAT"
/product="tRNA-Ala"
                                                                                                                                                                                                                                                                                                                                                                           /anticodon=(pos:716.
                                                                                                                                                                                                                                                                                                                                                                                              /note="codon recognized: ATT"
/product="tRNA-Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Ile-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="does not fit consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /anticodon=(pos:337. .339
join(303. .340,349. .384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Lys-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Schizosaccharomyces
/db_xref="taxon:4896"
join(303.340,349.384)
/gene="Lys-tRNA"
                                                                                                                                                                                                                                                                                                                                          'gene="Ile-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="Lys-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="Lys-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="tRNA-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="codon recognized: AAG; precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anticodon=(pos:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="tRNA-Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="codon recognized: TAT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Lys-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lys-trna"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Carbon, J. in Schizosaccharomyces pombe centromeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA PLN
Ala-1, Val-1 and Glu-2 tRNA
                                                                                                                                                                                      .1645)
                                                                                                                                                                                                                                              .865,aa:Ala)
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                                                                                                                                  .1598,aa:Val)
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                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-JAN-1994) Samuel L. Stanley, Washington School of Medicine, Medicine/Infectious Diseases, 660 Avenue, St. Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Entamoebidae; Entamoeba.

1 (bases 1 to 2639)
Yang,W.; Li,E., Kairong,T. and Stanley,S.L. Jr.
Entamoeba histolytica has an alcohol dehydrogenase homologous
the multifunctional adhE gene product of Escherichia coli
Mol. Biochem. Parasitol. 64 (2), 253-260 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Entamoeba histolytica mRNA, complete cds.
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                                                                                                                                                                                  /note-"The derived amino acid sequence of EhADH2 is homologous (48% identity) to the trifunctional enzyme product of the E. coli adhE gene described by Goodlove al., Gene 85:209-214, 1989 (Swiss Prot Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="does not fit consensus"
/cons.splice=(5'site:no,3'site:no)
complement(1608. .1645)
/gene="Val-trna"
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1599. .1607
/db_xref="g1:488430"
/translation="msTQQTmtvdehinqlvrkaqvalkeylkbeytqekidyivkka
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SVAALDQHQALAAAveeTGRGIFEDKATKNIFACEHYTHEMBHAKTYGIINVDPLYG
ITEIAEPVGVVCGVTPVTNPTSTAIFKSLISIKTRNPIVFSFHPSALKCSIMAAKIVR
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complement(2086..2157)
/genee-"Glu-tRNA"
375 c 321 g 787 t 1
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/gene="Glu-tRNA"
/note="codon recognized:
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                                                                     /evidence-experimental /product-"alcohol dehydrogenase /protein_id="ALA81906.1" /db_xref="PID:9488430"
                                                                                                                                                                                                                                                                                                                    /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
                                                                                                                                                                                                                                                                /standard_name="EhADH2"
                                                                                                                                                                                                                                                                                               /db_xref="taxon:5759"
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94.1%;
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Pred. No. 1.32e+02;
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University S. Euclid

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DAA IAAGAPEKCIQWIEEFGGIEASNKLIMNHPGVAT ILATGGNAWKAAYSSGKPALGV GAGNVPTY IEKTONI KQAANDVVMSKESDNGMICASEQAAI IDKEIYDQVVEEMKTLG AYFINBEEKAKLEKFWEGVNAYSADVNNAKRINPKCPGMSPQWFAEQVGIIVVPEDCNII CAVCKEVGPNEPLTREKLSPVLAILKAENTQDGIDKAEAMVEFNGRGHSAAIHSNDKA

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X77132.1
alcohol de
Entamoeba
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Bruchhaus, I. and Tannich, E.
Bruchhaus, I. and Tannich, E.
Purification and molecular characterization of the NAD(+)-dependent acetaldehyde/alcohol dehydrogenase from Entamoeba histolytica acetaldehyde/alcohol dehydrogenase from Entamoeba histolytica acetaldehyde, J. 303 (Pt 3), 743-748 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-JAN-1994) I. Bruchhaus, Bernhard Nocht Institute for Tropical Medicine, Bernhard-Nocht-Str. 74, 20359 Hamburg, FRG
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                /db_xref="SWISS-PROT:Q24803"
/translation="MANSTQQMTVDEHINQLVAKAQVALKEYLKPEYTQEKIDYIVK
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VRDAAIAAFDENCIQWIEFGGIEASNKLMNHFGVATILATGGVAMVKAAYSSCKPAL
GVGAGNVPTYIEKTCNIKQAANDVVMSKSFDNGMICASEQAAIIDKEIYDQVVEEMKT
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NIKKLADRRNNLQWFRVPPKIFFEPHSIRYLAELKELSKIFIVSDRMMYKLGYVDRVM
DVLKRRSGNEDEIEIFILDVEPDPSIGTVQKGLAVMNTFGPDNIIAIGGGSAMDAAKIM
LLYEHPEADFFAMKQKFIDLRKRAFKFPTMGKKARLICIPTTSGTGSEVTPFAVISDH
ETGKKKYPLADYSLTPSVAIVDPMFTMSLDKRAIADTGLDVLVHAFEAYVGVMAMBYDT
GLAREAVKLYPENLLKSYNGDLEAFEKMHNAYTIAGMAFASAFLGMDHSMAHKYGAF
HLPHGRCVAVLLPHVIRYNGQKPRKLAMWPKYNFYKADQRYMELAQMVGLKCNTPAEG
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                                                                                                                                                     /product="NAD--dependent alcohol dehydrogenase"
/protein_id="CAA54388.1"
/db_xref="PID:9443985"
/db_xref="GI:443985"
                                                                                                                                                                                                                                                                                     /gene-"ADH2"
/EC_number-"1.1.
                                                                                                                                                                                                                                                                   /note="alcohol dehydrogenase"
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JGAYF I NEEEKAKLEKFMFGVNAYSADVNNARLNPKCPGMSPQWFAEQVG I KVPEDCN
                                                                                                                                                                                                                                                /codon_start=
                                                                                                                                                                                                                                                                                                                                                         /gene="ADH2"
                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="trophozoite"
/clone_lib="lambda ZAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:5759"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="pathogen"
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Eukaryota; Fungi; Ascomyce
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Takahashi,K., Murakami,S., Chikashige,Y., Funabiki,H., Niwa,O. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               centromere; centromere 2; RNA-Ile; transfer RNA-Val.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-JUN-1992) K. Takahashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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1 (bases 1 to 3044)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lanagida, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fission yeast.
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                                                                                                                                                     1077
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· GGVEAFAKACEELMKATETITGFKQANIDEAAWMSKVPEMALLAFEDQCSPANPRVPM
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LLNIKRLADRRNNLQMFRVPPK.IFFEPHSIRYLRELKELSKIE IVSDRMMYKLGYVDR
VMDVLKREASMEVEIEIFIDVEEDPSIGJUVGKLAVMNTFGPDNIIAIGGGSAMDAKI
MRLLYEHPEADFFAMKQKFIDLRKRAFKFPTMGKKARLICIPTTSGTGSEVTPFAVIS
                                                                                                                                                                                                                    /product=":
2003. .207
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1 387 C 492 g
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                                                                                                                                                /product="transfer RNA-Val"
486 c 414 g 1058 t
                                                                                                                                                                                     /product="transfer RNA-Ala"
2676. .2750
                                                                                                                                                                                                                                                                                                                                                          /organism-"Schizosaccharomyces pombe"
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                                                                                                                                                                                                                                                                    note="homology with dhia"
                                                                                                                                                                                                                                                                                                       /chromosome="II"
                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4896"
                                                                                                                                                                                                                                                                                                                                            /strain="972"
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94.1%;
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                                                               Score 15; DB 27;
Pred. No. 1.32e+02;
0; Mismatches 1
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Pred. No. 1.32e+02;
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L14925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Cell Biology, University of Chicago,
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (28-APR-1993) Christopher C. Bauer, Molecular Genetics and Cell Biology, University of Chicago, Chicago, IL 60637 USA
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Anabaena sp.
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llarity 94.1%;
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                                                                                                                                                                                                                                                          /note="heptamers (CCCCAGT) x /rpt_type=tandem 3677...3710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKIIGEGTDNYAQGYFVYDSKKSGSMTVSHLRFGSQPIRSTYLIDQANFIGCHHWAFLERIEVLKRLLAATILLNSPYNAATVWEBULPLKVBLQILDKQLKLLVINANQVARDSGMGGRINTIMQVCFFALAGVLPEVQAILAKIKQALEKTYGKKGVEVVRMULQAVDQTLENLHEVKIPLEEKGKWIDEEALLSNQSPESTSAPKFVRDVLGKIMVWQGDDLDVSTLPPDGTFPTGTAKWEKRNVAQEIPVWDTDLCVQCSKCVMVCPHAAIRAKVYQPSELENAPPTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSQTFATIDGNEAVARYAYKLNEVIAIYPITPSSAMGEWADAWM AEGRPALWAYKLNEVIAIYPITPSSAMGEWADAWM AEGRPALWAYKOOGLILLMIENLYKIGG ELTSAWCHVAARSLATHALSIFGBHSDVMAARGTGFAMLCSASVQESHDFALIAHAFLIDTRVSFLHFFDGFRTSHEVQKYELLADDDVRSLINEDKIFAHRARALTEDSPLLRGT LQTRVSFLHFFDGFRTSHEVQKYELLADDDVRSLINEDKIFAHRARALTEDSPLLRGT AQNPDVFFQAREGANPYYNACPAIVQGIMDKFFGERTGRYYQIYEYHGASDADRLIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSYDAKDRDFANQKFTIQVAPEDCTGCAICVNYCPAKNKSEPSIKAINMANQLPIREQ
ERDNWDFFINLPNPDRRNLKLNQIRQQQLQEPIFEFSGACAGCGETPYYKLLTQIFGD
RSYIANATGCSSIYGGNLPTTPWTKNNDGRGPAWSNSIFEDNAEFGFGYRLSLDKQAE
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DNLAQATPKNHFTIGINDDVTHTSLEYDPSFSTEPDNVVRAMFYGLGSDGTVGANKNS
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EAFDGPSIIIAYSHCIAHGINMTTGMNQQKALVESGRWLLYRYNPLLQEQGKNPLQLD
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KIQNLKSLADYLVKKSVWIIGGDGWAYDIDFGGIDHVIASGRNVNILVMDIEVYSNTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="nitrogen fixation protein"
/protein_id="AAC36818.1"
/db_xref="PID:9289139"
                                                                                                                                                                                  /note="heptamers [(A/G)GGTAAT] x 5"
/rpt_type=tandem
835 c 907 g 1025 t
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/strain="PCC 7120"
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7120) nitrogen fixation protein (nifJ) gene.
                                                                  Score 15; DB 18; Le
Pred. No. 1.32e+02;
0; Mismatches 1;
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YSCRAD2G 3919 bp 1
S.cerevisiae RAD2 gene, 0
M10275 M13389
g172328
M10275.1 GI:172328
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Triticum aestivum leaf rust resistance kinase Lr10 (LRK10) gene, US1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 3878)
Feuillet,C., Schachermayr,G. and Keller,B.
Molecular cloning of a new receptor-like k
Lr10 disease resistance locus of wheat
Plant J. 11 (1), 45-52 (1997)
97177795.
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Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-MAR-1996) Catherine Feuillet, Plant Breeding, Swiss Federal Research Station for Agronomy, Reckenholzstr. 191, Zurich
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NIVRLLGFCSEGMRRALIYEFMPNESLEKYIFSDDSNIFQNLLVPEKLLDIALGIARG
MEYLHQGCNQRILHFDIKPHNILLDYNFNPKISDFGLAKLCARDQSIVTLTAARGTMG
                                                                                                                                                                                                                                                                                                                                   NGEELALTLETTQEEKDKVRQLAMVALWCIQWNPRNRPSMTKVVNMLTGRLQSLQMPP
KPFVSSENELMS"
. 833 c 831 g 1072 t
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/translation="MSKLLVIALLLLPLINHGIYLATAWDDQDFFKYCPPSKCSQHGP
MIRYPLCLESSNTSSSSSGGCAGRSIWKLACSGQDTILVHPVLGPYSVSAIDYRRSSM
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join(619. .1432,2270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                                                                                                                                                YIAPELYSRNFGGVSYKADVYSFGMLVLEMVSGRRNSDPRIGSQDDVYLPEWIYEKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MFYNFTETAKKIPSFAETAVSWDEGDCRECELSGRRCAFSSQRDREFCMPDPHGSHIK
VIAATSSVAAFVALLLTVATVLYLSLKTRYNAEIHMKVEMFLKTYGTSKPTRYTFSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KITPLVDPCLVLQQKLIISRSSSSPQVDVINDEKPSFDENFFESSSATIVHCSREFTP
AAAHADSIAGPVSCLSNTTHFFYLVNSDEDMSILPLDCKVVPVSDRGGISLPHMLKDQ
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519. .3487
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                                                                                                                                                                                                                                                      78.98;
94.18;
                                                                                                                                                                                                                                   Score 15; DB 28; 1
Pred. No. 1.32e+02;
0; Mismatches 1;
                                                             complete cds.
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JOURNAL
MEDLINE
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SOURCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                praft entry and computer-readable copy for [1] kindly provided be C.Nicolet, 09-DEC-1985. Draft entry and sequence in computer readable form for [2] kindly provided by C.Nicolet, 08-OCT-1986. The unidentified reading frame (positions 534-647) overlaps the start of the RAD2 coding region. The translation of the RAD2 protein might reinitiate from the 'atg' codon at position 652, encoding a RAD2 protein missing the 26-amino terminal residues. polyadenylation signal is present at positions 3532-3537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Madura, K. and Prakash, S.
Nucleotide sequence, transcript mapping, and regulation of the gene of Saccharomyces cerevisiae
J. Bacteriol. 166 (3), 914-923 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (strain 7799-4B)
Saccharomyces cerevisiae (strain 7799-4B)
Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 3919; 1 to 3919)
Nicolet,C.M., Chenevert,J.M. and Friedberg,E.C.
The RAD2 gene of Saccharomyces cerevisiae: nucleotide sequence
transcript mapping
Gene 36 (3), 225-234 (1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAD2 gene; RAD2 protein.
Saccharomyces cerevisiae
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                                                                                                                                                 /gene="RAD2"
562. .3841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="RAD2"
527. .3841
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/citation=[2]
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   /protein_id="AAA66928.1"
                  codon_start=1
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574. .3669
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558. .3841
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548. .3841
                                                                                                                                                                                                                                                            'gene="RAD2"
                                                                                                                                                                                                                                                                                                             /db_xref="PID:g808848"
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                                                                                                                citation=[2]
                                                                                                                                                                                                                                                                                              translation="MKKSIFGRTPNFRHGCAFILGYCRSYGKTGQAGILGR"
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(clone: pNF2005)
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) DNA.
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ORIGIN
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ACCESSION
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Best Local
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z73043.1
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Similarity 89.5%;
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/db_xref="SGD:L0001556" complement(366. .3461) /gene="RAD2"
                                                             complement(366. .3461)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3445.
                                                                                                                                            Location/Qualifiers
                                                /gene="RAD2"
                                                                                /chromosome="VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:1323469
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EDNSLKIVRHESSNATTAPQKRSNRSEDEGCDSDECEWEEVELKPKNVKFVEDESLKA
RRLPYMQGLNAMGSKSFLDKRHDQASPSKTTPTMTISRISVEDDDEDYLKQIEEIEM
MEAVOLSKMEKKPEADDKSKIAKPUTSKGTEARPDIVOGGLLGAQPDSKOPHIVTNLN
SKSESVIKRTSKTVLSEFRPPSQQEDKGAILTEGEQNLNFISHKIPQFDFNNENSLLF
QKNTESNVSQEATKEKSPIPBMFSWESSTASQQLYNPYNTTNFVEDKNVRNEDGESGAE
TTNKGSSYELLTGLNATEILERESEKESSNDENKDDDLEVLSEELFEDPPTKSQISKE
AEDNDSRKVESINKEHKKPLIFDYDFSEDEEDNIVENNIKEQEEFDTFKNTTLSTSAE
RNVAENNFVEDELFEQQMKDKDSDEVTMDMIKEVDELLSREGIPYITAPMBAEAQCA
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QEGNAVKNSHITGFFRRICKLLYFGIRPVFVFDDGVPVLKRETIRQRKERRQGKRESA
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SNKTFEKLMNSINGDGLEDIDLDTINPASAEFEELPKATQYLILSSLRLKSRLRMGYS
                                                   ELLQLNLVDGIITDDSDVFLFGGTKIYKNMFHEKNYVEFYDAESILKLLGLDRKNMIE
LAQLLGSDYTNGLKGMGPVSSIEVIAEFGNLKNFKDWYNNGQFDKRKQETENKFEKDL
RKKLVNNEIILDDDFPSVMYYDAYMRPEVDHDTTPFVMGVPDLDMLRSFMKTQLGWPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEQLETIFPNSMDFSRFQIDMVKRRNFFTQKLINTTGFQDGGASKLNEEVINRISGQK
SKEYKLTKTNNGWILGLGANDGSDAQKAIVIDDKDAGALVKQLDSNAEDGDVLRWDDL
EKSDEILIPLIRDVNKRKKKGKQKRINEFFPREYISGDKKLNTSKRISTATGKLKKRN
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/citation=[1] 1355 a 653 c 908 g 1003 bp upstream of NdeI site [1]; c Score 15; D Pred. No. 1. 0; Mismatc Mismatches DB 27; 1.32e+02; 2; 3 t chromosome 7 Length 3919; Indels [1]. 0, Gaps 0

Direct Submission
Submitted (14-MAY-1996) Data collected by MIPS on behalf of the European yeast chromosome VII sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org Panzeri,L., Agostoni Carbone,M.L., Melchioretto,P., Plevani,P., Martegani,E., Vanoni,M., Carignani,G., Clemente,M.L., Frontali, Fabiani,L., Marconi,A., Ruzzi,M. and Saliola,M. Unpublished Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales; Agostoni Carbone,M.L., Panzeri,L., Melchioretto,P., Carignani,G., Feroli,F., Frontali,L., Mazzoni,C., Rinaldi,T. and Ruzzi,M. Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 603) /organism="Saccharomyces /db\_xref="taxon:4932" DNA VII reading cerevisiae" frame ORF YGR258c Frontali, L.,

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567 CTTCATGAATGAACGAAGC 585
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                                               Direct Submission
Submitted (20-MAY-1997) Genetics, Groningen Biomolecular Sciences
Submitted (20-MAY-1997) Genetics, Groningen Biomolecular Sciences
                                                                                                                                                                                                                                          2 (bases 1878 to 2423)
Sanders, J.W., Venema, G., Kok, J. and Leenhouts, K.
Identification of a sodium chloride-regulated promoter in
Lactococcus lactis by single-copy chromosomal fusion with
                                                                                                                                                                                                                                                                                                                                                                A chloride-inducible acid resistance mechanism in Lactococcus lactis and its regulation Mcl. Microbiol. 27 (2), 299-310 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF005098 5565 bp DNA BCT 23-MAR-1998 Lactococcus lactis RNAseH II (rnhB) gene, partial cds, positive regulator GadR (gadR), GadC (gadC) and glutamate decarboxylase (gadB) genes, complete cds.
                                                                                                                      3 (bases 1 to 5565)
Sanders, J.W., Venema, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eubacteria; Firmicutes; Low G+C gram-positive bacteria; Streptococcaceae; Lactococcus.

1 (bases 1 to 5565)

Sanders, J.W., Leenhouts, K., Burghoorn, J., Brands, J.R.,
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                                                                                                                                                                                                                        reporter gene
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                         Biotechnology Institute, Unen 9751 NN, The Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                Kok, J
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SKSESVIKRTSKTVLSEFRPSOGEDKGAILTEGEQNLMFISHLIPOFONNENSLLF
OKNTESNVSOBATKEKSPIPEMPSWESSTASOOLYNPYNTTNIFVEDKNYNEDESGAL
TTNKGSSYELLTGLNATEILERESEKESSNDENKDDDLEVLSEELFEDVPTKSQISKE
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SNKTFEXLMNSINGDGLEDIDLDTINA,SAEFEELPKARQYLILSSLRLKSKLKKGYS
KEQLETIFPNSMDFSRFOIDMVKRHFFTQKLHTTGFQDGGASKLEEVINRISQK
SKEYKLTKTNNGWILGLGANDGSDAQKAIVIDDKDAGALVKQLDSNAEDGDVLRWDDL
EDNSLKIVRHESSNATTAPQKRSNRSEDEGCDSDECEWEEVELKPKNVKFVEDFSLKA
ARLPYMGQSLNNAGSKSFLDKRHDQASPSKTTPTMRISRISVEDDDEDYLKQIEEIEM
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RNVAENAFVEDELFEQQMKDKRDSDEVTMDMIKEVQELLSRFGIPYITAPMEAEAQCA
ELLQLNLVDGIITDSDVFLFGGTKIXKNMFHEKNYVEFYDAESILKLLGLDRKNMIE
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QEGNAVKNSHITGFFRRICKLLYFGIRPVFVFDGGVPVLKRETIRQRKERRQGKRESA
          Location/Qualifiers
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RKKLVNNEIILDDDFPSVMVYDAYMRPEVDHDTTPFVWGVPDLDMLRSFMKTQLGWPH
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/db_xref="PID:g1323470"
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/codon_start=1
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Pred. No. 1.32e+02;
Nismatches 2;
                                                                                                                           Kok, J. and Leenhouts, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="gadR"
1084. .1089
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1095. .1925
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/note="RnhB; similar to Escherichia coli paacou **"
                                                                   antiporter; Functions in glutamate dependent acid stre resistance. Expression induced by chloride and at low Homologue of Shigella flexneri GadC" (codon_start=1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FERIDLMLEEMQVPLSEYELI VNNFMPNFQEFFI LELEKAEFSQNRDKIKELYSEVKE
TGNHLLTVTVKTKLGNISQTEVKEIEAYICNIEEMGYFEUTLFVEVSDYLNVNQLELL
LENEDDKRCEMVKCRVLKYRRRLLQIAVKSVAIVAAKGERKKAENILEMTKKYRTYGVDU
YSEVLRHLARAII I FNFENAEIGEEKINVALEI LEEFGGKKIKEFYQNKMEKYLKRSI
                                                                                                                                                                                                                                                                                                                                         /gene="gadC"
1987. .1992
                                                                                                                                                                                                                                                                                                                                                                                                                  /note functions as terminator; dependent transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"positive regulator GadR"
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979. .1966
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                                                                                                                                                                   2069. .3580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lactococcus lactis"
/strain="MG1363"
/db.xref="rtaxon:1388"
/map="between ldh and leu-ilv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene=
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AEKIDEVNIYEATKIAMIQAVSKLSLKPEHLLIDAMVLDLPIAQTKIIHGDARSASIA
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                                                                                                                                                                                                                                                                                                                     'gene="gadC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref="GI:2352485"
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.969
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. .946
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.1967
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KEYWORDS SOURCE ORGANISM

VERSION ACCESSION RESULT LOCUS

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BASE COUNT ORIGIN

Query Match Best Local

Matches

REFERENCE AUTHORS

REFERENCE AUTHORS TITLE

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                                                                                                                                                                 9212880
M18060.1
                                                                                                                                                                                                           Chicken vitellogenin M18060
Phasianidae; Phasianinae; Gallus
1 (bases 1 to 5791)
                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
                                                                                              Gallus gallus
                                                                                                                         Chicken DNA.
                                                                                                                                          vitellogenin.
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LWFLPVALCAARMATVEGWKNGGIFSWYSQTLCERFGFBAIFFQWFQTITVGFVMYIYF

SVILFGLAAAYFIGGNEDLIKFIGLLIFWGLFFSQLGFGPRAKLYKAGFTVGFUIY

SVILFGLAAAYFIGGNEDLIKFIGLLIFWGLFFSQLGFTLAYMGVEASASHIN

ELENPKRNYPLAMILLVILAISLDAIGGFSVAAVIPOKELSLSAGVIQTEQFLILHFN

HHLGMLVKVIALMIAFGVMGEVSSWVVGPSRGMFAAAQRGLLPKFLRKTNTHEVPVPL

VMIQGIIVTLWGAVLTFGGGGNNLSFLVAISLTVVIXLVGYLLFFIVKTVLXKQNL

KRTYNVPGKIIGKTILAGIGFELLSIFALFISFVPPASIAKNETHTYQMILLISFVVTA

KRTYNVPGKIIGKTILAGIGFELLSIFALFISFVPPASIAKNETHTYQMILLISFVVTA
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/translation="IPVANVLAGAGILGVALGFAGRDLVADIINGFFIIVEHQINVAD
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DENISEKKAQIIEVNANYPQVKYLGIINIEDKLFLRTSLTAPLSKITPLKMEILDKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="g1:2352487"
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MIADLWNASEKGKIYGTSTIGSSEACMLGGMAMKFSWRKRAEKLGLDINAKKPNLVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="glutamate dependent acid stress resistance" /note="expression induced by chloride and at low pH; similar to Synechocystes sp. GadB"
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YGFDGYKAIHERTHKVAMYLAEEIEKTGMFEIMNDGAQLPIVCYKLKENSNRGWNLYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="glutamate decarboxylase"
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/db_xref="GI:2352486"
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94.18;
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Comparison of the organization and fine structure of a chicken and a Xenopus laevis vitellogenin gene
a Xenopus Chem. 262, 15377-15385 (1987)
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SLISAGASLWIHNENQGFALAAPGHGIDKLYFDGKTITIQVPLWMAGKTCGICGKYDA
ECEQEYRMPNGYLAKNAVSFGHSWILEEAPCRGACKLHRSFVKLEKTVQLAGVDSKCY
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SACPKEALQPIHDLADERISGGEDKNKLALKCIGNMGEPASLKRILKELPISSSAA
DIPVHIQOIAITALKKIJAKKDENYGGYLIQILADGSLPPEVENMACAU TETRRALA
DITYHTOLATITALKIJAKDENYGGYLIQILADGSLPPEVENMACAU TETRRALA
LITTIANVAMKESKTNMQVASFVYSHKKSLSKSRLPFMYNISSACNIALKLLSPKLDS
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GIRVEGLADVIMKRNLPFAEYPTYKQIKELKSALOGWEPSAIISKLMANSAGSVADLVEV
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GGIPLENGSYTTALARAAVSVEEKMTPPLTGDFRLSQLLESTMOIRSDLKPSLYVHTV
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ATMGVNTEYFOHAVEIGGEGVQTRMPMKFDAKIDVKLSHLKSTNPCREETEIVGTHK
ATMGVNTEYFOHAVEIGGEGVGTHRANGFDSMPRKOSH
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RSLGKAGVRLSSKLEISGLPENAYLLKVRSPQVEEYNGVWPDDDFTRSSKLTQVISSG
FTRLFKFEYSGSRIGNIYAPEDCPDLCVNIVRGILNMFQMTIKKSQNVYELQEAGIG
ICHARYVIQEDKNSRIYVTRTVDLNNCQEKVQKSIGMAYIYPCPVDVMKERLTRGTT
AFSYKLKQSDSGTLITDVSSRQVYQISPFNEPTGVAVMEARQQLTLVEVRSERGSAPD
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APQAVAYTVKGGWDCRDYKVSTELVTGRFAGHPAAQVLEWFVEVV
PGAAFMLGFSERMDKHSFRAGARWVALTSPRTCDVVVKLEWFVEVV
PRIPASELQPPIMNVFAEAPSAVLENLKARCSVSYNKIKTENEVKFNYSMPANCYHIL
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EVVQLCRIANADNLESIWRQVSDKPRYRRWLLSAVSASGTTETLKFLKNRIRNDDLNY
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/db_xref="PID:g212881"
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/db_xref="taxon:9031"
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MPsrch\_ntp  $\ensuremath{\text{n.a.}}$  -  $\ensuremath{\text{n.a.}}$  -  $\ensuremath{\text{m.a.}}$  -  $\ensuremath{\text{m.a.}$ 

Wed Nov 24 02:28:42 1999; MasPar time 0.37 Seconds 118.965 Million cell updates/sec

Tabular output not generated.

Run on:

Description:
Perfect Score:
N.A. Sequence:
Comp: Scoring table: >US-09-103-287-5 (1-19) from US09103287.seq 95 TABLE bktranslate2 1 CTTCATTAATGAACGATGC 19 GAAGTAATTACTTGCTACG

Gap 40

Nmatch

STD:

Dbase 0; Query 0

1479 seqs, 1162203 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: HIV-AA8 1:ALL

Statistics: Mean 37.456; Variance 38.083; scale 0.984

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	80	7	o,	<sub>5</sub>	4	w	2	μ.	Result No.
51	51	51	51	51	51	51	51	51	51	51	51	52	52	55	U U	55	56	56	Score
53.7	53.7	53.7	53.7	53.7	53.7	53.7	53.7	53.7	53.7	53.7	53.7	54.7	54.7		57.9	57.9		58.9	Query Match I
261	261	260	260	257	257	255	247	225	214	180	27	860	424	768	557	492	486	240	Length I
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NEF\$SMM9	NEF\$SMMPBJ	NEF\$2CAM2	NEF\$MMP11	NEF\$2BEN	NEF\$2D194	NEF\$2GH1	NEF\$MM251	NEF\$2UC1	NEF\$MNDGB1	NEF\$2NIHZ	ENV\$FLQ5R4	ENV\$2BEN	LOCUSSHUMT	ENV\$AGM155	ENV_U08804	GAG\$UG280	<b>ENVELOPE\$A</b>	NEF\$2D205	ID
SIVSMM9, NEF PROTEIN	SIVSMMPBJ, NEF PROTEI	HIV2CAM2, NEF PROTEIN	SIVMMP11, NEF PROTEIN	HIV2BEN, NEF PROTEIN	HIV2D194, NEF PROTEIN	HIV2GH1, NEF PROTEIN	SIVMM251, NEF PROTEIN	HIV2UC1, NEF PROTEIN	SIVMNDGB1, NEF	HIV2NIHZ, NEF PROTEIN	HIVFLQ5R4E, ENV	HIV2BEN, ENV POLYPROT	HUMAN IMMUNODEFICIENC	SIVAGM155, ENV POLYPR	HIVU08804, ENV POLYPR	HIVUG280, GAG POLYPRO	SIVAGMTB14, ENV POLYP	HIV2D205, NEF PROTEIN	Description
3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	2.28e+01	2.28e+01	8.11e+00	8.11e+00	8.11e+00	5.63e+00	5.63e+00	Pred. No.

RESULT

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T 1 NEF\$2D205 X16109; X61240;		50	50	50	50	50	50	50	50	50	50	50	50	51	51	51	51	51	51	51	51	51	51	51	51	51	51	
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	ALIGNMENTS	ENV_U08793	GAG\$NL43	GAG\$JH31	ENV\$AGMTB5	<b>VPR\$JRFL</b>	VPR\$NH52	VPR\$BCSG3C	VPR\$CPZ	VPR\$BRU	ENV_U0867	ENV_U08672	ENV_U08673	POL\$MNDGB1	<b>ENV\$SMMPBJ</b>	ENV\$SMP209	<b>ENVELOPESS</b>	<b>ENVELOPESS</b>	<b>ENVELOPESS</b>	<b>ENVELOPE\$</b> Z	ENV\$2D194	GAG\$MNDGB	NEF\$SMMH4	NEF\$MM1A1	NEF\$MM32H	NEFSMNE	NEF\$MM142	
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		4.29e+01	4.29e+01	4.29e+01	4.29e+01	4.29e+01	4.29e+01	4.29e+01	4.29e+01	4.29e+01	4.29e+01	4.29e+01	4.29e+01	3.15e+01		3.15e+01	3.15e+01	3.15e+01	3.15e+01		3.15e+01		3.15e+01	٠	3.15e+01	3.15e+01	3.15e+01	

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HIVUG280, GAG 1
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M29975
14-NOV-1989
                               M34079
HUMAN IMMUNODEFICIENCY VIRUS TAT TRANSACTIVATOR BINDING PROTEIN-1
C1 424
TAT BINDING PROTEIN-1
                       -1-5':N 3':Y
TRANSLATED USING PHASE
SEQUENCE 424 AA; 47345
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TRANSLATED USING PHASE
SEQUENCE 768 AA; 86858
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SEQUENCE 557 AA; 61964
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HIV2NIHZ, NEF PROTEIN
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03-FEB-1992
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SEQUENCE 27 AA; 3093 N
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SEQUENCE 225 AA; 25680
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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Nov 27 12:42:37 1999; MasPar time 1.71 Seconds 32.958 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-09-103-287-5 (1-19) from US09103287.seq 19

1 CTTCATTAATGAACGATGC 19 GAAGTAATTACTTGCTACG

Scoring table: TABLE default Gap 10

Nmatch STD: Dbase 0; Query 0

1052 seqs, 1486975 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

HIV-NA8 1:H\_PRI 2:H\_UNA 3:H\_VIR

Statistics: Mean 6.893; Variance 1.353; scale 5.094

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Query Match Length	BB	ID	Description	Pred. No
c 1	12	63.2	672	w	SIV2010G	Simian immunodeficien	2.53e-
c 2	12	63.2	781	ω	HIV27924A1	۳.	2.53e-01
ი 3	12	63.2	1773	ω	SIVAGMT49	2	2.53e-01
c 4	12		9170	w	SIVAGMTYO		2.53e-01
ი 5	12	63.2	9623	w	SIVAGM677		2.53
ი 6	12	63.2	13068	w	SIVMM239		2.53e-01
7	11	57.9	672	w	SIV2010G		2.36e+00
<b>&amp;</b>	11	57.9	781	ω	HIV27924A1	-	2.36e+00
ი 9	11	57.9	1217	Н	HUMB2M1	Human beta-2-microglo	2.36e+00
10	11	57.9	1773	ω	SIVAGMT49	Simian immunodeficien	2.36e+00
11	11	57.9	8344	w	EIAV	Equine infectious ane	2.36e+00
c 12	11	57.9	8344	ω	EIAV	Equine infectious ane	2.36e+00
13	11	57.9	9170	w	SIVAGMTYO	Simian (African green	2.36e+00
14	11	57.9	9623	ω	SIVAGM677		2.36e+00
c 15	11	57.9	9625	2	SIVAGM3		2.36e+00
	10	52.6	270	ω	HIVU08739	Human immunodeficienc	1.71e+0
17	10	52.6	275	ω	HIVU08675	Human immunodeficienc	1.71e+0
18	10	52.6	276	ω	HIVU08679	Human immunodeficienc	1.71e+0
19	10	52.6	276	ω	HIVU08672	Human immunodeficienc	1.71e+0:
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### ALIGNMENTS

CDS	FEATURES Source	÷		TITLE JOURNAL STANDARD COMMENT	ORGANISM REFERENCE AUTHORS	RESULT 1 LOCUS DEFINITION ACCESSION SOURCE
/clone"gagabz010" /strain="SIYbabz010" /organism="Simian immunodeficiency virus" /specific_host="papio cynocephalus-hamadryas" <1>672 <1.e>672 /gene="gag" /codon_start=1 /product="gag protein" /translation="VATVRQCCHLVKKEKSAAETSSGRQKNDRSTATSSGQSQNFPAQ	vervet subtype, including ver266 and ver385, and believe that this is the first evidence for simian-to-simian cross-species transmission of SIV in the wild.  Location/Qualifiers 1672	monkeys (animals ver266 and ver385). With this aim in mind, uncultured leukocyte DNA was PCR-amplified, cloned and sequenced over a 672 bp region of gag and a 906 bp region of env for animal 2010 (only the env region was analyzed for isolates ver266 and ver385). Jin et al. note that the viral strain derived from the yellow baboon (animal 2010) clusters with SIV strains of the	< 0 + +.	Infection of a yellow baboon with SIV from African green monkeys: evidence for cross-species transmission in the wild J. Virol. (In press, 1994) full staff review Two wild yellow baboons from Tanzania were identified in a previous	yellow baboon from Tanzania.  Simian immunodeficiency virus  Vira; Viruses; sRRA enveloped viruses; Retroviridae; Lentivirus;  Primate immunodeficiency viruses.  1 (bases 1 to 672)  Jin, M.J., Rogers, J., Phillips-Conroy, J.E., Allan, J.S.,  Descreters B.C. Shaw G.M. Sharn B.M. and Hahn B.H.	SIV2010G 672 bp DNA VRL 24-AUG-1994 Simian immunodeficiency virus (SIVbab) partial gag sequence, yellow baboon sample SIVbab2010. U10899 Simian immunodeficiency virus from PCR-amplified DNA extracted from uncultured leukocytes derived from an asymptomatic pregnant female

QQGNTWVHVPLSPRTLNAWVKAVEEKKFGAEIVPMFQALSEGCTPYDINQMLNVLGDH QGALQIVKEIINEEAAQWDIQHPPPAGPLPAGQLRDPRGSDVAGTTSTVQEQLEWIYT

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nes 12; Conservative
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Patient 7924 was a heterosexual 48-year old teacher from Guinea Bissau, who was living in the Washington, D.C. area. Originally he lived in an urban area in West Africa before traveling extensively and coming to the United States. After seeking medical care for a STD, patient 7924 was identified as HIV-2 positive. Subsequent Western blot analysis of peripheral blood cells showed HIV dual reactivity. Virus isolation was successfully performed at the University of Alabama at Birmingham. Sample 7924A clusters with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCATTAATGAAG
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Human immunodeficiency virus type 2

Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetic diversity of human immunodeficiency virus type 2: Evidence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gao, F., Yue, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 2 PCR-amplified DNA recovered from a 48 year old heterosexual male originally from urban Guinea Bissau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              approximately 304 bp downstream from the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full staff_review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hahn, B.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
                                                                                                                                                                                                                                                                                                                                                                                     the subtype A HIV-2 viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retroviridae; Lentivirinae.
1 (bases 1 to 781)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for five distinct sequence subtypes with differences in virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virol. 68, 7433-7447 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 a
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/translation="ANELDREGLAESLLESKEGCQRIISVLDPLVPTGSENLKSLFNT
VCVVWCIHAEEKVKDTEEAKKIVQRHLVAETGTAEKMPNTSRPTAPPSGKGGNYPVQS
IGGNYTHVPLSPRTLNAWVKLVEEKKEGAEVVPGFQALSEGCTPYDINQMLNCVGDHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANPRVDVGAIYRRWIILGLQKCVKMYNPVSILDIKQGPKEPFKDYVDRFYRTIRAEQA
                                                                               /codon_start=2
                                                                                                       /note="NCBI gi: 532146"
                                                                                                                            /gene="gag"
                                                                                                                                                            /partial
                                                                                                                                                                                                      /tissue_type="PBMC"
                                                                                                                                                                                                                                    /sequenced_mol-"DNA"
                                                                                                                                                                                                                                                           /proviral
                                                                                                                                                                                                                                                                                 organism="Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 c
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STANDARD
                                                                                                                                                       TITLE
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                                                                                                    JOURNAL
                                                                                                                                                                                                         AUTHORS
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This sequence was obtained from a lambda clone African green monkey imported from Kenya.
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Query Match
Best Local S
Matches 1
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Best Local Similarity 100.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             828 tcattaatgaag
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Miki,K., Kitamura,T. and Hayami,M. Sequence of simian immunodeficiency virus monkey, a new member of HIV/SIV group Nature 333, 457-461 (1988) full staff_review
                                                                                                                                     Simian (African green monkey) immunodeficiency virus, extra-
chromosomal closed-circular DNA, TYO-1 clone lambda-SAH12.
                                                                                                                                                                                                                                   Ol-MAR-1989 Simian (African green monkey) immunodeficiency virus, isolate TYO-1, complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       full staff_review Kindly submitted prior to publication by Dr. Vanessa Hirsch, Kindly submitted prior to publication by Dr. Vanessa Hirsch, Immunodeficiency Viruses Section, NIAID/NIH, Twinbrook II, Rockville MD 20852. SIVagm-tan strains cluster with other previously characterized agm strains taken from vervets and grivets. See related tantalus isolate sequences 17, 27, 40, 9 (accession numbers L19250-L19252, L19254).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hirsch,V.M., McGann,C., Dapolito,G., Goldstein,S., Ogen-Odoi,A., Biryawaho,B., Lakwo,T. and Johnson,P.R. Identification of a new subgroup of SIVagm in tantalus monkeys Virology (1993) In press full staff_review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ugandan tantalus monkey (Cecopithecus tantalus).
Simian immunodeficiency virus
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIVAGMT49 1773 bp ds-DNA VRL 09-JUN-1993
Simian immunodeficiency virus, isolate TAN-49, complete gag cds.
L19253
                                                                                                                                                                                                                                                                                       SIVAGMTYO
                                                                                                               Fukasawa, M., Miura, T., Hasegawa, A., Morikawa, S., Tsujimoto, H.
                                                                                                                                                                                                                    X07805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 63.2%;
Similarity 100.0%;
12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sequenced_mol="DNA"
4 a 375 c 480 g 324 t
upstream from the gag cds start.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="gag"
1..1773
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NPVPVGNIYRRWIQIGLQKCVRMYNPTNILDVKQGPKESFQS"
157 c 195 g 150 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_line="CEMss"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Simian immunodeficiency virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /proviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /haplotype="na'
                                                                                                                                                                                                                                                                                                                                                                                                                                 839
                                                                                                                                                                                                                                                                                    9170 bp ss-RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.53e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12; DB 3; 1
Pred. No. 2.53e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12; DB 3;
Pred. No. 2.53e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                     from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIVAGMTYO appears to lack a vpR coding region. [1] suggests that this may account for SIVAGMTYO's lack of pathogenicity. The env to the in-frame stop codon at positions 8077-8079, similar to the in-frame stop codons found in the SIV macaque and HIV-2 ROD35 envelope coding regions, except that SIVAGMTYO's stop codon is found 96bp downstream from the 3' splice junction of tat and rev, which is the location of the stop codon in the other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] finds that SIVAGMTYO is approximately equally distantly related to the HIV-1's and the HIV-2/SIV (macaque) group; over a "conserved" stretch of the pol protein, TYO is only 87% similar to AGM385 and 82% similar to AGM266, the latter two differing by 20%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences.
                                                                                                                                        /note="8201..8
                                                                                                                                                                                                                                                                                                            /note="tat, 5770..8367
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432..19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="5' LTR" <1634..4819
                   /note="R repeat 3'
9151..9156
                                                                                                                                                                                                                                                                                                                                               /note="rev
5764..7983
                                                                                                                                                                                                                                                                                                                                                                               /note="tat
5764..7983
                                                                                                                                                                                                                                                                                                                                                                                                              /note="rev protein, exon 2 (first expressed exon)"
5764..7983
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="tat protein, exon 2 (first expressed exon)"
5703..5763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="R repeat 5' copy"
220..237
                                                                                                                                                                                                        /note="tat protein, exon 3 (AA at 7985)"
7984..8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="gag polyprotein"
/codon_start=432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="genomic mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=5546
join(5703..5763,7984..8177)
/note="rev protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
/note="mRNA polyadenylation signal"
                                                                                                                                                                                                                                                          /note="env polyprotein (in-frame stop codon at 8077)"
/codon_start=5770
                                                                                                                                                                                                                                                                                            /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="vif protein"
/codon_start=4755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="tat, rev, nef subgenomic mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=5703/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1634
join(5546..5763,7984..8068)
/note="tat protein"
                                                                                                                   'note="nef protein"
                                                                                                                                                                                          'note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=5236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="vpx protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="pol polyprotein (NH2-terminus uncertain; AA at 634)"
                                                                   note="3' LTR"
                                                                                                     codon_start=8201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .9170
                                                                                                                                          . 8890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer (Lys-tRNA) binding site"
                                                                                                                                                                                                                                                                                                                            tat, rev, nef subgenomic mRNA intron
                                                                                                                                                                                                                                                                                                                                                            rev intron 2"
                                                                                                                                                                                       rev protein, exon 3 (AA at 7986)"
                                                                                                                                                                                                                                                                                                                                                                                              cat intron 2"
                                                                                                                                                       n-frame stop
                                                                                                                                                        5
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Query Match 63.2%;
Best Local Similarity 100.0%;
Matches 12; Conservative
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| Cocation/Qualifiers | Cocation/S93.6195,8370..8750) | Cone-"tat" | Cocation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Computation/Co
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Virology 182, 397-402 (1991)
full staff_entry
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Simian immunodeficiency virus from an African monkey), gri-1, lambda clone II (biologically proviral DNA, also denoted 677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 2438)
2 (bases 1 to 2438)
3 Johnson, P.R., Fomsgaard, A., Allan, J., Gravell, M., London, W.T., Olmstead, R.A. and Hirsch, V.M.
Simian immunodeficiency viruses from African green monkeys display
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIVAGM677 9623 bp ss-DNA VRL 02-APR-1991
Simian immunodeficiency virus from African Green Monkey;
gri-I lambdaII or 677 clone (from a grivet); complete genome.
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J. Virol. 64, 1086-1092 (1990)
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690..707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="The normal stop codon 'tag' in rev (position 8574) is 'cag' making rev in SIVgri-1 longer than rev in most other sequences. The gri-1 sequence is the most divergent primate lentivirus reported to date."
/codon_start=5683
5993..6195
                                                                                                                                      /codon_start=5214
5683..6039
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897..2438
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                                                                                                                                                                                                                                                                                      214..5873
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active clone);
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                                                                                                               4 (bases 6860 to 8434)
Burns, D.P.W. and Desrosiers, R.C.
Selection of genetic variants of simian immunodeficiency virus persistently infected rhesus monkeys
J. virol. 65, 1843-1854 (1991)
Desrosiers,R.C. Characterization of infectious molecular clones of simian immunodeficiency virus (SIVmac) and human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                    Regier,D.A. and Desrosiers, personal communication (12-91) personal communication from D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simian immunodeficiency virus (SIV) from a macaque, isolate 239 (Macaca mulatta Mm239-82); proviral DNA. Infectious clone, lambo siv239-1 [3]; clone-infected peripheral blood lymphocytes from rhesus macaques [4]; integrated proviral DNA in lambda vectors transfected into HUT-78 cells [5]. (bases 1 to 1035)

1 (bases 1 to 1035)

Regier, D.A. and Desrosiers, R.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIVMM239 13068 bp ss-RNA VRL 15-OCT-199 Simian immunodeficiency virus isolated from a macaque; isolate 239; complete proviral genome and flanking sequence. M33262 M61062-M61093
                                                   Naidu,Y.M., Kestler,H.W.III., Li,Y., Butler,C.V., Schmidt,D.K., Troup,C.D., Sehgal,P.K., Sonigo,P.,
                                                                                                                                                                                                                     Induction of AIDS in Rhesus monkeys immunodeficiency virus Science 248, 1109-1112 (1990)
                                                                                                                                                                                                                                                                         Desrosiers, R.
                                                                                                                                                                                                                                                                                      Kestler,H.,
Lackner,A.,
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                                                                                      (bases 9026 to 9145)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete nucleotide sequence of ian immunodeficiency virus
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/note="3'
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6202..8766
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Regier,D.,
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Sehgal,P., 1
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                                                                                                                                                                                                                                                                                                                                                      Regier, Dept. of Microbiology,
                                                                                                                                                                                                                                                                                      , Marthas,M.,
Daniel,M., K
                                                                                                                                                                                                                                                       by molecularly cloned simian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a pathogenic molecular clone
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                                                                                                                                                                                                                                                                                      King, N. and
                                                     Silva, D.P., Daniel, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-1991
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                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
[1, 2] Kindly submitted in computer readable form prior to publication by Dr. Desrosiers, New England Regional Primate Center, Harvard. 256 bases of 5' flanking cellular DNA and approximately 2500 bases of 3' flanking material were also determined.
                                                                                                                                                               Restler,H.W., Ringler;D.J., Mori,K., Panicali,D.L., Sehgal,P.K.,
Daniel,M.D. and Desrosiers,R.C.
Importance of the nef gene for maintenance of high virus loads and
for development of AIDS
Cell 65, 651-662 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                              Luciw, P.A. Shaw, K.E., Unger, R.E., Planelles, V., Stout, M.W., Pratt-Towe, E., Leung, N.J., Banapour, B. and Marthas, M.L. Genetic and Biologic Comparisons of Pathogenic and Non-pathogenic molecular Clones of Simian Immunodeficiency Virus (SIVmac)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type 2: persistent infection of rhesus monkeys with molecularly
cloned SIVmac
J. Virol. 62, 4691-4696 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                   AIDS Res. Hum. Retroviruses (1991) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 (sites; see <SIVMM1A11>)
                                                                                                                                                                                                                                                                                                                                      (sites)
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27 late-time-point clones obtained from 2 rhesus monkeys infected with SIVMM239 were used to quantify variation in the gpl20 region [3] describes the pathogenic potential of SIVMM239

COMMENT

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Macaque lymphocytes supported the replication of SIVMM239 and SIVMM251 but not SIVMM142 or HIV2ROD [5].

See also <SIVMM1A11> (accession number M76764); SIVMM239 and SIVMM1A11 show greater than 98% homology at the nucleotide level Analysis in [6] largely focuses on sequence differences in SIVMM and SIVMM1A11 which may account for differences in biologic properties [6]. in SIVMM239

entry replaces pages I-B-86 through I-B-89 HUMAN RETROVIRUSES AND AIDS. (APR 90) in

misc_binding	LTR	misc_feature	repeat_region	LTR	LTR	provirus	cellular				CDS				CDS	exon		EATURES exon	
10781105	710-ce mana scart (Pucarred) 951.1074 7notes 115 "	775	774950 /note="R"	257773 /note="U3"	2571074 /note="5/ltr"	25710535 /note="SIVmac239 provirus"	1256 /note="flanking cellular DNA"	RSPQD"	/translation-"MSNHEREEELRKRLRLIHLLHQTNPYPTGPGTANQRRQRKRRWR	/codon_start=1	Join (6784-6853,90629315) /notes "rev protein"	RPLEACYNTCYCKKCCYHCQFCFLKKGLGICYEQSRKRRRTPKKAKANTSSASNKPIS	/translation-"METPLREQENSLESSNERSSCISEADASTPESANLGEEILSQLY	/note="tat protein" /codon start=1	<pre>/note="rev protein, exon 2 (iffst expressed exon)" join(65586853,90629158)</pre>	<67846853	/note="tat protein, exon 2 (first expressed exon)"	Location/Qualifiers	

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misc_feature
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YTAFTLPSVMNAEPCKRYIYKYLPQCWKGSPALFQYTMKHYLFEPFRKANDDVTLVQYM
DDILIASDRTDLEHDRVYLQSKELLNSIGFSTPEKFGXDPPFQWMGYELMPTKWKLQ
KIELPQRETWYVNDIQXLVGYLNWAAQIYPGIKTKHLCELIRGKKTLTEEYQWTEMAE
AEYEENKIILSQEQEGCYYQEGKPLEATVIKSQDNQWSYKIHQEDKILKVGKFAKIKN
THTNGVRLLAHVIQKLGKEAIVIWGQVFKFHLPVEKDVMSQWTDYMQVTM1PEWDFI
STPPLVKLVENLVKNDDIEGEFTYYTDGSCCNKQSKEGKAGYITDRGKDKVKKLEQTTNQ
QAELEAFLMALTDSGPKANIIVDSQYVMGIITGCPTESESRLVNQIIEEMIKKSEIYV
AWVPAHKGIGGNQEIDHLVSQGIRQVLFLEKEEPADEEBKYHSWKELVFKFGLDRI
VARQIVDTCDKCHQKGEAIHGQANSDLTRYMQMDCTHLEGKIIVAVHVASGFIEAEVI
PQETGRQTALFILKLAGRWPITHLHTDNGANFASQEVKNVAWMAGIEHTFGCPYNPQS
QGYVEAMNHHLKNQIDRIREQANSDLTRYDKYMYAKRRGGIGDMTPAERLINMIT
                             ATKNRDTWGTTQCLPDNGDYSEVALNVTESFDAWNNTVTEQAIEDVWQLFETSIKPCV
KLSPLCITMRCNKSETDRWGLTKSITTTASTATASTAVDMYNETTSSCIAQDNCTGL
EQEQMISCKFNWTGLKRDKKKEYNETWYSASTYSTTASTASAKVDMYNETSSCIAQDNCTGL
EQEQMISCKFNWTGLKRDKKKEYNETWYSASTAVCEQGNUFESRCYMHCNTSVIQE
SCDKHYWDAIERFXCAPPGYALLRCNDTNYSGFWPKCSKVVVSSCTRWHCTGTSTWFG
FNGTRAENRTYIYWHGRDNRTIISLNKYYNLTMKCRRPGNKTVLPVTIMSGLVFHSQP
FNGTRAENRTYIYWHGRDNRTIISLNKYYNLTMKCRRPGNKTVLPVTIMSGLVFHSQP
TNDRFXQAWCWFGGKWIDAIKEVKQTIYKHPRYTGTNNTDKINTAPGGGDPRYTFMW
TNCRGEFLYCKMNWFLNWVEDRNTANQKPKEDKRNVYPCHIRQIINTWHKKVGKNYYL
PPREGDLTCNGTVTSLIANIDWIDGNQTNITMSAEVABLYRLELGDYKLVEITPIGLA
PTDVKRYTTGGTSRNKRGVFVLGFLGFLATAGSAMGAASLTLTAQSRTLLAGIVQQQQ
QLLDVVKRQQELLRLTYWGTKNLQTRYTAIEKKLKDQAQLNAWGCAFRQVCHTTVPWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MGVRNSYLSGKKADELEKIRLPNGKKKYMLKHVVWAANELDRF
GLAESILJENKEGCOKILSVLAFLVPTGSENLKSLVNTVCVIWCIHAEEKVKHTEEAKO
IVORHLVVETGTTETMPKTSRPTAPSGGRGNYPVQQIGGNYVHLPLSPFTLNAMVKL
IEEKKFCAEVVPGFQALSEGCTPYDINQMLNCYGDHQAAMQIINDIINEEAADMDLQH
PQPAPQOGQLREPSGSDIAGTTSSVDEQIQMMYRQQNPIPVGNIYRRWIQLGLQKCVR
MYNPTNILDVKQGFKEPFQSVVDRFYKSLRAEQTDAAVKNMMTQTLLIQNANPDCKLV
LKGLGVNPTLEEMLTACQTVGFYGKARLMAFALKFALAPVFIPFAAAQORGFKFNFL
LKGLGVNPTLEEMLTACQTVGFYGKARLMAFALKFALAPVFIPFAAAQORGFKFNFL
LKGLGVNPTLEEMLTACQTVGFYGKARLMAFALKFALAPVFIFFAAAQORGFKFNFL
CVNQGKEGHSARQCRAFRRQGCWKCGKMDHVMAKCPDRQAGFLCIGFWGKKFRNFPMA
CVHQGLMPTAPPEDPAVDLLKNYMQLGKQQREKQRESREKFYKEVTEDLLHLNSLFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation~"MEERPPENEGPQREPWDEWVVEVLEELKEEALKHFDPRLLTALG
NHIYNRHGDTLEGAGELIRILQRALFMHFRGGCIHSRIGQPGGGNPLSAIPPSRSML"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="meeekrwiavpTwriperlerwhslikylkyktkDLQkvCyvph
FKVGWAWWTCSRVIFPLQEGSHLEVQGYWHLTPEKGWLSTYAVRITWYSKNFWTDVTP
NYADILLHSTYFPCFTAGEVRRAIRGEQLLSCCRFPRAHKYQVPSLQYLALKVVSDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAKIIKDYGGGKEVDSSSHMEDTGEAREVA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mlelwergtlckamqspkktgmlemwkngpcygqmprqtggpfr
PWSMGKEAPQFPHGSSASGADANCSPRGPSCGSAKELHAVGQAAERKAERKQREALQG
NASLTPKWNNETWQEWERKVDFLEENITALLEEAQIQQEKNMYELQKLNSWDVFGNWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQGENPTWKQWRRDNRRGLRMAKQNSRGDKQRGGKPPTKGANFPGLAKVLGILA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEQEIQFQQSKNSKFKNFRVYYREGRDQLWKGPGELLWKGEGAVILKVGTDIKVVPRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDRGFAAPQFSLWRRPVVTAHIEGQPVEVLLDTGADDSIVTGIELGPHYTPKIVGGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="env polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note≖"vpR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSDPRERIPPGNSGEETIGEAFEWLNRTVEEINREAVNHLPREL
IFQVWQRSWEYWHDEQGMSPSYVKYRYLCLIQKALFMHCKKGCRCLGEGHGAGGWRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="vpX protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="vif protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="polypurine tract"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="gag polyprotein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MGCLGNQLLIAILLLSVYGIYCTLYVTVFYGVPAWRNATIPLFC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=:
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two wild yellow baboons from Tanzania were identified in a previous study with strong SIV(agm) seroreactivity. They lived in a national park where yellow baboons and African green monkeys share the same habitat. In this study, molecular characterization was performed for virus derived from one of the SIVagm seroreactive yellow baboons (animal 2010) and from two vervet African green monkeys (animals ver266 and ver385). With this aim in mind, uncultured leukocyte DNA was PCR-amplified, cloned and sequenced over a 672 bp region of gag and a 906 bp region of env for animal 2010 (only the env region was analyzed for isolates ver266 and ver385). Jin et al. note that the viral strain derived from the yellow baboon (animal 2010) clusters with SIV strains of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIV2010G
Simian in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jin,M.J., Rogers,J., Phillips-Conroy,J.E., Allan,J.S., Desrosiers,R.C., Shaw,G.M., Sharp,P.M. and Hahn,B.H. Infection of a yellow baboon with SIV from African green monkeys: evidence for cross-species transmission in the wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Virol. (In press, 1994)
full staff_review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simian immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simian immunodeficiency virus from PCR-amplified DNA extracted uncultured leukocytes derived from an asymptomatic pregnant fem
                                                                                                                                                                                                                                                                                                                                                                                                                                                      vervet subtype, including ver266 and ver385, and believe that this is the first evidence for simian-to-simian cross-species transmission of SIV in the wild.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simian immunodeficiency virus (SIVbab) partial gag sequence, yellow baboon sample SIVbab2010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vira; Viruses; ssRNA enveloped viruses; Retroviridae; Primate immunodeficiency viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yellow baboon from Tanzania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 672)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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/product="gag protein"
/translation="VATVRQCHLVKKEKSAAETSSGRQKNDRSTATSSGQSQNFPAQ
QQGNTWVHVPLSPRTLNAMVKAVEEKKFGAEIVPMFQALSEGCTPYDINOMLNVLGDH
QGALQIVKEIINEEAAQMDIQHPPAGPLPAGQLRDPRGSDVAGTTSTVQEQLEWIYT
ANPRVDVGAIYRRWIILGLQKCVKMYNPVSILDIKQGPKEPFKDYVDRFYRTIRAEQA
                                                                                                                                                                                                                                                        /clone="gagbab2010"
/strain="SIVbab2010"
/organism="Simian immunodeficiency virus"
/specific_host="Papio cynocephalus-hamadryas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9333..10124
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                                                                                                                                                               codon_start=1/
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Pred. No. 2.53e-01
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the cells was used for virus isolation.

Patient 7924 was a heterosexual 48-year old teacher from Guinea Bissau, who was living in the Washington, D.C. area. Originally he lived in an urban area in West Africa before traveling extensively and coming to the United States. After seeking medical care for a STD, patient 7924 was identified as HIV-2 positive. Subsequent Western blot analysis of peripheral blood cells showed HIV dual reactivity. Virus isolation was successfully performed at the University of Alabama at Birmingham. Sample 7924A clusters with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 6067K, 7312A, 7810A, 7924A, FA, F0784, FT, JA, ON, and PA) from six different West African countries, living in both urban and trural areas. Uncultured PBMC DNA was PCR amplified, and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 2 PCR-amplified DNA recovered from a 48 year old heterosexual male originally from urban Guinea Bissau who showed HIV dual seroreactivity.

Human immunodeficiency virus type 2

Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV27924A1 781 bp ds-DNA VRL 23-AUG-1994 Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag seque sample 7924A, clone 1, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up to now, HIV-2 sequences have been derived almost solely from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      approximately 304 bp
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NPVPVGNIYRRWIQIGLQKCVRMYNPTNILDVKQGPKESFQS"
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                                                                                   VCVVWCIHAEEKVKDTEEAKKIVQRHLVAETGTAEKMPNTSRPTAPPSGKGGNYPVQS
IGGNYTHVPLSPRTLNAWVKLVEEKKFGAEVVPGFQALSEGCTPYDINQMLNCVGDHQ
                                                                                                                                           translation="ANELDRFGLAESLLESKEGCQRIISVLDPLVPTGSENLKSLFNT/
                                                                                                                                                                                                                                                                                                                    /tissue_type="PBMC"
                                                                                                                                                                                                                                                                                                                                                                                                       organism="Human immunodeficiency virus type 2"
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                                                                                                     SIVAGMT49 1773 bp ds-DNA VRL 09-JUN-1993 Simian immunodeficiency virus, isolate TAN-49, complete gag cds. 119253 Simian immunodeficiency virus proviral DNA, isolate TAN-49 from Ugandan tantalus monkey (Cecopithecus tantalus). Simian immunodeficiency virus Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
Retroviridae; Lentivirinae.

1 (bases 1 to 1773)

Hirsch,V.M., McGann,C., Dapolito,G., Goldstein,S., Ogen-Odoi,A.,
Biryawaho,B., Lakwo,T. and Johnson,P.R.

Identification of a new subgroup of SIVagm in tantalus monkeys
Virology (1993) In press
                                                                                                                                                                                                                                                                                                                                                                                                                          383
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Guessow,D., Rein,R., Ginjaar,I., Hochstenbach,F., Seemann,(
Kottman,A. and Ploegh,H.L.
The human beta-2-microglobulin gene: Primary structure and
definition of the transcriptional unit
J. Immunol. 139, 3132-3138 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Draft entry and computer-readable sequence for [1] kindly provided by E.J.Baas, 03-DEC-1987.
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11; Conservative
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Similarity 100.0%;
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274 a 325 c 322 g 29
bp upstream of EcoRl site.
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/gene="B2M"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="intron A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="beta-2-microglobulin, mature peptide"
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'codon_start=1
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Pred. No. 2.36e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virology 158, 300-312 (1987)
full staff_review
2 (bases 324 to 5122)
Stephens,R.M., Casey,J.W. and Rice,N.R.
Equine infectious anemia virus gag and
                             7 (bases 1 to 8229; correction
Tronick,S.R. and Fuller,F.
                                                           of the env gene region
Virology 155, 309-321 (
full staff_review
                                                                           Lentivirus genomic organization: of the env gene region of equine Virology 155, 309-321 (1986)
                                                                                                                                     full staff_review
6 (bases 4769 to 8048; 8069 to 8228)
Rushlow,K., Olsen,K., Stiegler,G., Payne,S.L.,
                                                                                                                                                                                                                   Nature 317, 366-368 (1985)
full staff_review
5 (bases 4769 to 8048; 8069 to 8344)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIAV 8344 bp ss-RNA Equine infectious anemia virus proviral M16575 M11337 K03334 M14855
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Kindly submitted prior to publication by Dr. Vanessa Hirsch,
Immunodeficiency Viruses Section, NIAID/NIH, Twinbrook II,
Rockville MD 20852. SIVagm-tan strains cluster with Other
Unpublished,
                                                                                                                                                                                                         Payne, S
                                                                                                                                                                                                                                                                                                                                                               Unpublished (1985) Meloy Labs Inc,
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                                                                                                                               Issel,C.J
                                                                                                                                                                                   Unpublished (1987) Dept Biochem, Louisiana
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11; Conservative
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.u,I.-M., Yaniv,A., Dahlberg,J.E., Gazit,A., Skuatz,S.F.,
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4 a 375 c 480 g
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/cell_line="CEMss"
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Pred. No. 2.36e+00;
0; Mismatches 0;
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           155, 309-321 (1986
Louisiana St Univ,
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7060..7060
                                                                                    /note="g in [Virology 158, 300-312 (1987)], a 155, 309-321 (1986)],[Unpublished (1987) Dept Louisiana St Univ, Baton Rouge, LA]"
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155, 309-321 (1986)],[Unpublished (1987) Dept
Louislana St Univ, Baton Rouge, LA]"
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231, 589-594 (1986)]"
5312..7891
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uncertain)"
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/codon_start=5312
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[Unpublished (1985) Meloy Labs Inc, Springfield,
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Science 231, 589-594 (1986)]"
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231, 589-594 (1986)]"
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/codon_start=465
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Science 231, 589-594 (1986)]"
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Unpublished (1985) Meloy
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                        in [Virology 158, 300-312 (1987)], t in [Virology 321 (1986)],[Unpublished (1987) Dept Biochem, St Univ, Baton Rouge, LA]"
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Montelaro, R.C.

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Chiu,I.-M., Yaniv,A., Dahlberg,J.E.,
Tronick,S.R. and Aaronson,A.
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Equine infectious anemia virus proviral DNA,
M16575 M11337 K03334 M14855
 Unpublished (1987) Dept Biochem, full staff_review
                                                                full
                                                                                                           Nucleotide sequence
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                                                                                                                                                                                                                                                                      Equine infectious anemia virus gag
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Stephens, R.M., Casey, J.W. and Rice, N.R.
                                  Payne,S.L.
                                                                                            lentiviruses
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                                                                                                                                                                                                          Chiu, I.-M
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full staff_review
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                                                                                                                                                                                                                                                                                                                                                                                                  Kawakami,T., Sherman,L., Dahlberg,J., Gazit,A.,
Tronick,S.R. and Aaronson,S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equine infectious anemia virus (EIAV) proviral 409-2 \{1\}).
                                              ture 317, 366-368 (1985)
ll staff_review
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a 1358 c
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8048..8069
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uncertain)"
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155, 309-321 (1986)],[Unpublished (1987) Dept
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(1987)], gt in [Virology 155, 309-321 (1986)],[Unpublished
(1987) Dept Biochem, Louisiana St Univ, Baton Rouge, LA]"
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7909..8229
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155, 309-321 (1986)],[Unpublished (1987) Dept
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92.3%;
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Rushlow,K., Olsen,K., Stiegler,G., Payne,S.L.,
Issel,C.J.
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231, 589-594 (1986)]"
2865..2870
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[Science 231, 589-594 (1986)]"
4573..4573
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325..342
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2341..2341
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231, 589-594 (1986)]"
/note="a in [Virology 158, 300-312 (1987)],
155, 309-321 (1986)],[Unpublished (1987) Dep
                                               /note="envelope polyprotein (AA at 5312)
/codon_start=5312
                                                                                            /note="a in [Virology 158, 300-312
231, 589-594 (1986)]"
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uncertain)"
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/codon_start=465
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SIVAGMTYO appears to lack a vpR coding region. [1] suggests that this may account for SIVAGMTYO's lack of pathogenicity. The env cds contains an in-frame stop codon at positions 8077-8079, similar to the in-frame stop codons found in the SIV macague and HIV-2 ROD35 envelope coding regions, except that SIVAGMTYO's stop codon
                                                                                                                                                                                                      Fukasawa,M., Miura,T., Hasegawa,A., Morikawa,S., Tsujimoto,H., Miki,K., Kitamura,T. and Hayami,M.
Sequence of simian immunodeficiency virus from African green monkey, a new member of HIV/SIV group
Nature 333, 457-461 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                   SIVAGMTYO 9170 bp ss-RNA VRL 01-MAR-1989 Simian (African green monkey) immunodeficiency virus, isolate TYO-1, complete genome.
                                                                                                                                                                                                                                                                                                                                                                 Simian (African green monkey) immunodeficiency virus, extra-
chromosomal closed-circular DNA, TYO-1 clone lambda-SAH12.
                                                                                                                                                              This sequence was obtained from a lambda clone derived from
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155, 309-321 (1986)],[Unpublished (1987) Dept Biochem,
Louisiana St Univ, Baton Rouge, LA]"
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155, 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="g in [Virology 158, 300-312 (1987)], a in [Virology 155, 309-321 (1986)],[Unpublished (1987) Dept Biochem, Lausiana St Univ, Baton Rouge, LA]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="3' ORF protein
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92.3%;
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Pred. No. 2.36e+00;
0; Mismatches 1
                                                                                                                                      from Kenya.
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(1987)
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Matches 11; Conservative
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RESULT LOCUS

13

REFERENCE SOURCE ACCESSION DEFINITION

COMMENT

0;

Indels

0

Gaps

0;

JOURNAL STANDARD

TITLE AUTHORS Ç В BASE COUNT ORIGIN

Matches

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/note="genomic mRNA"
prim_transcript 1..9170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] finds that SIVAGMTYO is approximately equally distantly related to the HIV-1's and the HIV-2/SIV (macaque) group; over a "conserved" stretch of the pol protein, TYO is only 87% similar to AGM385 and 82% similar to AGM266, the latter two differing by 20%.
                                                                        a 1720 c 226 of genomic RNA.
                                                                                                                             /note="R repeat 3'
.9151..9156
                                                                                                                                                                                                                                                                             8077..8079
/note="in-frame stop
                                                                                       /note="mRNA polyadenylation
1720 c 2263 g 2015 t
                                                                                                                                                                  9054..9170
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8547..>9170
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5770..8367
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/codon_start=5770
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/codon_start=5236
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/codon_start=432
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join(5703..5763,7984..8177)
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join(5546..5763,7984..8068)
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codon_start=4755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="tat, rev, nef subgenomic
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Score 11; DB 3; I
Pred. No. 2.36e+00;
0; Mismatches (
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                                                                                                        signal"
                                  Length 9170;
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Johnson, P.R., Fomsgaard, A., Allan, J., Gravell, M., London, W.T.,
Olmstead, R. A. and Hirsch, V.M.
Simian immunodeficiency viruses from African green monkeys display
unusual genetic diversity
J. Virol. 64, 1086-1092 (1990)
full staff_entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fomsgaard, A., Hirsch, V.M., Allan, J.S. and Johnson, P.R. A highly divergent proviral DNA clone of SIV from a distinct species of African green monkey.
Virology 182, 397-402 (1991)
full staff_entry
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Simian immunodeficiency virus from African Green Monkey;
gri-1 lambdaII or 677 clone (from a grivet); complete genome.
M66437 M29973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other sequences. The gri-1 sequence is the most divergent primate lentivirus reported to date. Location/Qualifiers join(5993.6195,8370..8750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kindly submitted prior to publication and in a computer readable form by Phillip Johnson, NIAID/Georgetown University.
The typical stop codon "tag" in rev (position 8574) is "cag" making rev in SIVgri-1 (lambdaII) longer than rev in most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simian immunodeficiency virus from an African grivet (green monkey), gri-1, lambda clone II (biologically active clone); proviral DNA, also denoted 677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 9623
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codon_start=6202
                                                                                                                                                                                                'gene="vpx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="5' long terminal repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene≖"rev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=5993/
                                                            gene="rev"
                                                                                                                                                                                                                                  codon_start=5214
                                                                                                                                                                                                                                                                                                                                    gene="pol"
                                                                                                                                                                                                                                                                                                                                                  141..5314
                                                                                                                                                                                                                                                                                                                                                                                            gene-"gag"
                                                                                                                                                                                                                                                                                                                                                                                                                            note="primer (Lys-tRNA) binding site"
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                                          202..8766
                                                                                                                                                                                                                                                                                                              odon_start=2141
                                                                                                                                                                              odon_start=5683
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Best Local Similarity 100.0%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete proviral genomic DNA. Infectious clone.

1 (bases: 1 to 9625)

Baier,M., Garber,C., Mueller,C., Cichutek,K. and Kurth,R.

Complete nucleotide sequence of a simian immunodeficiency virus from African green monkeys: a novel type of intragroup divergence Unpublished (1990); Paul-Ehrlich-Institute, Paul-Ehrlich-Str-57-59,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was taken from an infectious molecular clone (used for heterologous infection of the pigtail macaque). The 3' LTR sequence does not appear to match the 5' LTR sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Draft entry and computer-readable sequence for [1] kindly submitted by M.Baier 20\text{-DEC-}1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6070 Langen 1, Federal Republic of Germany full staff_review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simian immunodeficiency virus from African Green monkey, complete proviral genomic DNA. Infectious clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIVAGM3 9625 bp ds-RNA UNA
Simian immunodeficiency virus from African
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8600..9271
//gene="nef"
/codon_start=8600
8937..9623
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/codon_start=431
<1687..4827
                      /rpt_type=R repeat 3' 9506..9511
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/gene="tat"
8368..8750
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/note="tat protein"
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                                                                                                                                                                                                                //note="pol polyprotein (NH2 terminus uncertain; AA
1687)"
                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=5554
join(5711..5771,8013..8221)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
/note="rev protein, exon 2 (first expressed exon)"
                                                                                                                                                                          /codon_start=1687
1763..5461
                                                                                                                                                                                                                                                    'partial
                                                                          codon_start=5244
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                                                                                                                                                                                                                            This sequence encodes a Staphylococcus aureus protein of unknown function, and represents a DNA Sequence of the invention.

The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. bylori infection.

Sequence 619 BP; 208 A; 117 C; 79 G; 215 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAY-1998.
24-SEP-1997; 307485.
24-SEP-1996; US-027032.
(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response induction; eye infection; respiratory infection; inhibitor; bacternal infection; cardiac infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
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V53479
 V80065;
                V80065 standard;
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WPI; 98-252940/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to identify modulators or specific receptors; in rational drug design and as an immunogen for vaccines. The MurC gene sequences useful in antisense/ribozyme therapeutics; to detect mutant MurC gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respiratory tract and central nervous system Claim 1; Page 146; 390pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid sequences from Staphylococcus aureus WCHU29 useful in vaccines and for treatment of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Black MT,
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Similarity 100.0%;
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the recombinant production of the polypeptide. Agonists or the Murc expression of the polypeptide. Antagonists, inhibitory nucleic acid or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide or expression of the polypeptide are useful for inhibiting the polypeptide e.g. bacterial (especially S. aureus) infections. They are also useful against Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agentification useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The Murc polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to identify modulators or specific receptors; in rational drug design and as an immunogen for vaccines. The Murc gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant Murc gene; for othermosomal mapping; to determine bacterial serotype; and for genetic immunisation. The present sequence represents a partial nucleotide sequence (Murc Ora) of the Murc gene.
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                                                                                                                                                                                                                                                                                                                                                                                          V99650 standard; DNA; 1351
V99650;
17-MAR-1999 (first entry)
07-JAN-1999.
26-JUN-1998; 305064.
03-JUL-1997; US-052720.
(SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                             UDP-N-acetylmuramate:L-alanine ligase (Murc polypeptide) encoding DNA. Murc gene; UDP-N-acetylmuramate:L-alanine ligase; Murc polypeptide; bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine; immunogen; drug; genetic immunisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a UDP-N-acetylmuramate:L-alanine li
(MurC polypeptide) encoded by the S. aureus MurC gene. Host containing an expression system comprising the MurC gene can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burnham MKR, Wallis WPI; 99-062655/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; W89199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Partial nucleotide sequence of the MurC gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcatcgttcattaatgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATCGTTCATTAATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA; 1351 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
larity 100.0%;
Conservative
                                                                                                                                                                                                                                                                            aureus
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                                                                                                                                                                                                                       Location/Qualifiers 22..1335
                                                                                                                                              /gene= "Murc"
/product= "UD
                                                                                                                                                                                                 /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide from :
eful in diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39pp; English.
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                                                                                                                          "UDP-N-acetylmuramate:L-alanine
(MurC polypeptide)"
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PLC.
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Pred. No.
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83 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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lcer; gastritis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>و</u>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a MurC gene encoding a Staphylococcus CC aureus UDP-N-acetylmuramate:I-alanine ligase (MurC polypeptide). Host CC cell containing an expression system comprising the MurC gene can be used CC for the recombinant production of the polypeptide. Agonists or the MurC CC polypeptide are used to treat conditions requiring increased activity or CC expression of the polypeptide. Antagonists, inhibitory nucleic acid or CC competitive polypeptide are useful for inhibiting the polypeptide e.g. CC bacterial (especially S. aureus) infections. They are also useful against CC the incobacter pylori infections and related cancers, ulcers and gastritis. CC The antibacterial agents are useful to treat in-dwelling devices for CC infection prevention or generally as wound treatments to prevent adhesion CC diagnosing or prognosing a (susceptibility to) disease, for raising CC drug design and as an immunogen for vaccines. The MurC gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant MurC gene; for chromosomal mapping; to determine bacterial serotype; and for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 1
                                                                                                                                Query Match
Best Local Similarity
                                                                                                               Matches
                                                                                                                                                                                                        Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                  New oligo:nucleotide probes detection and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shank DD, Spears PA; WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide probe MK14-A Oligonucleotide; DNA probe; n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 5
Q51746 standard;
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Claim 2; Pages 3-4; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated MurC polypeptide from Staphylococcus aureus and related nucleic acid - useful in diagnosis, treatment and prevention of
                                                                                                                                                                                                                                                                                                                                                                                                           samples
                                                                                                                                                                                                                                                                                                                                                                                                                               detection and
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                                                       vhhvvhhvhvsvvvvhhvv
     CTTCATTAATGAACGATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 100.0%;
Similarity 100.0%;
19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMITHKLINE BEECHAM PLC
                                                                                                            0;
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                                                                                                            Conservative
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(80.0%)
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Pred.
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                                                                                                         Score
Pred.
18; M
                                                                                                            Mismatches
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                                                                                                                                     No.
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9.92e-02;
9.92e-02;
                                                                                                                                                            B
                                                                                                                                   34e+00;
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                                                                                                                                                         Length 91;
                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                        MK14
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Claim 3: Page 14: 23pp; English.
Claim 3: Page 14: 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides (Q51735). It hybridized to all spp. of mycobacteria cross reacted to a few non-mycobacterial spp. The pr be useful as an initial screen for mycobacterial infe see also Q51735-45 and Q51747-59.
See also Q51735-45 and Q51747-59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1993;
24-MAY-1993;
26-MAY-1992;
                                       anti-S.aureus vaccines
Claim 1; Page 1287-1288; 3271pp; English.
This sequence represents one of 5191 Staphylococcus aureus DNA sequences
of the invention. The DNA sequences are recorded on a computer readable
medium, preferably selected from a floppy or hard disk, random access
memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
the S.aureus DNA sequences allows putative functions to be assigned so
that protein-encoding or regulatory regions of commercial, therapeutic or
industrial importance can be obtained. Specifically, sequences which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 93-378844/48.
New oligo:nuclectide probes detection and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V74703 standard;
V74703;
16-MAR-1999 (fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shank DD, Spears WPI; 93-378844/48.
                                                                                                                                                                         Polynucleotide(s) and proteins der stored on computer readable medium
                                                                                                                                                                                                                                   05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
EP-571911-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q51746 standard;
Q51746;
likely to encode antigens have been identified and these polypeptides be used in a vaccine composition against S.aureus infection. The molypeptides can also be used in a kit for the immunodetection of
                                                                                                                                                                                                         WPI; 97-374922/35.
                                                                                                                                                                                                                       Rosen
                                                                                                                                                                                                                                                                                 07-JAN-1997;
                                                                                                                                                                                                                                                                                                               EP-786519-A2.
                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                toxic shock syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BECT ) BECTON DICKINSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAY-1994
                                                                                                                                                                                                                                                                                               30-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aureus contig SEQ ID #392.
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 1141..1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          irst entry)
probe MK14-A
                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ds.
                                                                                                                                                                                                                                                                                                                        "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specific for Mycobacteria - used of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
18; 1
                                                                                                                                                                              derived
                                                                                                                                                                                                                                      Fannon MR, Kunsch CA,
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                                                                                                                                                                              from
used
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                                                                                                                                                                         staphylococcus aureus in the production of
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Best Local
                                                                                                               MO9810080-A1.
12-MAR-1998.
20-AUG-1997; E04755.
13-MAR-1997; EP-200744.
05-SEP-1996; EP-202444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             surgical wound infections, food poisoning, osteomyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating computer readable medium.

Sequence 2424 BP; 839 A; 302 C: 1500 poisoning, osteomyelitis, osteomythis are useful as primers or probes for isolating computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V11905 stand
V11905;
13-AUG-1998
      WPI; 98-193629/17.

P-PSDB; W59162, W59163, W59164, W59165, W59166.

Salt-inducible promoter - derived from lactic acid bacteria, used for the production of polypeptides in food Example 6; Fig 29; 111pp; English.

This sequence is a PstI-EcoRI fragment from the NS3 locus of the acid bacterium Lactococcus lactis which contains the C-terminal f
                                                                                                                                                                                                                                  CDS
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                                                                     (UNIL ) UNILEVER NV.
(UNIL ) UNILEVER PLC.
KOK J, Ledeboer AM, Sanders JW, Venema
WPI; 98-193629/17.
                                                                                                                                                                                                                                                                                      CDS
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                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                  RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                               -10_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
 full length gadR (also known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                processes; cheese production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         locus PstI/EcoRI genomic DNA e promoter; lactic acid; food
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/*tag=
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                                                                                                                                                                   /product= unknown ORF
/note= "reads in 3' t
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2069..3580
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/product= rnmb
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94.7%;
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                                                                                                                                                                                                                                                               gadC
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                                                                                                                                                                                                   (5075..5565)
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Pred. No. 1.34e+00;
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as rggL),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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gadC
C-terminal f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       food-grade inducer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                    lactic
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Best Local S
Matches 1
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Best Local
What receptor, Caenorhabditis frizzled gene 1; Cfz1 encoding a What receptor. Signal transduction; cancer; cell growth; cell proliferation; mammary tumour; oncogene; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a Staphylococcus aureus protein of unknown function: The present sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequence to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.

Sequence 517 BP; 131 A; 101 C; 75 G; 194 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T83852;
                                                                                                                                                                                               T89887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Orfx, gadB and the C-terminus of an unknown reading frame which reads in the reverse orientation. This fragment is also found to act as a salt-inducible promoter (SIP). Using this SIP, salt can be used as a food-grade inducer in food fermentation processes, e.g. in the production of cheese, dressings, water-containing spreads, sausages, or sour dough. Sequence 5565 BP; 1869 A; 771 C; 1073 G; 1852 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4783 atcgtttattaatgaag 4799
                                                                                                                                                                    T89887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aureus infection
Claim 9; Page 711; 989pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptide(s) from
to isolate antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Black MT, Burnham MK, E
Pratt JM, Reichard RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09730070-A1.
21-AUG-1997.
19-FEB-1997; U02318.
20-FEB-1996; US-011888.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; W27890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxic shock syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-1998
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                                                                                                                                                                                      standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers complement (296..424)
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94.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     compounds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus strain WCUH29 sompounds, and in vaccines against S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₿P.
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                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14; I
Pred. No. 5.
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Pred. No. 1.65e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 43;
5.52e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5565;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT
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           Claim 3; Page 7-y; ITE.

Claim 3; Page 7-y; ITE.

Claim 3; Page 7-y; ITE.

Claim 3; Page 7-y; ITE.

Claim 3; Page 7-y; ITE.

Claim 3; Page 7-y; ITE.

Claim 3; Page 7-y; ITE.

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Claim 3; Page 7-y; ITE.

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Claim 3; Page 7-y; IT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T89885-92) and are considered to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 29-30; 61pp; English.

This sequence comprises novel Caenorhabditis frizzled gene 1 (CfZ1) that encodes a putative transmembrane receptor, frizzled-1 (see W31269), a Wnt receptor (WntR). Novel frizzled family members have been identified in Drosophila, mouse, human and Caenorhabditis (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
CDS
                                                                                                                                                                                                                                                                                                       New plant expression vectors - co
from an ADP ribosylation factor g
Claim 3; Page 7-9; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-FEB-1996 (first entry)
ADP ribosylation factor gene regulatory region.
ADP ribosylation factor; promoter; ARF gene; ve
                                                                                                                                                                                                                                                                                                                                                                                                Hirota N, Ito K, WPI; 95-375210/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP-681028-A1.
08-NOV-1995.
07-APR-1995; 105287.
08-APR-1994; JP-071048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                              (SAPB ) SAPPORO BREWERIES Hirota N, Ito K, Kuroda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
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T05628 standard; DNA; 3088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nusse R, Samos CH, Wangy; WPI; 97-526631/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYJO ) UNIV JOHNS HOPKINS.
(STRD ) UNIV LELAND STANFORD
Andrew D, Bhanot P, Brink M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identification of Wnt
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11-APR-1997; U06049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9739357-A1.
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nes 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TTCATTAATGAACGATGC
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1..3027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function= ADP gene promoter region
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73.7%;
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                                                                                                                                                                                                                      factor (ARF) gene was isolated by DNA libraries prepd. from barley roots and omoter) region of the gene was identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14;
Pred. No.
0; Misma
Score 14; DB 16;
Pred. No. 5.52e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JUNIOR.
Hsieh J, Nathans
                                                                                                                                                                                                                                                                                                                                     contg. a regulating
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No. 5.52e+01;
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                                                                                                                                                              tissue-
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DAG : RESULT

10-FEB-1997

(first entry)

T43303;

standard; DNA; 1035

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RESULT OF THE PROPERTY OF THE 
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                                                                                                            Query Match
Best Local S
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02-MAR-1992.
05-JUL-1990; J76420.
05-JUL-1990; JP-176420.
(ENER-) SHIN ENERGY SANGYO.
(NENR-) NENRYOYO ALCOHOL KAIHAT.
WPI; 92-120685/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              023500 standa
023500;
023500;
26-AUG-1992
                           4523 ttaattaatgaccgatgc 4540
                                                                                                                                                                                         Disclosure; Fig. 1; 14pp; Japanese.

This is the sequence of plasmid pxlpx. The plasmid can be use transform Zymomonas cells. The transformants can be cultured express the xyla/B genes. Alcohol production from such transformants is comparable to that from yeast.
                                                                                                                                                                                                                                                                                                                             P-PSDB; R22720:
Vector for expression of heterogenes in
used for expression of xylose isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cds
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xylB; pzMlA; pyruvate decarboxylase; promoter; marker gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                 xylose and/or fructose
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    N
    TTCATTAATGAACGATGC
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                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                               7801 BP;
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= pMZlA
/note= "when included
allows replication in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /phenotype=
5414..7096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /phenotype=7361..7801
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1..219
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/note= "xylokinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= xylose_isomerase
/note= "see R22720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isomerase expression plasmid pX1PX
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                                                                                                               88.98;
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    19
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                                                                                                                                                                           lcohol production from su
to that from yeast.
A; 1910 C; 1918 G;
                                                                                                               Score 14;
Pred. No.
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Zymomonas"
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                                                                                                                                                                                                                                                                                                                               Zymomonas sp. -
for prodn. of ethanol from
                                                                                                                                      4.
                                                                                                                                 Length 7801;
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RESULTION ACCORDED TO SOLUTION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PN US5517188-A.

PN US5517188-A.

PN US551718-A.

PF 08-SEP-1992; 941523.

PF 08-SEP-1992; US-632072.

PF 08-SEP-1992; US-632072.

PR 21-DEC-1990; US-632072.

PR 21-DEC-1990; US-632072.

PR (ASUY-) ASSOC UNIVERSITIES INC.

PA (ASUY-) ASSOC UNIVERSITIES

PA (ASUY-) ASSOC UNIVERSITES

PA (ASUY-) ASS
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Best Local Similarity
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                     WPI; 96-505409/50.

Soluble recombinant forms of Borrelia lipo:proteins - useful for Vaccine prodn. for treatment of Lyme disease Example 9: Column 41-42; 49pp; English.

This sequence represents the coding sequence for a soluble recombinant Borrelia variable major protein 7 (0sp7) variant protein of the invention. Borrelia spirochetes are responsible for a variety of human disorders including Lyme borreliosis, and relapsing fevers. The spirochete is transmitted to humans and animals through the bite of a spirochete is transmitted to humans and animals through the bite of a spirochete is transmitted to humans and animals through the bite of a spirochete is transmitted to humans and animals through the bite of a spirochete is remained to the spirochete is transmitted to humans and animals through the bite of a spirochete is remained to the spirochete is transmitted to humans and animals through the bite of a spirochete is remained to the spirochete is remained to the spirochete is transmitted to humans and animals through the bite of a spirochete is remained to the spirochete is transmitted to humans and animals through the bite of a spirochete is remained to the spirochete is transmitted to humans and animals through the bite of a spirochete is remained to the spirochete is spirochete is spirochete is spirochete in the spirochete is spirochete is spirochete is spirochete is spirochete is spirochete in the spirochete is                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-1992; 941523.
21-DEC-1990; US-632072.
08-SEP-1992; US-941523.
(ASUY-) ASSOC UNIVERSITIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OspA; OspB; outer surface protein A; Borrelia; variable major protein 7; Borrelia hermsii; Vmp7; surface lipoprotein; spirochete; human; antigen; Lyme borreliosis; relapsing fever; dermatological disorder; Lyme disease; arthritic disorder; neurological disorder; vaccine; Borrelia lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barbour AG, Dunn JJ; WPI; 96-505409/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T43316 standard; DNA; 1110
T43316;
10-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinant proteins can also be used in immunoassays and other diagnostic screening methods to detect the presence of antibodies against Borrelia lipoproteins in the sera of infected pattents.

Sequence 1035 BP; 397 A; 141 C; 274 G; 223 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vmp7 soluble variant coding sequence.

OspA; OspB; outer surface protein 7;
Borrelia hermsii; Vmp7; surface lipoprotein; spirochete; human; antigen;
Lyme borreliosis; relapsing fever; dermatological disorder; Lyme disease;
arthritic disorder; neurological disorder; vaccine; Borrelia lipoprotein;
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Pred. No. 1.79e+02;
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Alterations were made to the TATA box sequence of the human and mouse GM-CSF genes (see Q55627 and Q55628, respectively) and the effects of the various alterations on gene expression were measured. Results indicated that resonances of the LFF type are most strongly affected by changes in the TATA box; it was further shown that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other pathogenic disorders in an infected host. This sequence is used to create recombinant host cells, and the encoded Vmp7 protein can be isolated from the cytosol of one of these cells without the use of detergent. The encoded recombinant proteins can be used as antigens for the production of vaccines against Lyme disease. The recombinant proteins can also be used in immunoassays and other diagnostic screening methods to detect the presence of antibodies against Borrelia lipoproteins in the sera of infected pattents.

Sequence 1110 BP; 432 A; 143 C; 286 G; 249 T;
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Q55627 standard; DNA; 1138
Q55627;
12-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       non-coding region; coding region; resonance; optimisation; promoter region; TATA box; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                   Granulocyte Macrophage Colony Stimulating Factor; GM-CSF; non-coding region; coding region; resonance; interaction;
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human GM-CSF gene.
                                                                                                                                     LFF resonances control
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22-JUN-1992; FR-0075
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Similarity 100.08;
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Pred. No. 1.79e+02;
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John F.	
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Release 3.1A John F. Collins, Biocomputing Research Unit.	
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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat Nov 27 12:42:58 1999; MasPar time 6.06 Seconds 271.193 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-09-103-287-5 (1-19) from US09103287.seq 19 1 CTTCATTAATGAACGATGC 19 GAAGTAATTACTTGCTACG

Scoring table: TABLE default Gap 10

Nmatch STD: Dbase 0; Query 0

Searched: 165359 seqs, 43243793 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: n-issued 1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1

Statistics: Mean 4.735; Variance 2.435; scale 1.945

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

uence 1, Application US/0841844A uence 1, Application US/0841844A ent No. 5773688 NERAL INFORMATION: APPLICANT: KURODA, HISAO APPLICANT: HIROTA, NAOHIKO APPLICANTON: FACTOR  NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSEE: OBLON, SPIVAR, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON STATE: VIRGINIA COUNTRY: USA APPLICATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PLOPPY disk COMPUTER: TEM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIA Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/418,444A FILING DATE: 07-APR-1995 CLASSIFICATION NUMBER: JP HEI 6-71048 FILING DATE: 08-APR-1995 CLASSIFICATION NUMBER: JP HEI 6-71048 FILING DATE: 08-APR-1995 CLASSIFICATION NUMBER: JP HEI 6-71048 FILING DATE: 03-APR-1994 ATTORNEY/AGENT INFORMATION: TELEPHONE: (703) 413-3200 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-220 TELES: 248855 OPAT UR FORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:	CC TELEFAX: (703) 4.13-22 CC TELEX: 248855 OPAT UR CC INFORMATION FOR SEQ ID NO: CC SEQUENCE CHARACTERISTICS	TE		2		CC PRIOR APPLICATION DATA:		,	CURRENT APPLI	OPERATING S			3	CC COUNTRY: USA	STATE:				NUMBER OF	ACTION OF	TITLE OF INV	APPLICANT:	APPLICANT:	APPLICANT:		Sequence 1,	Sequence 1.		
ਸੇ ਸੀ	: (703) 413-2220 248855 OPAT UR FOR SEQ ID NO: 1:	ELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-3000	V NUMBER: 24,618 CKET NUMBER: 2589-024-0	man	JP HEI	CION DATA:	: 07-APR-1995	NUMBER: US/08/418,444A		. Version #1.	IBM PC compatible	Floppy disk	ABLE FORM:	3A	VIRGINIA	JEFFERSON DAVIS HIGHW	IVAK, MCCLELLAND,	ADDRESS:		EXPRESSION REGULATING REGION	GENE EXPRESSION VECTOR USING	O, KAZUTOSHI		-	TION:				xxxxx

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                                                                               NAME/KEY: CDS
LOCATION: 3..911
SEQUENCE 913 BP; 363 A; 115 C; 223 G; 212 T; 0 OTHER
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Sequence
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SEQUENCE 3088 BP; 716 A; 761 C; 672 G; 939 T; 0 OTHER
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                     250 CATCGTACATTAATG 264
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Local Similarity 88.98;
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NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Relicuration DATA:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Frank, Glenn APPLICANT: Grieve, Rober
 CATCGTTCATTAATG 4
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                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Denver
STATE: CO
                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                               FILING DATE: 19-
CLASSIFICATION:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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VENTION: NUCLEIC ACID MOLECULES ENCODING
VENTION: PARASITIC HELMINTH PROTEINS
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                                                    .60e+01;
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LOCATION: 3..911
SEQUENCE 913 BP; 363 A; 115 C;
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 Sequence 22, Sequence 22,
                                          US-07-941-523-22 STANDARD; DNA; UNC; 1035
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                                                                                                    250 CATCGTACATTAATG 264
                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (303) 863-022 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                        18 CATCGTTCATTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tripp, Cynthia A.
APPLICANT: Frank, Glenn R.
APPLICANT: Grieve, Robert B.
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P4 PROTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, #3500
                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 80203
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                         ORGANISM: Dirofilaria immitis DEVELOPMENTAL STAGE: Larva IMMEDIATE SOURCE:
                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: 1
                                                                                                                                                                                                                  LIBRARY: L3 and/or L4 larval D. LIBRARY: expression library CLONE: p4
EATURE:
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FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                    14;
                                                                                                                                              Similarity
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T. U.S.A.
                                                                                                                                                                                                                                                                                                                                                         nucleic acid
Application US/07941523
Application US/07941523
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                     913 base pairs
                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                             Score 13; DB 2; L
Pred. No. 2.60e+01;
                                                                                                                                                                              223 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                      2618-13-1
                                                                                                                                    Mismatches
                                                                                                                                                                             212 T; 0 OTHER
                                                                                                                                                                                                                                                immitis cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
                                                                                                                                                      Length 913;
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CURRENT APPLICATION DATA:

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Best Local 9
                                                                                                                                                                    Sequence 20, Application US/07941523
Sequence 20, Application US/07941523
Patent No. 5571718
                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) SEQUENCE 1035 BP; 397 A; 141 C; 274 G; 223 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5571718
GENERAL INFORMATION:
                                                                                                                                                                                                                    US-07-941-523-20 STANDARD; DNA; UNC; 1110
                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              814 CGTTCATTAGTGAAG 828
                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         Local Similarity 93.3%;
                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,523
APPLICATION NUMBER: US/07/941,523
APPLICATION: 1920908
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 01730
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dunn, John J
APPLICANT: Barbour, Alan G
TITLE OF INVENTION: Cloning and Expression of Borrelia
TITLE OF INVENTION: Lipoproteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                    APPLICANT: Dunn, John J
APPLICANT: Barbour, Alan G
TITLE OF INVENTION: Cloning and Expression of Borrelia
TITLE OF INVENTION: Lipoproteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BNL90-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                              COUNTRY: U.S.A. ZIP: 01730
                                                               STREET: Two Militia I CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1035 base pairs
TYPE: NUCLEIC ACID
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                                                                                             ADDRESSEE:
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Two Militia Drive
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Pred. No. 2.60e+01;
0; Mismatches 1
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Best Local Similarity 93.3%;
Matches 14; Conservative
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INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 1110 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: 11near
MOLECULE TYPE: DNA (genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application Sequence 1, Application Patent No. 5441736
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SEQUENCE 1110 BP; 432 A; 143 C; 286 G; 249 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XXXXX
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                                                         TELEFAX: (415) 327-323
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 CGTTCATTAATGAAG 1
                                                                                        REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19921105
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GERLACH, GERALD F.
APPLICANT: WILLSON, PHILIP J.
APPLICANT: ROSSI-CAMPOS, AMAL
APPLICANT: POTTER, ANDREW A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: BN TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ACTINOBACILLUS PLEUROPNEUMONIAE OUTER TITLE OF INVENTION: MEMBRANE LIPOPROTEIN A AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 199209 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
            TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: ROBERTA L. ROBINS STREET: 635 BRYANT STREET
STRANDEDNESS:
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                                      1340 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNITED STATES OF AMERICA
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US/07971558
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Pred. No. 2.60e+01;
0; Mismatches 1
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linear

Best Local Similarity 88.2%; Matches 15; Conservative

Pred. No. 2.60e+01; 0; Mismatches 2;

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Query Match
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                   NAME/KEY: CDS
LOCATION: 169..1530
SEQUENCE 1675 BP; 417 A; 329 C; 375 G; 554 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 158..1252
SEQUENCE 1340 BP; 502 A; 183 C; 265 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application PC/TUS9210284
Sequence 12, Application PC/TUS9210284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US92-10284-12 STANDARD; DNA; UNC; 1675
                                                                                                                                                                                                         FILING DATE: 4 DECEMBER 1991
ATTORNEY/AGENT INFORMATION:
NAME: Floyd, Linda A.
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEPHONE: (302) 892-7949
                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Local Similarity 93.3%;
les 14; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                          MOLECULE TYPE: CU
                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1675 base pair
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION TO DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Browse, John, Kinney, Anthony J., APPLICANT: Pierce, John, Wierzbicki, Anna M., APPLICANT: Yadav, Narendra S., Perez-Grau, Luis TITLE OF INVENTION: Fatty Acid Desaturase Genes TITLE OF INVENTION: from Plants
NUMBER OF SEQUENCES: 32
                                                      FEATURE:
                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                      ORGANISM:
                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                    TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: POFILING DATE: 19921203
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                  835420
                                                                 pSFD-118bwp
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                                                                                                                                                              1675 base pairs
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1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                   Glycine max
                                                                                                                                 linear
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 68.4%;
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 Score 13;
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No. 2.60e+01;
DB 4;
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Length 1675;
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Sequence 1, Application PC/TUS9516930

C GENERAL INFORMATION:
C APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL TITLE OF INVENTION: HETEROLOGOUS POLYPETTIDE
C TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF TITLE OF INVENTION: NONSENSE-MEDIATED MRNA DECAY
C TITLE OF INVENTION: FUNCTION
C NUMBER OF SEQUENCES: 6
C CORRESPONDENCE ADDRESS:
C ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                               Matches
Sequence 1, Application US/08375300
Sequence 1, Application US/08375300
Patent No. 5679566
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PATENTIA Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/16930

FILING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/375,300

FILING DATE: 20-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Fasse, J. Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1639 ATCCTTCATTAATAAAG 1655
                                                                          T 9
US-08-375-300-1 STANDARD;
                                                                                                                                                                                                                               MOLECULE TYPE: DNA SEQUENCE 4080 BP; 1449 A; 645 C; 801 G; 1185 T; 0 OTHER.
                                                                XXXXXX
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                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4080 base pair
                                                                                                                                                                     68.48;
Local Similarity 88.28;
hes 15; Conservation
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                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
TELEFAX: (617)542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                        TOPOLOGY: 1in
                                                                                                                                                                                                                                                                                                                                  TELEX: 200154
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                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                  single
                                                                            DNA;
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                                                                                                                                                                                          Score 13; DB 4;
Pred. No. 2.60e+01
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                                                                                                                                                                              Mismatches
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                             Sequence 12, Application Sequence 12, Application
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                                                                                                                                                                                                                                                              XXXXX
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 4080 BP; 1449 A; 645 C;
                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                      635
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INFORMATION FOR SEQ ID NO:
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SOFTWARE: Patent....
CURRENT APPLICATION NUMBER: US/08/375,300
APPLICATION NUMBER: US/08/375,300
APPLICATE: 20-JAN-1995
                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fasse, J. P.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
TOPOLOGY: lim
MOLECULE TYPE:
                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                   TITLE OF INVENTION: TUTITLE OF INVENTION: RENUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Feng, He
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED mRNA DECAY FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                           STREET:
CITY: N
STATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
            COMPUTER: IBM PS
OPERATING SYSTEM:
                                                       COUNTRY: U
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ZIP: 02110-2804
                                                                                                            ADDRESSEE:
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15; Conse
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                                                                                      New York City
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llarity 88.2%;
Conservative
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                                                                            New York
                                                                                                 E: Felfe & Lynch
805 Third Avenue
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                                                                                                                                                   Brichard, Vincent; Van Pel, Aline;
Traversari, Catia; W lfel, Thomas; Coulie, Pierre;
Boon-Falleur, Thierry; De Plaen, Etienne
VENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
VENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (617)542-8906
                                                                 USA
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    Wordperfect
                       IBM PS/2
                                 Diskette, 5.25
                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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              PC-DOS
                                                                                                                                REJECTION ANTIGEN PRESENTED BY HLA-A2
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US/08370319C
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2.60e+01;
2.7 2;
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                                  360 kb storage
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Best Local :
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OTHER INFORMATION: 0
OTHER INFORMATION: 1
SEQUENCE 4129 BP; 1300 A;
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                                                                                                                                                                                                                                                                                                               Sequence 54,
Sequence 54,
                                                                                                                                                                                                                                                                                                                                                XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 838-388
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4129 base pair:
                                                                                                                                                                                                                                                                                                       GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     17 ATCGTTCATTAATGA 3
                                                                                                 ZIP: 19400-2.7.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
APPLICATION NUMBER: US 14
FILING DATE: 05-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                    SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      TITLE OF INVENTION: Vaccinal Polypeptides NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                    APPLICANT: Scott, Miller APPLICANT: Dillon, Susan B
                                                                                                                                                                                                                                                                                           APPLICANT: Shatzman, Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/2
FILING DATE: 8-JULY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                              STATE: F
                                                                                             OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                   STREET: U.S. Mailcode CITY: King of Prussia
                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                 FILING DATE:
                                                                           APPLICATION NUMBER:
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Application
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· 827 C; 728 G; 1273 T; 1
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PC/TUS9401149
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  US 013,415
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                                                                                                                                                                                                                                  1041 GCATCGTTCATTCAT 1055
                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 1879..2790
SEQUENCE 7616 BP; 1913 A; 1926 C; 1936 G; 1841 T; 0 OTHER
                                                                                                                                                                                    XXXXXX
                                                                                                                                                                                           T 12
US-08-441-591-60
                                                                                                    GENERAL INFORMATION:
APPLICANT: NIEUWLANDT, D., GOLD, I
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTII
TITLE OF INVENTION: TO THE TACHYK:
TITLE OF INVENTION: SUBSTANCE P
                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          19 GCATCGTTCATTAAT
       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.
COMPUTER: IBM compatible
COMPUTER: MS-DOS
                                                                                                                                                                                                                                                                                                                    LENGTH: 7616 base pairs
TYPE: nucleic acid
STRANUBLES: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 645,732 FILING DATE: 30-AUG-1984 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 2: FILING DATE: 02-NOV-1988 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 837,773 FILING DATE: 18-FEB-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 215-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 01-FEB-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 18-AUG-
                                                                                      CORRESPONDENCE ADDRESS:
                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 28-JUL-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                              CITY: Englewood
                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 30-AUC
                                         ZIP: 80111
                                                COUNTRY:
                                                         STATE:
                                                                       STREET:
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                                                                              ADDRESSEE:
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                                                        Colorado
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                                                                       8400 E.
                                                USA
 WordPerfect 5.1
                                                                      Swanson & Bratschun, L.L.C.
                                                                                                                                                                                           STANDARD; DNA;
                                                                                                                                                                                                                                                               68.4%;
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30-AUG-1991
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TO THE TACHYKININ
SUBSTANCE P
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Pred. No. 2.60e+01
0; Mismatches
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Best Local Similarity 37.5%;
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NAME: BAITY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: WEX2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-333
TELEPAX: (303) 793-2433
INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08418071
Sequence 1, Application US/08418071
Patent No. 5846705
                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-418-071-1.STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear SEQUENCE 47 BP; 10 A; 10 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                           XXXXXX
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.0
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APPLICANT: You, Li-Ru
APPLICANT: You, Li-Ru
APPLICANT: .Soong, Tai-Seng
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF TWO CIRCULAR SSDNA
TITLE OF INVENTION: ASSOCIATED WITH BANANA BUNCHY TOP VIRUS AN
TITLE OF INVENTION: BANANA BUNCHY TOP VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/714,1
FILING DATE: 10-JUNE 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,4
FILING DATE: 17-AUGUST-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11-JUNE-1990
PRIOR APPLICATION UDATA:
APPLICATION UDABER: 07/964,6:
FILING DATE: 21-OCTOBER-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/117,99 FILING DATE: 8-SEPTEMBER 1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                            ZIP:
                                                                                                         STATE: New York COUNTRY: United States
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                                                                                                                                                                                    ADDRESSEE:
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251 Avenue of the
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8; 1
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Pred. No. 9.75e+01
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Best Local S
Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Approximately Sequence 1, Approximately No. 572331
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08385187A Sequence 1, Application US/08385187A
                                                                                                                                                                                                                                                                                                                                                                                                                                                      XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-385-187A-1 STANDARD; DNA; UNC; 485 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 TCATTAATGAAG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 596-9090 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 63.2%;
Local Similarity 100.0%;
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 TCATTAATGAAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 287 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                APPLICATION NUMBER: US/08/385,187A FILING DATE: 07-Feb-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/US94/09089 FILING DATE: 10-AUG-1994 PRIOR APPLICATION DATE: 10-AUG-1994
                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                     TITLE OF INVENTION: AQUITITLE OF INVENTION: POLYNOMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: subgenomic DNA DESCRIPTION: /desc= "clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                       APPLICANT: Ogez, John APPLICANT: Reifsnyder, David
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hart, Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: DCB-1
          APPLICATION NUMBER: 08/110663 FILING DATE: 20-AUG-1993
                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Haley Jr., James REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/418,071 FILING DATE: 06-APR-1995
                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                   T: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                                        California
                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                          Builder, Stuart
                                                                                                                                                                                                                                                               Genentech, Inc.
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                                                                                                                                                                       3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-1995
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                                                                                                                                                                                                                                                                                       Polypeptide
9
                                                                                                                                                                                                                                                                                                              Aqueous Multiple-Phase Isolation
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Pred. No. 9.75e+01;
0; Mismatches (
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Query Match
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Matches 14; Conserv
                                           TOPOLOGY: linear SEQUENCE 485 BP; 117 A; 113
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Sequence 13, Application US/08240121
Patent No. 5487980
GENERAL INFORMATION:
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                                                                                                                                               APPLICATION NUMBER: 07/989844
FILING DATE: 23-NO. 5487980-1992.
ATTORNEY/AGENT INFORMATION:
NAME: HASAK, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 811D1
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 GCATCGTTGATGAATG 401
                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 GCATCGTTCATTAATG 4
                                                                                                                                                                                                                                                                                            SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
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LENGTH: 485 base pairs
TYPE: Nucleic Acid
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                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 485 bases
                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Method for Producing Polypeptide via Bacterial Fermentat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Swartz,
                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                           TELEFAX: 415/952-98
TELEX: 910/371-7168
                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/240,121 FILING DATE: 09-May-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                             COMPUTER: - IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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            63.2%;
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                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
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                                             C; 114 G;
          Score 12; DB 1;
Pred. No. 9.75e+01
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Pred. No. 9.75e+01
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                                             141 T; 0 OTHER
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                     Length 485
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Conservative

0;

Mismatches

Indels

0;

Gaps

0; \*

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MPsrch\_ntp n.a. n.a. Smith-Waterman search, using a protein database which has been backtranslated into n.a. using IUPAC symbols

Tabular output not generated. Run on: Wed Nov 24 02:29:41 1999; MasPar time 6.89 Seconds 663.259 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-09-103-287-5 (1-19) from US09103287.seq 95

1 CTTCATTAATGAACGATGC 19 GAAGTAATTACTTGCTACG

Scoring table: TABLE bktranslate2 Gap 40

Searched: Nmatch STD: Dbase 0; Query 0

122810 seqs, 120205779 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60
1:pir1 2:pir2 3:pir3 4:pir4

Mean 39.468; Variance 52.493; scale 0.752

Statistics:

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	n	a a	Re
14 16 17 18	110 113 113	27654221	Result
71 71 70 70 70	71177	76 776 772 772	Score
74.7 74.7 74.7 73.7 73.7 73.7	74.7 74.7 74.7 74.7	80.0 80.0 80.0 80.0 75.8 74.7	% Query Match
701 785 1030 148 180 308	162 213 244 293	421 496 592 1211 398 1113 1123 147	Length
212222	000001	งผมผมผม	DB
S51403 S46672 I39987 B43663 WZBE64 F64901	H70212 S29910 I40172 C71703 S73624	H70607 S16901 D64044 S65799 F64456 S28925 S73078	ID
probable membrane pro hypothetical protein lantiblotic subtilin host-inducible protei gene 64 protein - hum ABC-type transport pr	DD , DD:	hypothetical protein aromatase (EC 1.14.14 hypothetical protein chromosome scaffold phypothetical protein nuclear pore complex hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	Description
3.64e+01 3.64e+01 3.64e+01 5.22e+01 5.22e+01 5.22e+01	3.64e+01 3.64e+01 3.64e+01 3.64e+01 3.64e+01	5.60e+00 5.60e+00 5.60e+00 5.60e+00 2.53e+01 2.53e+01 3.64e+01	Pred. No.

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2 TTCATTAATGAACGATGC 19

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70.5	70.5	70.5	70.5	70:5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	71.6	73.7	73.7	73.7	73.7	73.7	73.7	73.7
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S57908	RRVUBY	S05603	RRXRBT	S73786	JH0266	S28857	S23416	E71403	D71631	S26873	A24872	S47527	JC2520	S40738	S56407	н70196	PN0013	S74698	JQ1661	JQ1662	S12319	A48440	E71660	H65214	A48457
hypothetical polyprot	genome polyprotein -	major merozoite surfa	RNA-directed RNA poly	hypothetical protein	glutamate receptor de	glutamate receptor de		protein	hypothetical protein	RNA pol	hypothetical protein	extracellular sucrase	beta-fructofuranosida	hypothetical protein	hypothetical 25.3K pr	adenine phosphoribosy	myosin heavy chain, n	UDP-glucose dehydroge	genome polyprotein .	genome polyprotein -	pre-mRNA splicing fac	ring-infected erythro	hypothetical protein	hypothetical 60.5 kD	EC 2.7
	1.49e+02			1.49e+02	1.49e+02	1.49e+02	٠	1.49e+02	1.49e+02	1.49e+02	1.49e+02	1.49e+02	1.49e+02	1.49e+02	1.49e+02	1.49e+02	1.49e+02		•	5.22e+01	5.22e+01	5.22e+01	5.22e+01	5.22e+01	5.22e+01

# ALIGNMENTS

Db F I Dt 1045 TTYAT	Query Match Best Local Similarity Matches 11; Conse	GENETICS #gene SUMMARY	##residues ##cross-referenc ##experimental_:	##status	#accession	#title	#journal				#authors	REFERENCE	DATE	ORGANISM	ENTRY	RESILT 1
FINEQC TTYATHAAYGARCARTGY 1062	80.0%; Score 76; DB 2; Length 421; Similarity 61.1%; Pred. No. 5.60e+00; 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;	Rv1194c #length 421 #molecular-weight 46097 #checksum 2032	##residues 1-421 ##label COL ##cross-references GB:293777; GB:AL123456; NID:g3261726; PID:e311071; ##cxperimental_source strain H37Rv	preliminary; nucleic acid sequence not shown; translation not shown	H70607	#title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. #cross-references MITTP-08295587	Taylor, K.; Whitehead, S.; Barrell, B.G. Nature (1998) 393:537-544	Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Squares, R.; Sulston, J.E.;	Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;	C.; Harris, D.; Gordon, S.V.; Elgimeler, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingmorth T. Concer B. Davide B. Doulin V.	Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,	A70500	17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change	(Strain H3/KV) #formal_name Mycobacterium tuberculosis	H70607 #type complete hypothetical protein Rv1194c - Mycobacterium tuberculosis	

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ACCESSIONS
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DATE
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ENTRY
TITLE
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1071 YTTYATHAAYGARWSNTGY 1089

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1 CTTCATTAATGAACGATGC 19

FINER C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436
                                                                #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors
                                                                                    #cross-references
##molecule_type DNA
##residues 1-592 ##label TIGR
                                            ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 80.0%;
Similarity 52.6%;
                                                                                                 Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman,
J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
Science (1995) 269:496-512
Whole-genome random sequencing and assembly of Haemophilus
                                                         nces MUID:95350630
D64044
                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Haemophilus influenzae
18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
18-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #length 496 #molecular-weight 56663 #checksum 3858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromoprotein; heme; iron; microsome; monooxygenase;
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                                                                                                                                                                                                                                                                                                                                                             Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D64044 #type complete
hypothetical protein HI0036 - Haemophilus influenzae (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily human cytochrome P450 CYP19; cytochrome
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13-Jan-1995 #sequence_revision 13-Jan-1995 #text_chango
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                                          nucleic acid sequence not shown; translation not shown
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
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424-431
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##residues 1-1211 ##label HOL
##cross-references EMBL:U40146; NID:g1103892; PID:g1103893
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CTTCATTAATGAACGAT 17
F I N E R
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Similarity 52.9%;
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Similarity 52.9%;
9; Conservative
                 Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C. Science (1996) 273:1058-1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565799 #type complete chromosome scaffold protein sudA - Emericella nidulans #formal_name Emericella nidulans, Aspergillus nidulans 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Sep-1998
Complete genome sequence of the methanogenic archaeon
                                                                                                                                                                                                                                                                                                             hypothetical protein MJ1255 - Methanococcus jannaschii
#formal_name Methanococcus jannaschii
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                           F64456
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#length 1211 #molecular-weight 138958 #
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Genetics (1996) 142:777-787
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#region nucleotide-binding motif A (P-loop)
#length 592 #molecular-weight 67903 #checksum 1875
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Pred. No. 5.60e+00
7; Mismatches
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Pred. No. 5.60e+00;
7; Mismatches 1
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KEYWORDS nuc:
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                                                                                               SUMMARY
                            Query Match 75.8%;
Best Local Similarity 55.6%;
Matches 10; Conservative
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##residues 1-25, A',27-535, G',537-719, P',721-1017, Y',1019-1022,

##residues 'Y',1024-1113 ##label WEN

##cross-references EMBL:Z15036; NID:g4075; PID:g4076

##note sequence extracted from NCBI backbone (NCBIP:117132)
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#accession $52896
##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                        #authors Wente, S.R.; Rout, M.P.; Blobel, G.
#journal J. Cell Biol. (1992) 119:705-723
#title A new family of yeast nuclear pore complex
#cross-references MUID:93054906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #title
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                                                                                                                                                                                                                                                                          #authors
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                                                                                                                                            ##cross-references SGD:S0004650; MIPS:YMR047c
                                                                                                                                                                                         ##residues 1-1113 ##label ODE
##cross-references EMBL: 248502; NID: g695715;
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##cross-references EMBL:X68108; NID:g4052; PID:g4053
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##residues 1-39
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Similarity 58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wimmer, C.; Doye, V.; Grandi, P.; Nehrbass, U.; Hurt, E.C EMBO J. (1992) 11:5051-5061
A new subclass of nucleoporins that functionally interact with nuclear pore protein NSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleoporin NSP116; protein YM9532.12c; protein YMR047c
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cerevisiae)
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                                                                                            #length 1113 #molecular-weight 116234 #checksum
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  translation not shown
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Pred. No.
6; Misma
                            Score 72; DB 2;
Pred. No. 2.53e+01
6; Mismatches
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No. 2.53e+01
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 Query Match
Best Local S
Matches 1
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Best Local Similarity 63.2%;
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#cross-references MUID:97055432
#accession $73078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #journal
#title
                                                                                                                                                                                                                         #authors Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov, Mitchell, W.P.; Olinger, L.; Tatusov, F. Koonin, E.V.; Davis, R.W.

#journal Science (1998) 282:754-759
#title Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.
                                                                                      #gene
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##cross-references GB:AE001282; GB:AE001273; NID:g3328466; PID:g3328474
##experimental_source serotype D, strain UW-3/Cx
                                                                                                                                                      ##molecule_type DNA
##residues
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h 74.7%;
Similarity 61.1%;
11; Conservative
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hypothetical protein CT079 - Chlamydia trachomatis (sero
D, strain UW3/Cx)
#formal_name Chlamydia trachomatis
13-Sep 1998 #sequence_revision 13-Sep-1998 #text_change
21-Nov-1998
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C.C.Y.; Liu, Q.Y.; Penny, S.L.; Young, F.; Schenk, M.E.;
Gaasterland, T.; Doolittle, W.F.; Ragan, M.A.; Charlebois,
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#length 147 #molecular-weight 17134 #checksum
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Mol. Microbiol.
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Score 71; DB 2; I
Pred. No. 3.64e+01;
5; Mismatches 2
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#cross-references MUID:98065943
                                                      ##status ##molecule_type DNA ##label AME 1-213 ##label AME ##rosidues 1-213 ##label AME ##cross-references EMBL:X57318; NID:g62239; PID:g62243 ##cross-references EMBL:X57318; with the contraction of the 
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##cross references GB:AE000799; NID:g2690224; PID:g2690279;
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                           Y Match 74.78;
Local Similarity 60.08;
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Similarity 55.68;
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S29907
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#length 162 #molecular-weight 19294
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13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change
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11 protein BBA48 - Lyme disease spirochete plasmid
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Score 71; DB 2; L
Pred. No. 3.64e+01;
6; Mismatches 0
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Pred. No. 3.64e+01;
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499 TTYATHAARGARMGNTGY 516
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2 TTCATTAATGAACGATGC 19
F I N E R C
                                                              #residues 1-293 ##label AND ##cross-references GB:AJ235271; GB:AJ235269; PID:g3861001
                                                                                         ##molecule_type DNA
##residues 1-29
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1 CTTCATTAATGAACG 15
                                               ##experimental_source strain
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#length 293
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                                                                                                                                                                         The genome sequence of Rickettsia of mitochondria.
                                                                                                                                                                                                                                       Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.C.M.; Podowski, R.M.; Naeslund, A.K.; Eriksson, A.S.; Winkler, H.H.; Kurland,
                                                                                                                                                                                                                                                                                                                                C71703 #type complete
hypothetical protein RP444 - Rickettsia prowazekii
#formal_name Rickettsia prowazekii
21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change
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orotidine-5'-phosphate decarboxylase homology
carbon-carbon lyase; carboxy-lyase
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orotidine-5'-phosphate decarboxylase
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12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
_05-Jun-1998
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translation not shown
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#molecular-weight 33724
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Pred. No. 3.64e+01;
viematches 2;
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8; NID:g312439;
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                                                                              NID:g3860788; PID:e1342745;
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Best Local Similarity 63.2%;
Matches 12; Conservative
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Nucleic Acids Res. (1996) 24:4420-4449

#title Complete sequence analysis of the genome of

Mycoplasma pneumoniae.

#cross-references_MUID:97105885
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#description
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                                                    map_position
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##rosidues 1-664 ##label HIM
##rcsidues 1-664 ##label HIM
##cross-references EMBL:AE000027; GB:U00089; NID:g1673941; PID:g1673969
##cross-references EMBL:AE000027; GB:U00089; NID:g1673941; PID:g1673969
##note the nucleotide sequence was submitted to the EMBL Data
Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
#residues 1-701 ##label MIL
#cross-references EMBL:U17244; NID:g577171; PID:g577184;
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Similarity 55.6%;
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                                                                                                                                                                                                   S51403
S51395
                                                                                                                                                                                                                              hypothetical protein L8479.13
#formal_name Saccharomyces cerevisiae
05-May-1995 #sequence_revision 12-May-1995
12-Dec-1997
*superfamily unassigned GAL4-type zinc cluster zinc binuclear cluster homology transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein M366 homolog G12_orf664 - Mycoplasma pneumoniae (ATCC 29342) (SGC3) #formal_name Mycoplasma pneumoniae ATCC 29342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #superfamily Mycoplasma genitalium hypothetical protein MG366
#length 664 #molecular-weight 76769 #checksum 452
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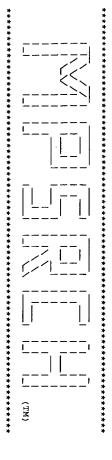
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930 YYTNATHAAYGARYTNTGY 948
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Similarity 47.4%;
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                                                                                                                                                                                                                                                                                                                                               hypothetical protein H9186.3
#formal_name Saccharomyces cerevisiae
28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change
12-Dec-1997
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hypothetical protein YHR182w -
cerevisiae)
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#domain transmembrane #status predicted #label TM1\
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Pred. No. 3.64e+01
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MPsrch\_ntp  $\ensuremath{\text{n.a.}}$  -  $\ensuremath{\text{n.a.}}$  -  $\ensuremath{\text{m.a.}}$  -  $\ensuremath{\text{m.a.}$ 

Tabular output not generated. Run on: Wed Nov 24 02:32:46 1999; MasPar time 4.78 Seconds 674.763 Million cell updates/sec

Perfect Score: N.A. Sequence: Description: >US-09-103-287-5 (1-19) from US09103287.seq 95

1 CTTCATTAATGAACGATGC 19 GAAGTAATTACTTGCTACG

Scoring table: TABLE bktranslate2 Gap 40

Nmatch STD : Dbase 0; Query 0

Searched: 77977 seqs, 84804879 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37

1:swissprot

Statistics: Mean 40.305; Variance 47.014; scale 0.857

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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RRP2_IAZII RRP2_IAZIF RRP2_IAZIF RRP2_IAZIF YHY2_YEASI SPAB_BACSU RPOB_GUITH NOLJ_RHIFR MS10_VZVD YDDO_ECOLI HXK_PLAFA YJCE_ECOLI PR06_YEAST	ATI2_VACCV DCOP_BACCL RPA3_SCHPO DHA4_HUMAN NU5M_RHIST	Y036_HAEIN MURC_STAAU N116_YEAST	ID
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# ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).  EMBL; U32689; G1572982;	"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."; SCIENCE 269:496-512(1995)i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE (POTENTIAL)i- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). STRONG, TO H. INFLUENZAE HI1467 AND M.TUBERCULOSIS MTCY1A11.24C.	SEQUENCE FROM N.A.  STRAIN-RD / KW20;  MEDLINE; 95350630.  MEDLINE; 95350630.  FLEISCHHANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,  KERLAVAGE A.R., BULT C.J., TOMB JF., DOUGHERTY B.A., MERRICK J.M.,  MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,  SCOTT J.D., SHIRLEY R., LIU LI., GLODEK A., KELLEY J.M.,  WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,  UTTERBACK T.R., HANNA M.C., MGUYEN D.T., SAUDEK D.M., BRANDON R.C.,  FINE L.D., ERITCHHAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,  GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,	TT 1  Y036_HABIN STANDARD; PRT; 592 AA.  Q57335; 005006;  Q1-NOV-1997 (REL. 35, CREATED)  Q1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)  Q1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  HAVOTHETICAL AGC TRANSPORTER ATP-BINDING PROTEIN HI0036.  HAEMOPHILUS INFLUENZAE.  BACTERTA; PROTEOBACTERTA; GAMMA SUBDIVISION; PASTEURELLACEAE;  HAEMOPHILUS.  [11]

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INNER MEMBRANE
TRANSMEM 58
TRANSMEM 102
TRANSMEM 191
TRANSMEM 214
TRANSMEM 299
                                                                  1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
LOWE A.M., DERESIEWICZ R.L.;
SUBMITTED (NOV-1997) TO EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O31211;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LICASE (EC 6.3.2.)
ACETYLMURANOYL-L-ALANINE SYNTHETASE).
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                          A S L I N GCNWSNYTNATHAAYGARG
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CTTCATTAATGAACGAT 17
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                                                                  1195
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Pred. No. 1.72e+00;
7; Mismatches 1
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No. 9.13e+00;
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EMBL; X68108; G4053; -.
EMBL; Z48502; G695727; -.
PIR; S28537; S28537.
PIR; S28925; S28925.
PIR; A44402; A44402.
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ODELL C., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: ESSENTIAL COMPONENT OF NUCLEAR PORE COMPLEX
NUCLEOPORINS MAY BE INVOLVED IN BOTH BINDING AND TRANS
THE PROTEINS DURING NUCLEOCYTOPLASMIC TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (REL. 26, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NUCLEOPORIN NUP116/NSP116 (NUCLEAR PORE PROTEIN
NUP116 OR NSP116 OR YMR047C OR YM9532.12C.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N116_YEAST
Q02630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=S288C / AB972;
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MEDLINE; 93099880.

WIMMER C., DOYE V., GRANDI P., NEHRBASS U., HURT E.C.;

"A new subclass of nucleoporins that functionally interact nuclear pore protein NSPI.";

EMBO J. 11:5051-5061(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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WENTE S.R., ROUT M.P., BLOBEL G.;
"A new family of yeast nuclear pore
J. CELL BIOL. 119:705-723(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEAR PROTEIN;
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                           19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: INTERACTS WITH KAP95.
SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX.
DOMAIN: CONTAINS G-L-F-G REPEARS.
SIMILARITY: BELONGS TO THE GLFG FAMILY OF NUCLEOPORINS.
GCATCGTTCATTAATGAA 2
A S F I N E
                                             A S F I N E GCNWSNTTYATHAAYGAR 2904
                                                                                                                                                                       Similarity
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37 X A APPROXIMATE R

G-L-F-G.
G-> A (IN REF. 1).
S-> G (IN REF. 1).
S-> Y (IN REF. 1).
S-> Y (IN REF. 1).
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MBL outstation -
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p46535;
01-NOV-1995 (REL. 32, CR
01-NOV-1995 (REL. 32, LA
01-NOV-1997 (REL. 35, LA
OROTIDINE 5'-PHOSPHATE D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 91310644.

AMEGADZIE B.Y., ANN B.-Y., MOSS B.;

AMEGADZIE B.Y., ANN B.-Y., MOSS B.;

"Identification, sequence, and expression of the gene encoding a Mr
35,000 subunit of the vaccinia virus DNA-dependent RNA polymerase.";

J. BIOL. CHEM. 266:13712-13718(1991).

-i- FUNCTION: MATURE VIRUSES ARE OCCLUDED INTO THE ATI, AND IT HAS
BEEN ASSUMED THAT SUCH BODIES PROTECT THE VIRUS DURING

DISSEMINATION FROM ANIMAL TO ANIMAL.

-i- A CHARACTERISTIC FEATURE OF ATI IS THE FORMATION OF LARGE MASSES

WITH NO SURROUNDING MEMBRANES IN THE CYTOPLASM OF INFECTED CELLS

WITH NO SURROUNDING MEMBRANES IN THE CYTOPLASM OF INFECTED CELLS

-i- SIMILARITY: TO COMPOX VIRUS A-TYPE INCLUSION PROTEIN C-TERMINUS.
                         GHIM S.Y., NIELSEN P., NEUHARD J.;
"Molecular characterization of pyrimidine biosynthesis of thermophile Bacillus caldolyticus.";
MICROBIOLOGY 140:479-491(1994).
-!- CATALYTIC ACTIVITY: OROTIDINE-5-PHOSPHATE - UMP + CONTACT ACTIVITY OROTIDINE-5-STRUMAY: SIXTH AND LAST STEP IN THE BIOSYNTHESIS OF -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P24758;

D1-MAR-1992 (REL. 21, CREATED)

O1-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)

O1-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)

PUTATIVE A-TYPE INCLUSION PROTEIN (PROTEIN A26).

VACCINIA VIRUS (STRAIN WR).

VIRUSES; DSDNA VIRUSES, NO RNA STAGE; POXVIRIDAE; CHORDOPOXVIRINAE;
   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M61187; G335786; -.
EMBL; X57318; G62243; -.
PIR; S29910; S29910.
SEQUENCE 213 AA; 25037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORTHOPOXVIRUS [1]
                                                                                                                                                                                                                               BACILLUS CALDOLYTICUS BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                       MEDLINE;
                                                                                                                                                                    STRAIN-DSM 405;
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             DECARBOXYLASE).
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Pred. No. 1.37e+01
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15-DEC-1998
                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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15-DEC-1998
                                                               entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                              OLIVER K., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WOOD V.; SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                        SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPA3
                         EMBL; Z99165; E1132708; -. TRANSFERASE; DNA-DIRECTED
                                                                                                                                                                                                                                                -!- SUBUNIT: RNA POLYMERASE I CONSISTS OF 14 DIFFERENT SUBUNITS
                                                                                                                                                                                                                                                                            RIBOSOMAL DNA UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRIMIDINE BIOSYNTHESIS; LYASE; DECARBOXYLASE ACT_SITE 61 61 BY SIMILARITY. SEQUENCE 244 AA; 26579 MW; 2188344B CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00156; OMPDECA PFAM; PF00215; OMPdecase;
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                                                                                                                                                                                                                                                                                                                                                                       STRAIN-972;
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THREE DISTINCT ZINC-CONTAINING RNA POLYMERASE ARE FOUND IN
EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR,
POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR 5S
                                                                                                                                                                                                                                                                                                    OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES SUBSTRATES. RNA POLYMERASE A IS ESSENTIALLY USED TO TRANSCRI
                                                                                                                                                                       AND TRNA GENES.
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larity 61.1%;
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CTED RNA POLYMERASE I 49 KD
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Pred. No.
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1.37e+01;
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01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-THE SECONDAID DEHYDROGENASE (EC 1.2.1.3) (ALDEHYDE DEHYDROGENASE, MICROSOMAL) (CLASS 3).
ALDH10 OR FALDH.
                                 <del>:</del>
                                                                                                                                                                       ---
                                                                                                                                                                                                                                               patients with Sjogren-Larsson syndrome.";
HUM. MUTAT. 12:377-384(1998).
-i- FUNCTION: CATALYZES THE OXIDATION OF LONG-CHAIN ALIPHATIC
ALDEHYDES TO FATTY ACIDS. ACTIVE ON A VARIETY OF SATURATED
                                                                                                                                                                                                                                                                                                        SILLEN A., ANTON-LAMPRECHT I., BRAUN-QUENTIN C., SAYLI B.S., AYUSO C., JAGELL S., KUESTER W., WADD "Spectrum of mutations and sequence variants in the sequence variants in the sequence variants."
                                                                                                                                                                                                                                                                                                                                                       VARIANTS SLS R-106; W-226; S-315; L-365; R-412, MEDLINE; 99045371.
                                                                                                                                                                                                                                                                                                                                                                                                  SILLEN A., JAGELL S., WADELIUS C.;
"A missense mutation in the FALDH gene syndrome patients originating from the HUM. GENET. 100:201-203(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue-dependent expression."; GENOMICS 40:80-85(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. ROGERS G.R., MARKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aldehyde
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
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                          DISEASE: DEFECTS IN FALDH ARE THE CAUSE OF SJOEGREN-LARSSON SYNDROME (SLS). SLS IS AN AUTOSOMAL RECESSIVE NEUROCUTANEOUS DISORDER CHARACTERIZED BY A COMBINATION OF SEVERE MENTAL RETARDATION, SPASTIC DI- OR TETRAPLEGIA AND CONGENITAL ICHTHYOSIS (INCREASED KERATINIZATION). ICHTHYOSIS IS USUALLY EVIDENT AT BIRTH, NEUROLOGIC SYMPTOMES APPEAR IN THE FIRST OR SECOND YEAR OF LIFE. MOST PATIENTS HAVE AN IQ LESS THAN 60. ADDITIONAL CLINICAL FEATURES INCLUDE GLISTENING WHITE SPOTS ON THE RETINA, SEIZURES, SHORT STATURE AND SPEECH DEFECTS.
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TOATTAATGAACGAT 17
F I N E R
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ET. 12:52-57(1996).
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WARKOVA TO EMBL/GENBANK/DDBJ DATA BANKS.
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MARKOVA N., RIZZO W.B.;
caused by mutations in the fatty
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produced through a collaboration
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of Sweden.";
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 RHIZOPUS
          ND5 OR NAD5
                  NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).
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(RHIZOPUS NIGRICANS)
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S -> L (IN SLS).

S -> L (IN SLS).

AEYY -> KYQAVLRRK

AEYY -> KYQAVLRRK
                                                                                                                                                  Score 71; DB 1;
Pred. No. 1.37e+01
6; Mismatches
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Best Local Similarity
Matches 9; Conser
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01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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P13175;
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PFAM; PF00361; oxidored_q1; 1.

PFAM; PF00662; oxidored_q1_N; 1.

OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.

OXIDOREDUCTASE; NAD; 72818 MW; AD926718 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-DAOM 148428;
PAQUIN B., ROEWER I., WANG Z., LANG B.F.;
PAQUIN B., ROEWER I., WANG Z., LANG B.F.;
"A robust fungal phylogeny using the mitochondrially encoded nac protein sequence.";
CAN. J. BOT. 73:S180-S185(1995).
-I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                                                                                                                                                                             OKAZAKI K., KAWAOKA Y., WE "Evolutionary pathways of VIROLOGY 172:601-608(1989)
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 90021190.
                                                                                                                                                                                                                                                                                                                                                                INFLUENZA A VIRUS (STRAIN A/SWINE/IOWA/15/30)
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; ORTHO
INFLUENZA VIRUS A AND B GROUP.
                                                                          PFAM; PF00603; Flu_PA; 1.
RNA-DIRECTED RNA POLYMERASE.
                                                                                                       EMBL; M26076; G325070;
                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN).
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                                                             SEQUENCE
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                                                                                                                                  send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                      P1 (OR PB1), P2 (OR PA), AND P3 (OR PB2).
                                                                                                                                                                                                                                                              SUBUNIT: INFLUENZA RNA POLYMERASE IS COMPOSED OF THREE SUBUNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A P F I N E GCNCCNTTYATHAAYGARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNGI; ZYGOMYCOTA; ZYGOMYCETES; MUCORALES; MUCORACEAE;
                                                             716
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                                                             ΑĄ;
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63.28;
                 74.78;
                                                             82566 MW;
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                                                                                                                                                                                                                                                                                                           WEBSTER R.G.;
  Score 71; DB 1;
Pred. No. 1.37e+
6; Mismatches
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                         PA genes of influenza A viruses.";
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                                                             E1FDF31E CRC32;
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DB 1; L.
1.37e+01;
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Matches 9; Consei
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P13177;
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., I DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTI KUCABA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y., LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MECZES S., NHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VIVIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.
                                                                                                                                                                                                                                                                           SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995
01-FEB-1996
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-!- SUBUNIT: INFLUENZA RNA POLYMERASE IS COMPOSED OF
                                                                                                                                                                                 STRAIN-S288C
                                                                                                                                                                                                                                                      SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                 YHR182W
                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA-DIRECTED RNÁ POLYMERASE.
SEQUENCE 716 AA; 82872 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFLUENZA A VIŘUS (STRAIN A/SWINE/TENNESSEE/26/77).
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; ORTHOMYXOVIRIDAE.
INFLUENZA VIRUS A AND B GROUP.
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(REL. 13, LAST SEQUENCE UPDATE)
(REL. 22, LAST ANNOTATION UPDATE)
D RNA POLYMERASE SUBUNIT P2 (EC 2.7.7.48)
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larity 60.0%;
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31, LAST SEQUENCE UPDATE)
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KD PROTEIN IN OYEZ-GND1 INTERGENIC REGION
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                                                                                                 COOPER J., DING H., DOVER J., S., GEISEL C., KIRSTEN J.,
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(See http://www.isb-sib.ch/announce/
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p39774; p33114; p36360;
p19774; p33114; p36360;
01-FEB-1995 (REL. 31, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPD;
15-JUL-1998 (REL. 36, LAST ANNOTATION UI
SUBTILIN BIOSYNTHESIS PROTEIN SPAB.
SPAB OR SPAE.
BACTILUS SUBTILIS.
BACTILUS SUBTILIS.
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                                                                                                                                                                                               CHUNG Y.J., HANSEN J.N.;
"Determination of the sequence of spaE promoter in the subtilin (spa) operon i J. BACTERIOL. 174:6699-6705(1992).
                                                                                                                                                                                                                                                                                                                                                                                          KLEIN C., ENTIAN K.D.; "Genes involved in self-protection against the produced by Bacillus subtilis ATCC 6633."; APPL. ENVIRON. MICROBIOL. 60:2793-2801(1994).
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                                "Analysis of genes subtilin.";
                                                                              MEDLINE; 92171481.
KLEIN C., KALETTA C.,
                                                                                                                                STRAIN-ATCC
                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                              STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC 6633;
MEDLINE; 94368094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Growth phase-dependent regulation and membrane localization of SpaB, a protein involved in biosynthesis of the lantibiotic subtilin."; APPL. ENVIRON. MICROBIOL. 60:1-11(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GUTOWSKI-ECKEL Z., KLEIN C., ENTIAN K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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:||:||:||:||:||
1 CTTCATTAATGAACG
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VTCC 6633;
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93015727.
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          MICROBIOL.
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                                                       SCHNELL N., ENTIAN K.-D.; rolved in biosynthesis of the lantibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACILLUS/CLOSTRIDIUM
                                                                                                                                                       N.A
       58:132-142(1992)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIEGERS K., BOHM K.,
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1.37e+01;
                                                                                                                                                                                                                           E and identification in Bacillus subtilis
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EMBL; U09819; G595316; --
EMBL; M99263; G143564; A:
EMBL; M99263; G143555; A!
EMBL; M86869; G143714; --
EMBL; M86869; G143714; --
EMBL; M86869; G143714; --
EMBL; M86869; G143558; AI
EMBL; U38418; G1109688; AI
EMBL; U38418; G1109688; AI
EMBL; M45740; A45740.
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078485;
15-DEC-1998
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SEQUENCE OF 852-1030 FROM
STRAIN-ATCC 6633;
----- 92138640.
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DOUGLAS S.E., PENNY S.L.;
"The plastid genome from the cryptomonad complete sequence and conserved synteny cancestry with red algae.";
                                                                                       GUILLARDIA THETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: POSSIBLY ASSOCIATED WITH,
THE CYTOPLASMIC SIDE OF THE MEMBRANE.
-!- SIMILARITY; TO S.EPIDERWIDIS EPIB AND L. LACTIS
-!- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. BACTERIOL. 174:1417-1422(1992).
-!- FUNCTION: INVOLVED IN THE POSTTRANSLATIONAL MODIFICATION LANTIBIOTIC SUBTILIN.
                                              SEQUENCE FROM N.A
                                                                                 CHLOROPLAST
                                                                                                        RPOB
                                                                                                                   DNA-DIRECTED
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                                                                      EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSPORT
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1 CTTCATTAATGAACGATGC 19
F I N E R C
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A43935;
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                                                                                                                                                                                                                                                                                                   74.78;
Similarity 47.48;
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37, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
POLYMERASE BETA CHAIN (EC 2.
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                                                                   CRYPTOMONADACEAE;
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LA -> AG (IN REF. 3).
H -> K (IN REF. 3).
N -> I (IN REF. 3).
F -> L (IN REF. 3).
P -> A (IN REF. 3).
E -> V (IN REF. 3).
MW; 831CCCC3 CRC32;
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Pred. No. 1.37e+01;
7; Mismatches 3
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          d alga,
groups
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                                                                   GUILLARDIA
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            Guillardia theta: confirm its commo
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                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collar between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                       BOUNDY-MILLS K.L., KOSSLAK R.M., TULLY K.E., PULTYNE S.G.,
LOHRKE S.M., SADOWSKY M.J.;
"Induction of the Rhizoblum fredii nod box-independent nodulation
"Induction of the Rhizoblum fredii nod box-independent nodulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Two host-inducible genes of Rhizobium the inducing compound.";
J. BACTERIOL. 170:171-178(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1989
01-FEB-1996
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  EMBL; M19019; G152249; -. EMBL; L26967; G435107; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHIZOBIUM FREDII.
BACTERIA; PROTEOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSCRIPTION;
                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              NODULATION DÉLAY.
-!- INDUCTION: BY PLANT 4',7-DIHYDROXY-ISOFLAVONE OR DERIVATIVES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 88086864.
SADOWSKY M.J., OLSON E.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHIZOBIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NODULATION
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FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
SUBSTRATES.
CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
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                                                                                                                                                                                                                                                                                                                  FUNCTION: INVOLVED IN
                                                                                                                                                                                                                                                                                                                  requires a functional nodD1 gene.";
PLANT MICROBE INTERACT. 7:305-308(1994)
FUNCTION: INVOLVED IN EFFICIENCY OF SOYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YYTNATHAAYGARMGNY 2017 ::| ||:||:||::| :
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F I N E R
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PTION; DNA-DIRECTED RNA
1096 AA; 123294 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        æ
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non-profit institutions as long
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(REL.
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NODULATION.
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                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virus genome.";
J. GEN. VIROL. 66:207-220(1985).
-i- SIMILARITY: BELONGS TO A FAMILY THAT
EHV-1 66, EHV-4 ORF3, AND VZV 64/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 85107111.
DAVISON A.J., SCOT
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.complete DNA sequence of varicella-zoster virus.";
EN. VIROL. 67:1759-1816(1986).
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993–1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_ntp n.a. - n.a. Smith-Waterman search, using a protein database which has been backtranslated into n.a. using IUPAC symbols

Run on: Wed Nov 24 02:31:07 1999; MasPar time 9.78 Seconds 636.263 Million cell updates/sec

Tabular output not generated.

Title: >US-09-103-287-5
Description: (1-19) from US09103287.seq
Perfect Score: 95
N.A. Sequence: 1 CTTCATTAATGAACGATGC 19
Comp: GAAGTAATTACTTGCTACG
Scoring table: TARLE betranslate2

Scoring table: TABLE bktranslate2
Gap 40

Nmatch

STD:

Dbase 0; Query 0

Searched: 179066 seqs, 163739223 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

sptremb19
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 38.972; Variance 46.490; scale 0.838

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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71 71 71	72 71 71	76 76 76 77 76	Score
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147 153 162	2374 2531 111 112	405 181 265 421 517 541 1211 1211 398	% Query Match Length
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HYPOTHETICAL 17.1 KD P HYPOTHETICAL PROTEIN ( HYPOTHETICAL 19.3 KD P	F22G12.5 PROTEIN. SIMILAR TO TENASCIN. POLYMERASE (FRAGMENT). ORF C06011.	T07D10.5 PROTEIN.  1-EVIDENCE-PREDICTED B CADHERIN 10 (T2-CADHER HYPOTHETICAL 46.1 KD P COSMID B1764.  M03C11.4 PROTEIN. CHROMOSOME SEGREGATION HYPOTHETICAL PROTEIN M RUST RESISTANCE KINASE	Description
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## ALIGNMENTS

22 무망

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CRC32

Mismatches

Indels

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Gaps

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DB 11; 2.39e+00;

Length

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Query Match
Best Local s
Matches 1
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                                         SEQUENCE AND STRAIN=C57BL/6; TISSUE=TEDALOW, STRAIN=C57BL/6; TISSUE=TEDALOW, MEDLINE; 97033837.
MEDLINE; 97033837.
MUNRO S.B., BLASCHUK O.W.;
"A comprehensive survey of the cadherins expressed in the testes "A comprehensive and adult mice utilizing the polymerase chain for the polymerase chain f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JLT 3
P70408
P70408;
P10408;
01-FEB-1997
01-FEB-1997
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     046041
046041;
046041;
01-JUN-1998
01-JUN-1998
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDH10
                                                                                                                                                                                                                                                                                                                                                                                                                                        MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1131
     SEQUENCE FROM N.A.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                MEDLINE; 96211873.

MUNRO S.B., DUCLOS A.J., JACKSON A.R., BAINES M.G.,

"Characterization of cadherins expressed by murine cell. IMMUNOL. 169:309-312(1996).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 117-203 FROM N.A. STRAIN=C57BL/6; TISSUE=TESTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CADHERIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA EMBL; AL009193; E1202173; -. SEQUENCE 181 AA; 20734 MW; CFB29EC7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MURPHY L., HARRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSE
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-EVIDENCE-PREDICTED EG:103B4.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DROSOPHILIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F I N E L C
21 YTTYATHAAYGARYUNTGY 339
21 (||:||:||:||:||:
21 CTTCATTAATGAACCATGC 19
F I N E R C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Н
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CTTCATTAATGAACGATGC 19
F I N E R C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F N N E R C
YTTYAAYAAYGARMGNTGY 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HARRIS D., (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TREMBLREL.)
(TREMBLREL.)
(TREMBLREL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TREMBLREL 02, CREATED)
(TREMBLREL 02, LAST SEQUENCE UPDATE)
(TREMBLREL 08, LAST ANOTATION UPDATE)
(T2-CADHERIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               larity 52.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , BARRELL B.;
TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06, CREATED)
06, LAST SEQUENCE UPDATE)
06, LAST ANNOTATION UPDAT:
CONTENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
7; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           re 76; DB 5; Le
d. No. 2.39e+00;
Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . No. 4.05e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                        BLASCHUK O.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSECTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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DO5296

C 005296;

TREMBLREL. 04, CREATED)

DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDAT'

DT 01-JUL-1997 (TREMBLREL. 08, LAST ANNOTATION UPC

DE HYPOTHETICAL 46:1 KD PROTEIN.

GN MTC1364.06C.

OS MYCOBACTERIUM TUBERCULOSIS.

OS BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOB

TOTAL ACTINOBACTERIUM TUBERCULOSIS.
RESULT 5
ID Q50018;
AC Q50018;
DT 01-NOV-1996
DT 01-NOV-1996
DT 01-NOV-1996
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Best Local
Matches
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Best Local S
Matches
                                                                                                                                                                                                                                                                                1045
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SUBMITTED (
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRÔC. NATL. ACAD. SCI. U.S.A. EMBL; 293777; E311071; -. HYPOTHETICAL PROTEIN. SEQUENCE 421 AA; 46097 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 96181548.
PHILIPP W.J., POULET S.,
BALASUBRAMANIAN V., HEYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6; TISSUE-TESTES;
MUNRO S.B., BLASCHUK O.W.;
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U69137; G1546833; -
EMBL; U69137; G1546833; -
MGD; MGI:107436; CDH10.
PFAM; PFO1049; Cddhrin_C_term; 1.
NON_TER 1:
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BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLE S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "An integrated map of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eprae."
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7 YTTYATHAAYGARMGNY 583
:||:||:||:||:||:
1 CTTCATTAATGAACGAT 17
F I N E R
                                                                                                                                                                                                                                                                                                                                                    Similarity
11; Conserv
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(TREMBLREL.
(TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHURCHER C
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llarity 52.9%;
Conservative
                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                       Conservative
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01,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIGLMEIER K.,
B., BERGH S.,
                                                                                                                                                                                                                                                                                                                                                    Score 76; D
Pred. No. 2.
6; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 76;
Pred. No.
7; Misma
CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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A; ACTINOBACTERIDAE; MYCOBACTERIUM.

5 5

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RESULT RESULT OF ACT OF

RESULT PO ACC PO

93:3132-3137(1996).

of the tubercle, and comparison

with Myco

Mycobacterium

PASCOPELLA BLOOM B.R.,

JACOBS

Σ

. R

JR.,

DATA

BANKS

DATA

BANKS

1DFF8D9D CRC32;

Mismatches

Indels

0

Gaps

0

DB 2; L 2.39e+00;

Length 421;

PRT;

517

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RESULT
ACC WAX
                                                                                                                                                          pr polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter

Pr infection, and to detect Helicobacter

Pr claim 61; pages 1035-1036; 1481p; English.

CC The present sequence is a Helicobacter pylori cytoplasmic protein cytoplasmic polypeptide binding cytoplasmic cytoplasmic cytoplasmic protein cytoplasmic cyt
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                                       Query Match
Best Local
       Matches
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06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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                 The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial infections, especially conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection.
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Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; cardiac infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid sequences from Staphylococcus aureus WCHU29 useful in vaccines and for treatment of bacterial infections respiratory tract and central nervous system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 329; 390pp; English.
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Reichard RW, Rosenberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC homology to N-acetylmuramate Alanine ligase.

CH Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention care used to evaluate compounds, especially activators or inhibitors of CC bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are calso useful for generating vaccines for immunising subjects against H. CC pylori or for use in detecting the presence of Helicobacter species in calso useful for generating vaccines for immunising subjects against H. CC pylori or for use in detecting the presence of Helicobacter species in calso useful to inhibit expression of a gene from Helicobacter species in CC aspler. Inher adapters in 100-1000 fold molar excess. These linkers are CC pylori whole genomic DNA was isolated and nebulised to a median size of C2 pylori whole genomic DNA was isolated and nebulised to a median size of C3 pylori whole genomic DNA was isolated and nebulised to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor construct to each of the 20 pMPX vectors to construct a series of cannenced.

CC sequence libraries. The purified DNA samples were then
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This sequence represents an H. pylori cyto
outer membrane or cell wall biosynthesis.
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15-NOV-1996; U18542.
17-NOV-1995; US-561469.
(ASTR ) ASTRA AB.
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04-AUG-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                        the related
                             YLEKLDYTNIKEALETFGGYKRRFNETTIANQYIVDDYAHHPREISATIDTARK--KYPH
                                                                                                                                                        PIYYYGFKDSDDIYAQNIQ-ITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAIS
                                                                                                                                                                                                                                                                                       FLSYKPDYAIMTNIDFDHPDYFK-DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The ORF/protein reference number for this sequence was obtained the related specification, WO9640893.
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                                                                                                                                                                                                                                                                                                                                                                                                                  n 7.7%;
Similarity 28.3%;
63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 239; DB 22;
Pred. No. 6.71e-09;
55; Mismatches 88
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PIYYYGFKDSDDIYAQNIQ-ITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAIS ai---vl-ekkdiy--niqyilkdgepytsf-elknlgaflvwglgehnatna-slails 119 FLSYKPDYAIMTNIDFDHPDYFK-DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADV

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Query Match
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Matches 63; Conser
                                                                                                                  The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contides generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide(s) useful for vaccines to infection, and to detect Helicobacter Claim 61; Page 335; 1481pp; English. This sequence represents a H. pylori cyto outer membrane or cell wall biosynthesis.
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misc_difference 133
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Cytoplasmic; vaccine; prevention; treatment; infection
identification; binding compound; bacterium; life cyc
bacteria; inhibitor; duodenal ulcer disease; chronic
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06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405
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Pred. No. 6.71e-09;
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14-APR-1997;
. 18-JUN-1996;
14-APR-1997;
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                                                                                           drug design; resistance; Streptococcus pneumoniae US5834270-A.
                                                                                                                                                                     uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligase;
                                                                                                                                                                                           S. pneumoniae MurD protein.
Biosynthesis; recombinant; antibacterial; bacterial cell wall;
                                                                                                                                                                                                                                                                     W68551;
                                                                                                                                                                                                                                                                                         W68551 standard; Protein; 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents Streptococcus pneumoniae MurD protein (uridine-diphosphate-N-acetylmuramy1-y-laiany1-p-isoglutamate ligase). The MurD protein is useful in a method for identifying compounds that inhibit Streptococcus pneumoniae MurD activity. Compounds identified are potentially useful as antibacterial agents.
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18-JUN-1996; US-665435.
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US-843309.
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No. 6.65e-02;
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                                                                                                                                                                                                                                                                      Streptococcus pneumoniae; antigen; vaccine; inf detection; pneumonia; otitis media; meningitis.
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             Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis Claim 11; Page 72; 118pp; English.
                                                                             WPI; 98-272224/24.
N-PSDB; V27378.
                                                                                                                                                                                                                                                       Streptococcus
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                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
Choi GH, Hromockyj A, Johnson LS,
                                                                                                                                              31-OCT-1996;
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89; Mismatches 117
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Best Local
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This sequence represents the protein encoded by the Brevibacterium flavum murF gene of the invention. The DNA sequence is contained within the chromosomal DNA fragment of the invention. The chromosomal DNA fragment to the invention of the chromosomal DNA fragment contains a segment which has a SphI site at one end, a BamHI site at the other end, and when it is digested by XbaI gives two fragments of 1.2 kb and 2.1kb. The murF gene encodes a UDP-N-acetylmuramoyl-L-alanyl-D-glitamyl-meso-2,6-diaminopineryl-D-alanyl-D-alanine synthetase. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 murF gene; synthetase;
suicide vehicle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein, gene and DNA fragment can be used to make an artificial cell replication control, and an antilytic strain breeding. They can also be used in the development of suicide vehicle by artificial lysing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T99927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-DEC-1996; 343877.
28-FEB-1996; JP-041439.
(MITU ) MITSUBISHI CHEM CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-1998
          380
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les 66; Consel
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mlvlgdmlelgdleetfhkecgavispdkidrvftygklgafiae-galkqfe-kdrvsh
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                                                                  KLDVTNIKEALETFGGVKRRFN-ETTIANQVIVDD-YAHHPREISATID-TAR-KKYPHK
                                                                                                                                                                                                          YGFKDSDDIYA-QNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAI-SYLE
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Similarity 53.8%;
21; Conservative
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larity 24.18;
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Pred. No. 1.72e-01;
7; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 128; DB 26;
Pred. No. 6.97e-01;
64; Mismatches 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence corresponds to a Plasmodium falciparum strain K1 pre-erythrocytic liver stage antigen-3 (LSA-3) protein. The encoding gene sequence was isolated by screening a P. falciparum strain T9/96 library with serum from a missionary treated by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones isolated, clone 7295 was used to screen a library generated from Thai strain K1. One clone contained a 6.85 kb insert including the genomic sequence T78867. The gene comprises a 1.8 kb region encoding 3 major blocks of tetrapeptide repeats (especially the amino acid sequence WEES, VEEN, VEEN, VAPT, etc) and a 3' hydrophobic region corresponding to a glycosyl-phosphatidyl-inositol membrane anchoring sequence. The invention relates to new polypeptides of at least 10 amino acids derived from the LSA-3 protein with the acception of the protein services and the second of the control of the contro
Yr 13
1543; standard; Protein; 370
W71543;
09-NOV-1998 (first entry)
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Claim 1; Fig 2A-I; 69pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum; pre-erythrocyte; liver stage antigen; serum; prophylaxis; Thai strain; gene organisation; exon; intron; hydrophob glycosyl-phosphatidylinositol membrane anchoring sequence; antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            derived from the liver stage antigen-3, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Daubersies P, .Dru
WPI; 97-065464/06.
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27-DEC-1996.
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13-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum poly:peptide(s) and related nucleic acids
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                                                                                                                                                                                                                                                391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 IAISYLEKLDYTNIKEALETFGGVKRRFNETTIANQVIVDDYAH-HPREISATIDTARKK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855 vvttilenveetta-esvttfsnileeigentitndtieekleelhenvlsaalentgse 913
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                                                                                                                                                                                                                                                                                                                     972 --ek-lnetvfntvldkveetveisgeslennemdkaffsei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.8%;
Local Similarity 19.1%;
les 31; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ytekkdllqavkenaskgdlilfkasrgm-klee 470
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FR-007007.
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Sclaim 1: Page 282: 362pp; English

This claimed Helicobacter pylori polypeptide, designated GHPO 208, can be used in vaccination methods for preventing or treating the second control of the invention also provides:

(See V52009-93) that encode them. The invention also provides:

(See V52009-93) that encode them. The invention also provides:

(See V52009-93) that encode them and related expression cassettes, vectors and transformed or transfected host cells; live vaccine vectors that contain the polynucleotides of the invention and which can be used to prevent or treat Helicobacter infection; therapeutic and/or prophylactic methods involving administration of polynucleotide of prophylactic methods involving administration antibodies; methods for detecting the presence of Helicobacter in samples using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.6%;
Best Local Similarity 29.3%;
Matches 24; Conservative
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29-JUL-1997; US-902615.
14-NOV-1996; US-749051.
01-APR-1997; US-831309.
01-APR-1997; US-833457.
01-APR-1997; US-833705.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detecting the presence of Helicobacter in samples using e.g. the polypeptides or monospecific antibodies; and methods for purifying the polypeptides by antibody-based affinity
                                                                                                                                                                                                                                                                                                                endonuclease 2; DNA polymerase; Pyrococcus furiosus; rare cutter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromatograph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Al-Garawi A, Haas R, Kleanthous H, Meyer T, Odenbreit S, Tomb J; WPI; 98-297855/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc_difference
                                                                                                                                 19-MAR-1996.
02-SEP-1994; 209619.
02-SEP-1994; JP-209619.
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                                                                                                                                                                                                                                                                                            cleavage; cloning; sequencing
                                                                                                                                                                                                                                                                                                                                                           Endonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                     W01107 standard; Protein; 536 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; V52078
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(HUMA-) HUMAN GENOME SCI INC
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GHPO 208; infection; therapy; diagnosis; vaccine; gastritis;
                                                                                                                                                                                                                                 J08070864-A.
                                                                                                                                                                                                                                                              Pyrococcus furiosus
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                                                                                                   ( MYOT)
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                                                                  4) ТОУОВО КК.
96-203145/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAIS-YLEKLDVTNIKE-ALE 290
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MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 AA;
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
2 derived from super-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "encoded by TCN"
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                                                                                                                                                                                                                                                              strain KOD1
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Pred. No. 9.12e+00;
19; Mismatches 34
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      archaebacteria
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Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                     of ca. 41 kD, cleaves double stranded DNA into large fragments, leaves a 3'-sticky end and is therefore useful in genetic engineering. Chromosomal DNA obtd. from a 95 degrees C P. furios KODI culture was PCR amplified using primers designed and synthesised according to the base sequence of P. furiosus derive pfu polymerase. The amplified fragment was used for Southern hybridisation against a restriction enzyme treated KODI chromosomal DNA, to give a DNA polymerase encoding fragment of chromosomal DNA, to give a DNA polymerase encoding fragment of chromosomal DNA, to give a DNA polymerase encoding fragment of chromosomal DNA, to give a DNA polymerase encoding fragment of contents of the process of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-1994; JP-208631.
(TOYM ) TOYOBO KK.
WPI; 96-203144/21.
N-PSDB; 728861.
Endonuclease I from super-thermophilic archaebacteria, P.furiosus useful for genetic engineering Claim 5; Pages 7-14; 18pp; Japanese.
The present sequence is the P. furiosus strain KOD1 (a super-thermophilic archaebacteria) DNA polymerase, which contains the claimed enzyme, endonuclease I. The endonuclease has a mol. wt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rare cleavage site, for cutting DNA into large fragments Claim 9; Page 14-16; 19pp; Japanese.
The present sequence is that of endonuclease 2, isolated from DNA polymerase of Pyrococcus furiosus strain KOD1. The endonuclease 2 is an approx. 62 KDA protein, and is a rare cutter (see T14693), cleaving DNA into large fragments. The specification states that the sequence is 537 residues but only 536 residues are given.
                                                        1144 kgrnp 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA polymerase, contg. endonuclease I.
KOD1 strain; super-thermophilic; archaebacteria; DNA polymerase;
endonuclease I; 3'-sticky end; genetic engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R97048 standard; Protein; 1670
R97048;
19-NOV-1996 (first entry)
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01-SEP-1994;
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   422 KLQNA 426
                                                                                                                     364 RVFLCEIFGSIRENSGALTIQDLID-KIGG-ASFINEDLINVLEQFDNAVVLFMGAGDIQ 421
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JP-208631.
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larity 30.8%;
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larity 30.8%;
Conservative
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Pred. No. 1.06e+01;
17; Mismatches 25;
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Pred. No. 1.06e+01;
17; Mismatches 25;
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Run on: MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Wed Nov 24 00:43:35 1999; MasPar time 7.05 Seconds 738.334 Million cell updates/sec

Description: Perfect Score: Sequence: Title: >US-09-103-287-2 (1-437) from US09103287.pep 3121 1 MTHYHFVGIKGSGMSSLAQI......GDIQKLQNAYLDKLGMKNAF 437

Searched: 122461 seqs, 11912985 residues Scoring table:

PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics: a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1 Mean 32.583; Variance 165.756; scale 0.197

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Result	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	147	4.7	446	2	US-08-934-	Sequence 2, Applicatio	.36e-0
2	4	4.6	450	μ	-08-66	2, Applicat	e,
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17			687	۳	-80-	e 10, Appl	٠
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21		٠	1098	2	US-08-290-	82	
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Local Similarity 24.1%;
les 74; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
 FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 1FORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                          APPLICANT: Hoskins, Joann
APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: Biosynthetic Gene MurD
                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Biosynthet
                                                                                                                                                                                                                                                                                                                              APPLICANT: Skatrud, Faux
APPLICANT: Peery, Robert
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPDYFKDINDVFDAFQEMAHNVKKG-IIAWGDDEHL-RKIEADVPIYYYGFKDSDDIYAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIDYHGSFSEYVAAKWNIQNKMTAADFLVLNFNQDLTSKTEATV-VPFSTLEKVDGAYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VMNGDKKTSFLIGD-G--TG-MGL--PESDYFAFEACEYR-RHFLSYKPDYAIMTNIDFD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLTAAGQHGLLSGNIGYPASQVAQTASDKDTLVMELSSFQLMGVQEFHPEIAVITNLMPT 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSH 121
                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         COUNTRY: UZIP: 46285
                                                                                                                                                                                                   CITY: Indianapolis
STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                             E: Eli Lilly and Company
Lilly Corporate Center
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                                                                                US/08/665,435A
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Pred. No. 1.36e-02;
91; Mismatches 117; Indels
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Best Local
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                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Skatrud, Paul
APPLICANT: Skatrud, Paul
APPLICANT: Hoskins, Johnn
APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: Blosynthetic Gene Mur D of Streptococcus
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08843309 Patent No. 5834270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 AYLEDGQLYFRG---EV-VMAA--NEIGVP--GSHNVENALATIAVAKLRDVDNQTIKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 -VVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 ALMVKNPGIPYNNPMIEKALAKRIPVLTEVE-LAYLISEAPIIGITGSNGKTTTTTMIGE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 LGLAKSGESA-ARLLDKLGAIVTVNDGKPFEDNPAAQSLLEEGIKVITGGHPLELLDEEF 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 VGIKGSGMSSLAQIMHDLGHEVQGSDIENYV-FTEV-ALRNKGIKILPFG-ANNI-KEDM
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
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                          CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSAFGGVKHRL 314
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            APPLICATION NUMBER:
                                                                                                                     COUNTRY:
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Similarity 24.4%;
76; Conservation
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450 AA; 48579 MW; 1010380 CN
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DATE:
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Lilly Corporate Center
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            US/08/843,309
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Pred. No. 2.58e-02
89; Mismatches 11
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                                       Version
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Best Local :
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SEQUENCE 4:
                                                                                                                                                                                      Sequence 4, Application US/08934481
                                                                                                                                                                                                                                              US-08-934-481-4
                                                                                                                                                                                                                                                                                                                                                                                                122 VMNGDKKTSFLIGD-G--TG-MG-LP-ESDYFAFEACEYR-RHFLSYKPDYAIMINIDFD
                                                                                                                                                            Sequence 4, Application US/08934481 Patent No. 5929045
                                                                                                                                                                                                                                                                                   289 LETFGGVKRRF 299
                                                                                                                                                                                                                                                                                                     304 LSAFGGVKHRL
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                                                                                                                                                                                                                                                                                                                                                                                                                    133 VLTAAGQHGLLSGNIGYPASQVAQIASDKDTLVMELSSFQLMGVQEFHPEIAVITNLMPT 192
                                                                                                                                                                                                                                                                                                                                                                               193 HIDYHGSFSEYVAAKWNIQNKMTAADFLVLNFNQDLAKDLTSKTEATV-VPFSTLEKVDG
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Local Similarity 24.4%;
les 76; Conservative
                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 ALMYKNPGIPYNNPMIEKALAKRIPVLTEVE-LAYLISEAPIIGITGSNGKTTTTTMIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 LGLAKSGESA-ARLLDKLGAIVTVNDGKPFEDNPAAQSLLEEGIKVITGGHPLELLDEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 VGIKGSGMSSLAQIMHDLGHEVQGSDIENYV-FTEV-ALRNKGIKILPFG-ANNI-KEDM 62
                                                                                                   APPLICANT: Wallis, Nichola G. APPLICANT: Fueyo, Joanna L. APPLICANT: LONetto, Michael A. TITLE OF INVENTION: NOVEL MUTD NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                           COMPUTER READABLE FORM
                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                         AYLEDGQLYFRG---EV-VMAA--NEIGVP--GSHNVENALATIAVAKLRDVDNQTIKET 303
                                                                                                                                                                                                                                                                                                                                                             HPDYFKDIND-VFD--AFQEMAHNVKKGIIAWGDD-E-HL-RKIEADVPIYYYGFKDSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                      -VVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
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                                                             STREET: 4000 Bell A
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COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                     COUNTRY: UZIP: 19103
                  MEDIUM TYPE:
                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LE TYPE: protein
450 AA; 48579 MW; 1010380 CN;
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                                                                         E: Dechert Price &
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                   Diskette
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Pred. No. 2.58e-02;
89; Mismatches 117;
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Tower,
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Query Match
Best Local S
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261 GDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRF 299
                           93 GSHNVENALATIAVAKLRGVDNQTIKETLSAFGGVKHRL
                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                        TOPOLOGY:
                                                                                                                                                       STRANDEDNESS: single
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                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                NAME: Dickinson, Toda
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                       4.3%;
Similarity 53.8%;
21; Conservative
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267 AA; 29079 MW; 348410 CN;
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                                                         Score 134;
Pred. No. 1.
7; Mismatc
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                                                            Mismatches
                                                                                         DB 2;
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                                                                                       Length 267
                                                            Indels
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                                                          Gaps
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XXXXXX US-08-271-364A-7 STANDARD; PRT;

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Sequence 7, Application US/08271364A

Patent No. 5756334
GENERAL INFORMATION: TITLE OF INVENTION: NUMBER OF SEQUENCES: APPLICANT: PERLER, FRANCINE B.
APPLICANT: SOUTHWORTH, MAURICE W. FROM ARCHAEBACTERIA RECOMBINANT THEROMSTABLE DNA POLYMERASE

CORRESPONDENCE ADDRESS:
ADDRESSEE: NEW ENGLAND BIOLABS,
STREET: 32 TOZER ROAD STATE: M STREET: CITY: B BEVERLY MASSACHUSETTS INC

LIFE: FORM:
LUMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA PC-LOATION DATA:
APPLICATION NUMBER: US/08/271,364A
FILING DATE: 06-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435 Version

FILING DATE: 18-DEC-1991 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA APPLICATION NUMBER: US 0 FILING DATE: 17-APR-1991 US 07/686,340

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Local Similarity 21.38;
les 13; Conservation
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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FILING DATE: 11-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/51
APPLICATION NUMBER: US 07/51
FILING DATE: 26-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
                                                 ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/167,238
FILING DATE: 15-DEC-1993
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS
                                                                                                                                                                                                                                                APPLICANT: Perler, Francine
APPLICANT: Kucera, Rebecca
APPLICANT: Jack, William E.
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE FROM ARCHAEBACTERIA
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (508) 927-5054
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STRANDEDNESS: unknown
TOPOLOGY: unknown
                                               APPLICATION NUMBER: US/0 FILING DATE: 04-APR-1994
                                                                                                                                                                                      STREET: 32 TO CITY: BEVERLY
                                                                                                                                                            COUNTRY:
                                                                                                                                                                            STATE:
                                                                                                                                                                                                               ADDRESSEE
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                                                                                                                                                                                                                                                                                                                                                   NO.
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1019 AA; 118920 MW; 5466116 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  larity 21.3%; Pred. No. 2.98e+01;
Conservative 22; Mismatches 23; Indels
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Pred. No. 2.98e+01
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Best Local Similarity 21.3%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,726A
FILING DATE: 12-UU-1996
CLASSIFICATION: 424
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION: NAME: Connell, Gary J.
                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                            APPLICANT: Haanes APPLICANT: Frank,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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FILING DATE: 26-APR-1990
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0:
FILING DATE: 11-DEC-1990
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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CITY: Denver
STATE: Colorac
                                                                                                                                  COUNTRY: U.S.A. ZIP: 80203
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TELEFAX:
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                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                        Colorado
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1700 Lincoln Street, Suite 3500
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                                                                                                                                                                                                                                                      Haanes, Elizabeth J.
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Pred. No. 2.98e+01
22; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
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Local Similarity 21.8%;
hes 36; Conservative
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TELEFAX: (303) 863-9223
INFORMATION FOR SEQ ID NO: 54-
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,151
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
        REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,118
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PAOLETTI, ENZO
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein JENCE 345 AA; 40609 MW; 660444 CN;
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                      CLASSIFICATION:
                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                          CITY: NEW YORK
STATE: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 SFLIGDGTGMGLPESDYFAFEACEYRRHF-LSYKPDYA-IMTNIDFDHPDYFKDINDVFD 187
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19,
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                      TELEFAX: (212) 840-0712 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide FRAGMENT TYPE: N-terminal JENCE 345 AA; 40609 MW; 6
                                           REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                        FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
              SEQUENCE CHARACTERISTICS:
                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                            STATE: NEW YORK
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                                                                                                                                                               FILING DATE:
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Similarity 21.8%;
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345 amino acids
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29-MAR-1995
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NUCLEOTIDE AND AMINO ACID SEQUENCES OF CANINE HERPESVIRUS 9B, 9C, AND 9D AND
                                                                                                                                                                                            Release #1.0, Version
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                                                                                                                           US 08/220,151
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Pred. No. 4.58e+0:
45; Mismatches
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                        19:
                                                                    454310-2670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
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                                                                                   TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO:
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Local Similarity 21.8%;
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STRANDEDNESS: sin
TOPOLOGY: linear
MOLECULE TYPE: pept:
FRAGMENT TYPE: N-te:
DUENCE 345 AA; 40609
                                                                                                                                   NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2540
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 30-MAR-19
CLASSIFICATION: 435
MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morri
STREET: 530 Fifth Avenue
                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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APPLICANT: Limbach, Keith J.
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                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rolesco "."
                                             LENGTH: 345 amino acids
                                                                                                         TELEFAX:
                                  STRANDEDNESS:
                         TOPOLOGY:
                                                                                                                      TELEPHONE:
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peptide
internal
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Pred. No. 4.58e+01;
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      SEQUENCE
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                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
BENCE 345: AA; 40609 MW; 660444 CN;
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PAOLETTI,
APPLICANT: LIMBACH,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, N
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                                                      LENGTH: 345 L...

TYPE: amino acid

mype: sin
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                                                                                                                                                     NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45
                                                                                                                                                                                                                                             FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                   CITY: NEW YORK
STATE: NEW YORK
                                           TOPOLOGY:
                                                    STRANDEDNESS:
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Similarity 21.8%;
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                                                                                                                                                                                                                                                                                                          IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                         linear
                                                                                                                                                                                                                                                                                                                                  Floppy disk
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NUCLEOTIDE AND AMINO ACID SEQUENCES
CANINE HERPESVIRUS 9B, 9C, AND 9D AN
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AVENUE, 25TH FLOOR
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Pred. No. 4.58e+01;
45; Mismatches 70;
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Sequence 20, Application US/08220151 Patent No. 5529780
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TELEFAX: (212) 840-0712
TELEX: 42506 CURTMS
INFORMATION FOR SEQ ID NO: 20
                                                                              MOLECULE TYPE:
FRAGMENT TYPE:
QUENCE 345 AA; 4
                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: SCORRESPONDENCE ADDRESS
                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acid
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APPLICANT: Limbach, Keith
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                                                                                                                                                                                                                                                                                  FILING DATE: 30 CLASSIFICATION:
                                                                                                                  TOPOLOGY:
                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                            NAME: Frommer, William S. REGISTRATION NUMBER: 25,5
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                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
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                                               Similarity
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amino acid
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Conservative
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IVENTION: NUCLECTIDE AND AMINO ACID SEQUENCES OF IVENTION: CANINE HERPESVIRUS 9B, 9C AND 9D AND U
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N-terminal
40609 MW; 660444 CN;
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                                              Score 94; DB 1; 1
Pred. No. 4.58e+01
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                                                                                                                                    SEQUENCE
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 270 AVIAISYLEKLD 281
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                                                                27 VSSTTPKIEFNSIAENDDI-PTNYDSDEEFEDGDTFIQSTLIHQFNASQVTTTTIIIIPM
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                                                                                                                                                                                                     TELEFAX: (617) 832-70 INFORMATION FOR SEQ ID NO:
                                                                                                  Local
                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P
                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Damagnez, Veroni
APPLICANT: Draetta, Guilio
                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 832-1299
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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ADDRESSEE: Foley, Ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                     MVTTIIYLQKLD 97
                                            IEADVP-IYYYGFKDSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLN-AL
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                                                                                                                                                       TYPE: amir
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REFERENCE/DOCKET NUMBER: MI
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                  Similarity
                                                                                                                                   LE TYPE: protein
411,AA; 47663 MW; 877573 CN;
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Human Pathogens, and Uses Related
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Pred. No. 4.58e+01;
24; Mismatches 28
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Best Local Similarity 24.4%;
                                                                                             Sequence 2, Application US/08949637
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                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                       169 EQFEPLVPEGRDIFDVWGNDSNYTKIVAAVDMFFHMFKKHE 209
                                                               Sequence 2, Application US/08949637 Patent No. 5910414
     GENERAL INFORMATION:
APPLICANT: Gwynn, Michael
APPLICANT: Kallendar, Howard
TITLE OF INVENTION: No. 5910414el Topoisomerase
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9606053
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Yale University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein JENCE 422 AA; 47409 MW; 925810 CN;
                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 652:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-990
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/I
FILING DATE: 01-MAY-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
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Pred. No. 5.28e+01
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Best Local Similarity 20.3%;
Matches 24; Conservative
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                                                                                                                                                                                                           SEQUENCE
                                                                  369 SKPE-OHFTOPPARYSEATLIK-TLEENGVGRPSTYAPTIETIOKRYYVRLAAKRFEP 424
                                                                                                                       312 TAAVFDTMAVKLSQKGVQFAANGSQVKFDGYLTI-YNDSDKNKMLPDMVVGDVVK-QV-N 368
                                         285 IKEALETFGGVKRRFNETTIANQVIVDDYAHHPREISATIDTARKKYPHKEVVAVFQP 342
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PSTELECOMMUNICATION INFORMATION TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/028,370
APPLICATION NUMBER: 60/028,370
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: DC
                                                                                                                                                                                                        MOLECULE TYPE: protein JENCE 496 AA; 56064 MW; 1299408 CN;
                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                             SDDIY-AQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTN 284
                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/949,637 FILING DATE: 14-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SmithKline
STREET: 709 Swedeland
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                              amino acid
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Pred. No. 4.58e+01;
35; Mismatches 53
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time: 44 secs

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Staphylococcus aureus 0.00e+00 Bacillus subtilis comp 0.00e+00 Bacillus subtilis rrnB 0.00e+00 Bacillus subtilis UDP- 3.44e-255 Porphyromonas gingival 1.51e-13 Sequence 14 from paten 1.51e-13 Treponema pallidum sec 1.51e-13 Borrelia burgdorferi (1.8e-13 Synechococcus PCC7942 4.74e-10 Aquifex aeolicus secti 9.00e-10 Escherichia coli UDP-M 3.26e-08 Escherichia coli murG 3.26e-08	Description Pred. No.	250.084; scale 0.278 s predicted by chance to have a e score of the result being printed, total score distribution.	3:em_fun 4:em_htg 5:em_hum1 6:em_hum2 em_cr 10:em_ov 11:em_pat 12:em_ph 15:em_sts 16:em_vi 12:19:gb_htg1 20:gb_htg2 21:gb_in1 124:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl1 130:gb_pr2 31:gb_pr3 32:gb_ro 130:gb_pr2 31:gb_pr3 32:gb_ro	, e s	bases x 2			pep YGTTNGGNATGAARAAYGCNTTY 1311 RCAANCCNTACTTYTTRCGNAAR	); MasPar time 2384.79 Seconds 1523.811 Million cell updates/sec	search, using a protein query l into n.a. using IUPAC symbols	ins, Biocomputing Research Unit. University of Edinburgh, U.K. hts by Oxford Molecular Ltd	

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31 31					
PFAASN5514 PFAASN5514 EACMVT MSGB27CS ECOUW87 YSCKEX2AA E02040 YSCKEX2AA A46392 A46392 A30798 CEF58H1 SCCXIV39K AC004993	2	HPAE0005/6 I70976 I70975 ATAC005313	D90916 AE001670 G12491 AB015023	RPXX02 AF012886 AE001348 AE001489	U32794 AE000118 EC2MIN EC0110K AC005903
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## ALIGNMENTS

	CDS	gene	FEATURES source	JOURNAL	TITLE	REFERENCE	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	RESULT 1 LOCUS DEFINITION
/gene="murc" /function="cell wall biosynthesis" /functe-"MurC; UDP-N-acetylmuramate-alanine ligase" /codon_start=1 /transl_table=11 /product="UDP-N-acetylmuramoyl-L-alanine synthetase"	/gene="murc" 1. 1314	/organism="scaphylococcus aureus" /db_xref="taxon:1280" 1. 1314	ocation/Qualifiers	Submitted (11-NOV-1997) Channing Laboratory, Brigham and Women's Hospital and Harvard Medical School, 181 Longwood Ave, Boston, MA 02115, USA	Direct Submission	2 (bases 1 to 1314)	Unpublished	Cloning and sequencing of Staphylococcus aureus murC, a gene involved in cell wall biosynthesis	Lowe, A.M. and Deresiewicz, R.L.	Bacillaceae; Staphylococcus. 1 (bases 1 to 1314)	Eubacteria; Firmicutes; Low G+C gram-positive bacteria;	Staphylococcus aureus	Staphylococcus aureus.		92642658 AF034076.1 GI:2642658	AF034076	AF034076. 1314 bp DNA Staphylococcus aureus UDP-N-acetylmuramoyl-L-alanine synthetase

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BASE COUNT
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Best Local
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/db_xref="plD:g2642659"
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NKGIKILPFDANNIKEDMVVIQGNAFASSHEEKARAHQMKLDVVSYNDFIGQIIDQYT
SVAVTGAHGKTSTTGLLSHVMNGDKKTSFLIGDGTGMGIPESDYFAFEACEYRRHFLS
YKPDYAIMTNIDFBHPDYFKDINDVFDAFOEMAHNVKGIIAWGDDEHLARIEADVFI
YYYGFKDSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISY
YYYGFKDSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISY
LEKLDYTNIKEALETFGGVKRRRUSTTLANQYIVDDYAHHPREISATIETARKKYPHK
EVVANFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKIEG
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317; Mismatches 202;
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Kunst, F., Ogasawara, N.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viari,A., Wambutt,R., Wedler,E., weuler,n., netrompyor, Winters,P., Wipat,A., Yamamoto,H., Yamane,K., Yasumoto,K., Yoshida,K., Yoshikawa,H.E., Zumstein,E., Yoshikawa,H. and
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Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
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                                                                                            /gene="ribR"
/function="regulation of riboflavin biosynthesis genes"
/note="alternate gene name: ytnK"
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                                                                                                                                                                                                                                                                                                                DIDALPIEEKTGLPYASKHKGIMHACGHDFHTAALLGAAFLLKENQDSLKGKIRLLFQ
PAEEAGAGATKVIEDGQLDGIDAVIGLHKRPDIAVGTVGLKTGELMAAVDFRKVEDIEG
KGAHAALPHKGEDPIIGASQLIVALQTIVSRNVNPLQSAILTYGKINGGSTWNVIPOV
VVIEGTVRTFDSEVRNQVKQRFFAVTEQISAAFSLKANVKWHSGPPPLCNDEAITGLV
                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:034980"
/translation="MSLDYWRNIEGSYPYQTTGNDILTLKEESNPVNLSTLEKQLIGI
RRHLHQYPELSKEEFETTAFIKKCLKEKGIQIRPTALKTGVFADIAGESEGPAIALRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPILLSRKGLSPRKVVGTVDTSEFAIAVSATAGFLISLGWEDVNWLWVFSLMAGGIIA
APIAAWLVQKFHPQLMGVLVGGFIILVNARTLINEWIANTAVHPLIYTAIGAIWLSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKKLIVFAFIGLLSQLIDGSLGMAYGVTSTSLLLAFGITPAVAS
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ISLFLLLLGGYVLIRFLFQYKPALEKKHVPLNRKQSIPLGVIAGFADATGGGGWGPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(8. .1001)
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                                                                                                                                                                                                                                                                     KASYFLYESAKRLLDSNEESKISD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(99. .1001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(8. .24)
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., Wipat,A., Yamamoto,H., Yamane,K., Yasumoto,K., Yata,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="hipO"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ∕organism="Bacillus subtilis"
                                                                     transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db_xref="GI:2635413"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref-"SPTREMBL:034430"
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                                                                                                                                                                                                                                           ement(2288.
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                                                                                                                                                                                             .2980)
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                                                                                                                                                                                                                             complement (5649.
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DLGVGKAPGGFQLSTDALQAEYKKPVRQFDEKLEELTHFVRDDFPDTHRYAALRAPRQ
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complement(4352...4633)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(4352. .4633)
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                                                                                                                                                                                                                                                                                                                            VDRKPGIFLLGGSTESAISAAKLGISFVFAYFINGEEEVLKEARRAFDAHLPPGSEAE
FHLAPAVFAAHTKEEAEKHIVSRESIKVVLKDGRKVNVGSREQAEAYLENVTEPYDII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ytm0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ytni"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="SPTREMBL:034974"
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'db_xref="PID:e1185804"
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                                                                                               codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="ytmo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _table=11
                                                                                                                                                            .6428)
                                                                                                                                                                                                                             .6428)
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CDS

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Note: remainder
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                                                                                                                                                                                                                                                                                                                 50048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       861
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GTCAAATACATCGTCAATGCTTGAGAAGTAATCAGGGTGATCAAAATCAATATTCGTCAT
                                                                             CTCATCGTCTCCGCAGGCAATAATGCCTTTGTTGACTTGAAGAGCCATCTCTTTGGAAAGC
                                                                                                                                                   ATTTTCTTCCCCCGTGCCATAATACACAACCGGGACGTTCGCATGGATTTTCGGCAGATG
                                                                                                                                                                                                                                                           NACRTANACRTCRAANGCNGTNCCYTTRTCNGTDATYTGDATRTTYTGNGCRTADATRTC
                                                                                                                                                                                                                                                                                                            GACAAAGACATCAAAAGTTGTCCCTTCCGTGCTTTTACGATGTTTCTGGCTTGAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                 GTTTAATACATTGTGGTGGCCGTACGCAGGAATATAAAACGTATCATAGAACGTATTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTCYTTDATRTINGTNACRTCNARYTTYTCNARRTANSWDATNGCDATNACNGCNARNGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCTTAATGATGCTGGAATCAATTTCTTCATAATGGCATAACGCAATGACCGCCAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YIGRTINGCDAINGINGIYTCRITRAANCKNCKYTINACNCCNCCRAANGIYTCNARNGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGATCCCCAAGCTGCTTCTCATTGAATCTGCGTTTGACGCCCCCCAAAGGATTTGAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCKNSWRAANGTRTGNGGYTGRAANACNGCNACNACYTCYTTRTGNGGRTAYTTYTTNCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGGGTAAATGTATGAGGCTGGAATACCGCGACAATTTCCCGATCAGGATACTTCTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NARRAANACNCKRTCNGCYTTRCANARNSWYTCNGCRAAYTCRTTNARRAANGCYTGNGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAATACACAGTCGGCGCCGCTCAGGCTTTCTGCAAATTCGTCAAGGAACTGCTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATNARRTCYTGDATNGTNARNGCNCCNSWRTTYTCNCKDATNSWNCCRAADATYTCRCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGAGATCACCGATCGTCAGCTTTCCGGCATTCTCACGGGCTGAGCCGAAAATATCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAAYTGYTCNARNACRTTDATNARRTCYTCRTTDATRAANSWNGCNCCNCCDATYTTRTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAGCTTTTAAAACAGATGTGTCATCTTCTTCAATCAGCTTGGCATTATGAATTTTTTCC 49627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTANGCRTTYTGNARYTTYTGDATRTCNCCNGCNCCCATRAANARNACNACNGCRTTRTC
                                                  YTCRTCRTCNCCCCANGCDATDATNCCYTTYTTNACRTTRTGNGCCATYTCYTGRAANGC
                                                                                                                                                                                                                                                                                                                                                              RTTNARNACNGTRTGRTCNCCRTAYTGNGGNSWNARRAARTGRTCRTARAAYTCNCCRTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGCNGTRTCDATNGTNGCNSWDATYTCNCKNGGRTGRTGNGCRTARTCRTCNACDATNAC
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606; Conser
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larity 47.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(6425. .7132)
/gene="ytmM"
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/gene="ytmM"
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/codon_start=1
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1 (bases.1 to 7430)
Green,C.J., Stewart,G.C., I
Nucleotide sequence of the
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AF008220
g2293135
Seki,T., Yoshikawa,H., Takahashi,H. and Saito,H. Cloning and nucleotide sequence of phop, the regulatory alkaline phosphatase and phosphodiesterase in Bacillus s. J. Bacteriol. 169 (7), 2913-2916 (1987)
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Nucleotide sequence and organization of dnaB gene
genes on the Bacillus subtilis chromosome
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Connors,M.J., Mason,J.M. and Setlow,P.
Cloning and nucleotide sequencing of genes for three
acid-soluble proteins from Bacillus subtilis spores
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                  regulatory gene for 
Bacillus subtilis
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Grundy, F.J., Waters, D.A., Takova, T.Y. and Henkin, T.M.
Identification of genes involved in utilization of acetate acetoin in Bacillus subtilis
Mol. Microbiol. 10 (2), 259-271 (1993)
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11 (bases 162129 to 164080)
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A Bacillus subtilis spore coat polypeptide
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regulatory sequence in multiple tRNA synthetase
J. Bacteriol. 174 (4), 1299-1306 (1992)
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Seki,T., Yoshikawa,H., Takahashi,H. and Saito,H.
Nucleotide sequence of the Bacillus subtilis pho
J. Bacteriol. 170 (12), 5935-5938 (1988)
                                                                                                                                                                                                                                                                                                                                                          genes
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                                                                     (bases 25258 to 31212)
                                                                                                                                                                                                                                                                                                                                       Bacteriol. 176 (15), 4669-4679 (1994)
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                                      Driscoll, J. and Taber, H. cillus subtilis operon en
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17 (bases
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Kappes, R.M., Kempf, B. and Bremer, E.
Three transport systems for the osmoprotectant operate in Bacillus subtilis: characterization
J. Bacteriol. 178 (17), 5071-5079 (1996)
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Varqn,D., Brody,M.S. and Price,C.W.
Bacillus subtilis operon under the dual
Stress transcription factor sigma B and
transcription factor sigma H
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22 (bases 1 to 220060)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-JUN-1997) Laboratoire de Genetique Microbienne, Domaine de Vilvert, Jouy-en-Josas cedex 78352, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lapidus, A., Galleron, N., Sorokin, A. and Eh. Sequencing and functional annotation of the in the 200 kb rins-dnaB region Microbiology 143 (Pt 11), 3431-3441 (1997)
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Location/Qualifiers
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             .udon recognized:
/product="tRNA-Leu"
5905. .5981
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/product="tRNA-Thr"
5543. .5618
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/db_xref="taxon:1423"
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/product="tRNA-Leu"
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/product="tRNA-Lys"
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TATGGCACGGGGAAGAAATGATTTTCAAGCCAGAAACATCGTAAAAAGCACGGAAGGG 130357
                                                                                                                                             GAYATHAAYGAYGTNTTYGAYGCNTTYCARGARATGGCNCAYAAYGTNAARAARGGNATH
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                                                                                                                                                                                                                                                                  TATCAGCCAGATTATGCGATTATGACGAATATTGATTTGATCACCCCTGATTACTTCTCA 130177
                                                                                                                                                                                                                                                                                                                                     YTHCCHGARWSHGAYTAYTTYGCHTTYGARGCHTGYGARTAYMGHMGHCAYTTYYTHWSN 480
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/product="tRNA-Ala"
6172. .6248
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/product="tRNA-Met"
6531, .6607
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5997. .6073
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/product="tRNA-Ser"
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Varon,D., Brody,M.S. and Price,C.W.
Bacillus subtilis operon under the dual
stress transcription factor sigma B and
transcription factor sigma H
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Bacillaceae; Bacillus.
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Bacillus subtilis.
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llus subtilis UDP-N-acetylmuramate-alanine ligase gene, partial
and 3 ORF's.
                                                                                                                                                                                                             Microbiol. 20 (2), 339-350
coli enzyme"
                                                      /sub_species="Marburg"
/db_xref="taxon:1423"
                                                                                                        /strain="168"
                                                                                                                          /organism="Bacillus subtilis'
                                                                                                                                                                   Location/Qualifiers
                     /note="identification based
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                                                            GINGINWSNTAYAAYGAYTIYYINGGNCARATHAIHGAYCARTAYACNWSNGINGCNGIN 318
                                                                                         GTGATACGTTATCATAAGTTTTTAGGCGACTACATGAAAAATTCACGAGTGTTGCCGTT
ACNGGNGCNCAYGGNAARACNWSNACNACNGGNYTNYTNWSNCAYGTNATGAAYGGNGAY
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DAFGEMALQYMKGIIACGDDEHLPKHANVPVVYYGTGEENDFQARNIYKSTEGTTFD
VFVRNTFYDTFYIPAYGHHNVLNSLAVIALCHYEEIDSSIIKHALKSFGGVKRRFNEK
QLGDQYLIDDYAHHFTEIKVTIEAARQKYPDBEIVAAFQPHTFTRTQQFLDEFAESLS
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/db_xref="GI:556017"
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(including the TGA stop) into the
reported by Bolotin et"
                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mmskdginskdfiligtliggiigattalflapksgkelrddlgs
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Dktdsstamqdmreeamqaadetkdqvlqtkedvkdelkdaqkqaeqlnr"
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1670
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1123. .1127
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/db_xref="GI:556016"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="similar to"
                                                                                                                                                                                                                                 translation="MAKQLIQSEEEFKRIAEQEGVFVFLKHSTTCPISQAAFHEFDAF"
                                                                                                                                                                                                                                                                                              /transi_table=:
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Pred. No. 3.44e-255;
206; Mismatches 326;
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2 (bases 1 to 2454)
Ansai, T. v=---
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A murC gene in Porphyromonas gingivalis 381
Microbiology 141 (Pt 9), 2047-2052 (1995)
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                                                                                                                                                                                                                                                                          VVEADEFDRSFHHLKPFMAIITSADPDHMDIYGTAENYRDSFEHFTSLIQSGGALVLK
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339. .1640
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                                                                                                          1630. .>2454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'codon_start≖
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function="peptidoglycan synthesis"
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                                                                    RTTRTANSWNACNACRTCNARYTTNARYTGRTGNGCNCKNACDATYTCYTCRTGNSWNSW
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NGCRAANGCRTTNCCYTGDATNACNACCATRTCYTCYTTDATRTTRTTNGCNCCRAANGG
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166494
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Similarity 41.4%;
79; Conservative
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178; Mismatcl
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35; Mismatches 77
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d. No. 1.51e-13;
Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                               1929
                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                               368 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YYYYYYYYYYGTACCAAAT 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-MAR-1998) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser, C.M., Norris, S.J., Weinstock, G.M., White, O., Sutton, G.G., Dodson, R., Gwinn, M., Hickey, E.K., Clayton, R., Ketchum, K.A., Sodergren, E., Hardham, J.M., McLeod, M.P., Salzberg, S., Peterson, J., Khalak, H., Richardson, D., Howell, J.K., Chidambaram, M., Utterback, T., McDonald, L., Artiach, P., Bowman, C., Cotton, M.D., Fujil, C., Garland, S., Hatch, B., Horst, K., Roberts, K., Watthey, L., Weidman, J., Smith, H.O. and Venter, J.C.
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Science 281 (5375), 375-388 (1998)
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Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete genome sequence of Treponema pallidum, the syphilis
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1 (bases 1 to 14838)
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                                                                                                                                                                               /db_xref="pid:g3322607"
/db_xref="g1:3322607"
/db_xref="G1:3322607"
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Qelidqrsyvkliasenysslavqaamanlltdkyaegfphhryyggcqnvdsiesaa
AAEACALFGABHAYVQPHSGADANLVAFWALLSRQIEMPTLSSLGYTAATHLSEEQWE
VLRQKMGNQKLMGLDYFSGGHLTHGYRQNVSGRMFRVVSYAVDRDTGLLDYAAIEAQA
KRERPLILLAGYSAYPRSINFSIFREIADKVCAVLMADMAHFAGLVAGGVFTGDEDPV
                                                                                IDCGVTLNRNSLPFDPNGAWLTSGLRIGTPAVTSLGMGPEEMKRIARLIARVLGAATP
VRTKTGALSKSAAEVPGEVRSSVCSEVRELLARFTLYPELDEPFLRAHFTRRPAGQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    putative"
                                                          CRRRDLNPYGVTPTDFESVVSASFTTSARAQPITRGTKGTAVHVVFLREAPCLPLREF
                                                                                                                                                                                                                                                                                                                                                                                /product="serine hydroxymethyltransferase (glyA)"
/protein_id="AAC65317.1"
                                                                                                                                RNAAFKTYAHAVRDNARALADACIQQGMQLQTGGTDNHLLLLDVRPFGLTGRQAERAL
                                                                                                                                                            RWSHIVTSTTHKTLRGPRGAFILCKKEFAEAVDKGCPLVLGGPLPHVMAAKAVAFREA
                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identity: 48.52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="TP0329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to SP:P39148 PID:556886 GB:AL009126 percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ∕organism="Treponema pallidum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ′gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .14838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GI:332609"
/translation="MGADIGFIGLAVMGENLYLNIERNGFSVAVFNRTTTVVDRFLAG
RAHGKRITGAHSIAELVSLLARPRKIMLMVKAGSAVDAVIDQILPLLEKGDLYLDGGN
RAHGKRITGAHSIAELVSLLARPRKIMLMVKAGSAVDAVIDQILPLLEKGDLYLDGGN
SHYQDTIRRMHALEAAGIHFIGTGVSGGEEGALRGPSLAPGGSNQAWPLVSPIFCAIA
AKADDGTPCCDWYGSDGAGHYVKMIHNGIEYGDMQIIAEGYRWKHALGMSYEMHHHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GB:L42023 SP:P43774 PID:1003990 PID:1222490 PID:1204804 percent identity: 55.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3814. .5280)
/gene="TP0331"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVSGSDLEAILVRAQLTAAMENRTMYTTQDITRTIEDFIPPAYPHEIELQNLVAVLEC
TGKEMLPARYQHLDRSKLVADIRELKLLMGEK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Translation="MHSGQQLLEKNSIIISGLPPWAQELSKKYCSKTVNLYFVHGNIR
DFLPHRDIGGSFSFVRINDYISEVIFGNRDIIVFYDKSAGLIFCLQEMLSAVLERMHA
QYPTEALADFLSRDPVKAFAYLERYFIMNMKQNKRMVLIIDYSESLVPSEDIANLSET
DRYCFVTLNRWANDPYFTNEDISVVMLTENITDINSRETASPSTVKIHIPLPWEETRI
RFLEYLKTQEEILVLERGLNTEKIGKLTSGLNLVNLHQLAAETYOTIDANGKPEDNIS
RLSHTDSATLQFLKRKKQEIIEHEAGGLLEFVDTSCDLSYVAGNYFVKKRLYNAVRAI
KRISHTDSATLQFLKRKKQEIIEHEAGGLLEFVDTSCDLSYVAGNYFVKKRLYNAVRAI
KOGRADVLPMGYLISGFIGTGKSFMVSAFAGEIGIPMVRLCNFQATQDGITGSNLEKT
LNILKALIPVAVMVDEADAVFGRRNAPAGESRIFAQIAGFMGNTQHRCNIIWFLLTSR
DDLLPIDLKRQGRAPEHLALFYPETTKEKTEIFEALKKKLRIKGNTVPVAIHHRIKF
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/gene="trna-Leu-3"
                                                                                                                                                            /product="T. pallidum p.
/protein_id="AAC65327.1
/db_xref="PID:g3322617"
/db_xref="GI:3322617"
                                                                                                                                                                                                                                                                                                                           putative'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDYFGAHTYERTDAPRGEFFHTNWTGTGGDTIAGTYSI"
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/protein_id="AAC65318.1"
/db_xref="PID:g3322608"
/db_xref="GI:3322608"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1788. .3584)
                                                                                                                                                                                                                                                                                                                                                                          5296. .5421
/gene="TP0332"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIVSYAQGFELLSHTAKRRGWTLDFSRIASLWRGGCIIRSGFLSKISAAFAQQHDLEN
LVLAPFFAEELKRACPGWRTIVAESVRQALPVPALSAALAWFDGFTGAALPANLLQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTRWNTGRLHSYLIEITAAILAHQDTDGTPLLEKILDAAGQKGTGRWTCVAALEEGSP
LTLITESYMARSLSAQKQARCKAHRVFGSPVKVSKAETLSAQQREELVSALEDALYCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="phosphogluconate dehydrogenase (gnd)"
/protein_id="AAC65319.1"
/db_xref="PID:g3322609"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="TP0331"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="tRNA-Gly-1"
complemen+/201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    putative"
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/product="Leu CAA"
                                                                                                                                translation="MRAECSAFRYFLKGDGDLVLSVYIRVLCVFLEPVQRGSCSL"/
                                                                                                                                                                                                                                                                transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                  ′gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="tRNA-Gly-1"
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/transl_table=11
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'note="similar to
                           'gene="TP0333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=
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                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                              note="hypothetical protein; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dentity: 29.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="similar to GB:L43967
                                                    .6151
                                                                                                            .6151
                                                                              TP0333"
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GB:AE000783 percent identity: 31.40
                                                                                                                                                                                                                         predicted coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ກ protein, putative"
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by sequence similarity;
                                                                                                                                                                                                                                       region TP0332"
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YAADLAMSTGSGTRAHLRAKVIFKYPDRLRLDFSSPAEQTIVETGDSLTIYLPTSRV
ALVQSVAKDDTVSAASLASPHGLALMKREYTLAYETSSSPVPLGPDSGEMVVALVLNR
KSAAETFKSLRVLVSAHTKLIRRIEAWPLSGEKITFDFSHYRLNVGIPDTRELYDVPP
TANVVHNFLFAD"
                    /translation="mlstnaysytaaaacstcgvlrkgercisvegcnriggrgyrah
Ispayvmaiaavggfygthyygvpepyaffgayqacvlcigcilvrsgygefskrgay
Riwrrwgiaytsvcrccutiffyefecglcvacvartslryoqaplotlaqppklrvlti
Hllqdpkpagtrfrvbarvlgagyidgasfsahgvctvlfpaevilqqyatlmtddab
ARVCQYYARGLRCQIRGRFASSAPKLFISSSTPPRFYGWSSYFAQMRAQMRVALMRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="TP0334"
6176. .7393
                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="TP0336"
7775. .9475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="T. pallidum predicted /protein_id="AAC65328.1" /db_xref="pID:93322618"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(7390.
/gene="TP0335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MPDIGELLKTTRERKHLSLEQAAHETSIARRYLEALENDEYDVF
PGEPYILGFLANYCEYLOLDTEQCIARVHLKIQEMSLPTETLLPSKRWGSFPLLKGV
ACVLELGGVLGVYYAAHRALGELSRTVFFGRAQRTPRELSPDDATGAVREETVSLSSAQ
HEERARRTRSSASRYTLAEEKFEHTVFPGDVLVISSGGNAYELTVSRTTPHLYLDTPI
SPWGRAGGLLLALLSADSVFLSDEMRVAFRHAGLAHVLALSGMHLSLVGASATFLGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALCTAVHALWNAYAIAAAAR"
7775. .9475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MAITTAGDICALYPLCPILLHCSTLMHLSPLRNTPHVLHAAAAY
TEYAFVLSTLVFPSFCFSLPSPFPFPEGEGGAFYVRLFLNALSEEVLFRAYIPERLCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(7390. .7932)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTQVISLGQRLVMDLNTDVQPDVEISVEDIEAHQADGGARVRVFTGSLVQTLRDRSAQ
SFVPTSGVNVSGQTGVAAGARYQVLFEGGVAYPVTMNATFRSYCLFRYEADRTRREER
                                                                                                                                                                     /db_xref="PID:g3322612"
/db_xref="GI:3322612"
                                                                                                                                                                                                                          /product="comE protein,
/protein_id="AAC65322.1"
                                                                                                                                                                                                                                                                                                                                 /note="similar to PID:1652202 percent identity: identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                  /gene="TP0336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GI:33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="TP0335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YYQKGEQLTVQANNGIRVWASNGNVVQLQIVAGGKTVDVGLSRPGEVLVKDIKWIKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="conserved hypothetical protein"
/protein_id="AAC65321.1"
/db_xref="PID:93322611"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GP:1842438 percent identity: 31.48; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="TP0334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="conserved hypothetical
/protein_id="AAC65320.1"
                                                                                                                                                                                                                                                                                  'transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GI:3322611"
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Note: remainder Query Match Best Local

of.

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omitted

Similarity 75; Conser

5.9%; llarity 36.9%; Conservative

Score 319; DB 18; Pred. No. 1.51e-13; 46; Mismatches 82

Length 14838;

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Gaps

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DEFINITION ACCESSION
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SOURCE
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g2688755
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Lathlgra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K.,
Gwinn,M., Dougherty,B., Tomb,J.-F., Fleischmann,R.D.,
Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J.,
Rainderg,S., Hanson,M., van-Vugt,R., Palmer,N., Addams,M.D.,
Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L.,
Gocayne,J.D., Weidman,G., Garland,S., Fujli,C., Cotton,M.D., Horst,K.,
Artiach,P., Bowman,C., Garland,S., Fujli,C., Cotton,M.D., Horst,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van-Yugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L., Artiach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Horst, Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C. Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Clayton, R. Lathigra, R., White, O., Ketchum, K.A., Dodson, R., Hickey, E.K., Gwinn, M., Dougherty, B., Tomb, J.-F., Fleischmann, R.D., Bichardson, D. Betterson, T. Verlage, A. B. Onsetherberg, A. B. Der B. Verlage, A. B. Onsetherberg, A. B. D. B. D. B. D. B. D. B. D. B. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-DEC-1997) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roberts,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 390 (6660), 580-586 (1997)
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a burgdorferi
3 AE000783
                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Borrelia burgdorferi"
/db_xref="taxon:139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
/gene="BB0814"
                                                                             LFPSIIFEWFVFLF"
                                                                                                                                                                                      /transl_table=11
/product="B. burgdorferi
/protein_id="AAC67176.1"
/db_xref="PID:g2688771"
                                                                                                             translation="MRNGILYAILLYVFMFVLWFCFAYFIDTSTTIFNIPLWFFLSGI"
                                                                                                                                                      /db_xref="GI:268877:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="BB0813"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="BB0813"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hatch, B., Smith, H.O. and Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Research,
                                                                                                                                                                                                                                                                   region BB0813"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="hypothetical protein; identified by Glimmer;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MRLDKYIFLEVLANDNGKRLDSILIKILNFSKASIIKHIRKGDI
RINGLKSHFSCRYCKGDKIYLYKSLAQNLNLTTDKCFKSNIDFQYIRKRIIYEDSDIL
VLDKQKGILIVHGGKNSLDFLVNSVLLSQNLRSLSFKPSAVHRLDRNTSGIIIFAKNI
TARKLSBAFSGGSIIKKYFAILLGEVKSPVVYKHLFRNKRLRKTFVLEDKNFVVANIT
KVNPILSCKRATLVEIVIETGETHQIRSQCSFNNHPLINDKKYCNKFKKSDYFLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               riu:1045895 percent identity: sequence similarity; putative"
                                                                                                                                                                                                                                                                                        /note="similar to GB:L42023 SP:P45066 PID:1006469 PID:1221261 PID:1205384 percent identity: 28.70; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="BB0816"
2578. .3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="BB0815"
1666. .2559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMLVSSVILFSKMLDLGGGINNLFKTATSSLDKSLLLFSNADLKPQYIISFWILIGIG
ILGQPQIINNFIAFKDENAIKFSLFISTFIISFLIVLMHLIGFFAIILFPDLSPNDKV
VLNVALKVLNPFSCFMFFIGLLSAIMSTVDSNLLLLITSVLIKSIFIYKEDLKEDVKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identity: 33.64; identified putative"
                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="BB0817"
3518. .4924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISRQMGEHVVPAAAFEITSIRPNLLLNSIKVFFKSGWFFARKKNYIRSVVRPHFYEEG
VLSISKRAVRQIIEHCVSEYDRNYIVYDLKIKKDGNNYLFKLFLNIPLGNNLLNNTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"MMSMNFQNFSSDFFLKKILSKVKDFAISIKHKFVRVKVYALVGS
AGTGKSFRSHLVADKYSIPLIIDDGVLIKNMKIIAGSSAKFEDNVFKAVRRSVFEDDA
HCREMLEVLAKEEFNKILILGTSLKMIDKIISKLLLPNVFKIIYITDVSTRQEIEKAR
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FFSMFLISAQLIGGAKLIEVFWGIDYVVGLTFFAFLVFIYVFFGGFKAVAYTDLIQGF
                        YTDEILSNNKISYYDNIYEFSLKQLDRSFDLIYYSSAYNKDGLQVLLEAKELNIPILS
YPEALGELSRKYYSIGIAGSHGKTTTTAFLGVLFNKLGLNPNVIVGSSVKDFKDNSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="B. burgdorferi predicted coding region BB0816"
|protein_id="AAC67175.1"
|/db_xref="pib:92688770"
|/db_xref="GI:2688770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKFNGTFFKKNEFCSKPSLDF"
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/protein_id="AAC67167.1"
/db_xref="pID:g2688762"
/db_xref="GI:2688762"
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/protein_id="AAC67168.1
/db_xref="pID:g2688763"
AGISNIFIVETCEYKKHFLNFSPNMLILTNVDYEHVDFFKNYEALEEAFLQYINNLKK
                                                                                /db_xref="G1:2688761"
/translation="MKVDFDDLNNIFFVGIKGSGACSLACFLNSKGYCVEGVDVSDKF
                                                                                                                                             /product="UDP-N-acetylmuramate--alanine ligase (murC)"
/protein_id="AAC67166.1"
/db_xref="PID:g2688761"
                                                                                                                                                                                                                                                                                                                                                                                       /gene="BB0817"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRTYIITNVLKYTIINILSIDIVIHKFYDKKDYLEESYEG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="BB0815"
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/translation="MLLNKYFLANRNINFIVMALLFSSSYISASSFISGPSAVYKYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="BB0814"
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1"
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:KRSLEVYYQTGIPISQFQKKQSSEFKNIVIIGLKRSFEDLKTRISIRINEMLNSGLL

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identity: putative"
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5798. .6340
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NVELKTVLFHNVLNFSAALLALNIFLESNGKSIFDFSKIIAKNYSGIKRRVEVVK
EENGVIYMDDYAHHPREIKNTLFGIKNFYKNKRIILDFMPHTFTRTKEFFADFVEVLS
AADILILHNIYLSNRENFNPDELSVKLFLNIKKINKNTYFFKDVKDSINFIKSLLISG
/translation="MKEDRVVFIFGPTAVGKSNILFHFPKNKAEIINVDSIQVYKEFN
IASSKPSKNLMKHIKHHLVDFLDPEKDYTIGIFYEQALKIVKEIRQKKKIPIFVGGTA
FYFKHLKDGFPSTPLVTSKIRIYVNNLLELKGKSYLLKELKNVDPIRFNMLNKNDIYR
                                                                                                  modification enzyme (mid/protein_id="AAC67163.1"/db_xref="PID:92688758"
                                                                                                                                                                                                                                     /gene="BB0821"
/note="similar to GP:216567 percent identity:
/note="similar to GP:216567 percent identity:
                                                                                                                                                                                                                                                                                                                                       /gene="BB0821"
6563. .7483
                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GI:2688769"
/translation="MTKVPLKKIQDFDGNFYELVVATIMRTEQIIDNISLAEHAIFDD
KILGQAFNDYLTGKFRYSIEGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Translation="WKIALSGKSGCGNTTVSGMIAKHYGLEFINYTFHDIAREHNIPF
SEFYEKEIIGRNDYYMDKYLDNRLSVLSRKNNTVLASRLAIWISKSADLKIYLYAKME
VRAERIMTREGGMYSDVLSSTFIRDENDKKRYLAIYNIDIDDYFSETDLVIDVTNINP
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DLDIRNLISKYISRGNVFLNYGYKELVPSVNFTINPNYIEAISELRDSLAHTNINIKN
ELSILODFLSLKKGALIILDEDSEHQEETYGLFKOVLEEBALLHYNNGRSFBESENTKSDIVS
TLVLIERDLKIVKDACSDINVKLFASIKENISKLMDEFRDLNIAEEAAKMAIRLDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="cytidylate kinase
/protein_id="AAC67164.1"
/db_xref="pID:g2688759"
/db_xref="GI:2688759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIMRLDSHIETFYKNLEYEICGKALEFISQEMHREITTMSNKAVDLDIKNLILNMKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
/protein_id="AAC67165.1"
/db_xref="PID:92688760"
/db_xref="GI:2688760"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLFITMGAGNNFILHDFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="B. burgdorferi
/protein_id="AAC67174.1"
/db_xref="PID:g2688769"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               putative
                                                                                                                                                     /product="2-methylthio-N6-isopentyladenosine
modification enzyme_(miaA)"
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/transl_table=11
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                                                                               'db_xref="GI:2688758"
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by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4542 TGGACGATTATGCTCATCATCCTAGGGAAATTAAAAATACTCTTTTTGGTATTAAAAATT 4601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNTTYYTNAAYGARTTYGCNGARWSNYTNTGYAARGCNGAYMGNGTNTTYYTNTGYGARA 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATTTTTTGCCGATTTTGTTGAAGTTCTAAGTGCTGCCGATATATTAATTTTTGCACAATA 4721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARTAYCCNCAYAARGARGTNGTNGCNGTNTTYCARCCNCAYACNTTYWSNMGNACNCARG 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTATAAGAATAAACGTATAATTTTGGATTTTATGCCTCATACCTTTACAAGAACAAAAG 4661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATATCTTTCAAATAGGGAAAATT 4745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THTTYGGNWSNATHMGNGARAAYW 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPU86147 2268 bp DNA BCT 16-FEB-1997 Synechococcus PCC7942 UDP-N-acetylmuramate-alanine ligase (murc) gene, partial cds, UDP-N-acetylenolpyruvy/glucosamine reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submitted (22-JAN-1997) Plant Sciences, Hebrew University, Jerusalem 91904, Israel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyanobacterial mutants concentration of zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechococcus PCC7942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes, complete cds. U86147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 2268)
Kirzner, S. and Kapla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kirzner, S. and Kaplan, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eubacteria; Cyanobacteria; Chroococcales; Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechococcus PCC7942.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jnpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (murB),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 77; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 2268)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mercuric resistance operon regulatory protein
                       RSAA"
854.
                                                                                      /product="UDP-N-acetylmuramate-alanine ligase"
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GMDFASIREGLAGFEGARRFEFERGSAGGIQFVDDYAHHPSELAATILAAARIAACHL
                                                                                                                                                                                                                                                                                                       /note="similar to slr1423 in the cyanobase (the genome sequence of Synechocystis sp. PCC 6803); translation of murC probably starts upstream of
                                                                                                                                                                                                                                                                                                                                                                                         /gene="murC"
<1. .843
                                                           TLADA I AQYQANVHY APDLEAVEQRLHQLLQPGDLALFLGAGNLNQVI PRLLDHYACD
                                                                              SRLPEVPKRLVAIFQPHRYSRTQAFLAEFAQSFGPADLVLISDIYAAGERNPGQLSGQ
                                                                                                                                                                                                                                                                                      sequence"
                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Synechococcus
/strain="PCC7942"
/gene≖"murB"
                                                                                                                                                                                                                                                                                                                                                                    /gene="murC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:1140"
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37.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of growing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCC7942"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15079;
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REFERENCE
AUTHORS
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SOURCE
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ORIGIN
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DEFINITION
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Best Local Similarity 38.2%;
Matches 63; Conservative
TITLE
                                                                                                      MEDLINE
                                                                                                                             JOURNAL
                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1127 ARAAYWSNGGNGCNYTNACNATHCARGAYYTNATHGAYAARATHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTGGCTATTTTCAACCCCATCGCTATAGCCGCACCCCAAGCATTTTTGGCCGAGTTTG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNGARWSNYTNTGYAARGCNGAYMGNGTNTTYYTNTGYGARATHTTYGGNWSNATHMGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCAGAGTTTTGGCCCAGCTGACCTCGTGCTAATCAGTGATATCTATGCAGCGGGTGAGC 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNGTNGCNGTNTTYCARCCNCAYACNTTYWSNMGNACNCARGCNTTYYTNAAYGARTTYG
             2 (bases 1 to 15862)

Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox
Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,
Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson
                                                                                                                                                                    Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L. Graham,D.E., Overbeek,R., Snead,W.A., Keller,M., Ajay,M., Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V. The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                         Aquifex aeolicus. Aquifex aeolicus
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g2983763
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Aquifex aeolicus section
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                                                                                                      98196666
                                                                                                                                                                                                                                                         Eubacteria; Aquificales; Aquificaceae; Aquifex 1 (bases 1 to 15862)
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                                                                                                                           392 (6674),
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a 582 c 670 g 562 t
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/gene="merR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to murB in
a hypothetical protein in
(Cyanobase N. slr1424)"
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/transl_table=11
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                                                                                                                           353-358 (1998)
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Pred. No. 4.74e-10;
37; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                           n 68
                                                                                                                                                                                                                                                                                                                                                                                                                                           of 109
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-JUL-1997) Diversa Corporation, Genomics, CA 92121
                                                                                                                                                                                                                                                                                                     /gene="aq_1349"
1950. .2756
/gene="aq_1349"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="aq
939. .146
                   /gene="aq_1350"
2753. .4234
                                                                           /translation="MSGFLIALEWVIFSKYVFDVLFFREAKIEREIFGNKNLALSLSY
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NAGAGITOGIYFLSLGILISASFWRKESFILSVIYSLIYLSLGMVMLFISTLLMSRLL
KLNFEEEVKKENFSASLVLGSITLGVSVVLYGAISGEFMGSLLFDLFSFVLYFVVSQV
LDVJFYVVEFLLFRKVILSSEVYENNLSASLILSATFIASAFITLAVMG"
                                                                                                                                                                                                                                                                                                                                                                          1950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mGFLERIKKLFSKEEEKQEESILSNPLERLKKGDIIEIDGETWE
VTDVALYDYGASKEKEWEIRSASRRGFLSLEEGKIYFFEEIDPEELEPDPGEHFRKYG
KPPEYVTYKGKRYRLKYAGKAKYIKNLESYPVTIWEFRSEDGEMIDLEIWDEYEIEAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="PID:g2983774"
/db_xref="GI:2983774"
/trans1.+:
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MEALAQVKASQIREBEARNEKERAKALVKKAESLLLQAQEGKISPEEAEKLAELIQ
KAELHEKNARRLEEEAKROREMAVKLOAKIDELKVQIAKVEAELKTLKARHATARAV
KYNKQIAKVDPSDTIAMLERMKEKVEEEETLAQAYEELAKQEVALDVESEAEKKLKEV
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233. .937
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233. .937
                                                                                                                                                                              /product="putative protein"
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                                                                                                                                                                                                                                                                                                                                                                                                               SKPEEFFLKNYEKGIYRYAILENKPQDTEYCKVHLKDLIKEGEYILSLPSRYKVEREK
LSTKLYCELFSKGRFLEVAGERFTPPSALKVVTFVELKEGLFLWFLERVRAQGGGGGG
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/db_xref="PID:g2983773"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Aquifex aeolicus".
/strain="VF5"
                                                                                                                                                                                                                                                                                                                                                                                              I IFLPLP I PWGGGYNY EGRYRT PTGRYGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:2983775"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative protein"
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/db_xref="pID:92983775"
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/product="putati
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'gene-"aq_1350"
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                                                                                                                                                                                                                                                                                                                                                   complement(5649.
/gene="lipA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REEKELEEEVILITHRKKAIVPKTETQKKYVEAIKKNDIVFGIGPAGTGKTYLAMAMA
LQHLKEGKVNKIILTRPAVEAGEKLGFLPGTIAEKVHPYLTPLYDALYDMVDYDKANY
MLERNIIEIAPLAFMRGRTLNDAFIILDEAQNATRDQMKNFLTRIGFGSKAVITGDVT
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FYGEBIIHFBQTPYQKIVLTRGKHYSLYLDGHLQFSTLDEKKRHETLVHVPASFLKR
YEKALILGGGDGLALBELKKYPFGEHLVDLDPKMIEFSKKNLVMRK I NENSFYDTEL
KVFSEDAFNFVKKTKEKYDFVIVDLIDPRTPSSARVYSLEFYMSLKNKLKEDGIFITQ
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                                                                                                                                                                                                                                                                                                    6505.
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/note="aq_1355"
/gene="lipa"
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TEFLNRERALAFYTLGKSLECPNVEVNTLLKPVLIYYYYKIQN"
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5230. .5682
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/protein_id="AAC07324.1"
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/transl_table=11
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1260. .5306
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGTCCGTAATCGTC 10434
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                                                                                                                                                                                                                                                                              U67892
g2177093
U67892.1
Origin of mutant strain 2 (bases 1 to 1998) Eveland, S.S., Pompliano
                                                                                          Matsuzawa, H., Matsuhashi, M., Oka, A. and Sugino, Y.
Genetic and biochemical studies on cell wall peptidoglycan
Synthesis in Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.1%;
Similarity 44.9%;
61; Conservation
                                                                                                                                                                                                                      Escherichia coli.
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                         Escherichia
                                                               69286442
                                                                                                                                                                                                Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                             Biophys.
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YLEGGKAYLASFFDAVNYSTPYRFVHNFLAGVITGAIFVAGISAYYLKKHLDVAG
ESFRIAVTIGNIASLLQIIAGDLHGYQVARTQPLKLAMMEDKNETESGAGLEIVPGIE
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                                                                                                                                                                                                                                                                                GI:2177093
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7056. .8462
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ITEEEIPPTWIPFWSLRGMVFLGFFFAFITSLGFIFTVQDTIEQRRWLLKLFFYSIPL
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/product="cytochrome oxidase
/protein_id="AAC07328.1"
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7056. 8462
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                                                                                                                                                                                                                                                                                                                                                     1998 bp DNA BCT 11-JUN-1997 coli UDP-MurNAc:L-alanine ligase (murC3) gene, complete
  Pompliano, D.L. and Anderson, M.S.
                                                                               Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 279; DB 18;
Pred. No. 9.00e-10;
26; Mismatches 49
                                                                               Commun.
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Best Local Similarity 42.4%;
Matches 72; Conservative
                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                            1599 GACCTGTATGATGTTCGCCAATGTGCTGACGCAGGTTGATACCCTGTT 1648
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Escherichia coli Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                    ECMURGC 2793 bp DNA BCT 19-JUL-1995 Escherichia coli murG and murC genes for an unidentified read frame and UDP-N-acetylmuramate:L-alanine ligase (EC 6.3.2.8)
                                                                                        X52644.1 GI:42053 ligase; murC gene; murC gene; UDP-N-acetylmuramate:L-alanine ligase; unidentified reading frame.
                                                                                                                                                                                             X52644
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                                                                  Escherichia coli.
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IPVIRRAEMLAELMFFRHGIAIAGTHGKTTTAAVVSSIYAEAGLLPFFVNGGLVKAAG
VHARLGHGRYLLAEADESDASFLHCPMVAIVINIEADHMDTYQGDFENLKQTFINEL
HNLPFYGRAVMCVDDPVIRELLPRVGRQTTTYGFSEDADVRVEDYQQIGPQGHFTLLR
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/strain="CGSC 5988"
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Ikeda,M., Wachi,M., Jung,H.K.,
Nucleotide sequence involving m
region of Escherichia coli
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/note="put. ribosome binding site"
1203. 2678
/gene="murc"
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PVRTVYLALPLEQORLAGREGPVRVLVVGGSQGARILNQTMEQVYAKLCDSVTIMPOS
GKGSQOSVEQAYAEAGQPQHKYTEFIDDMAAYAMADVVCRSGALTVSEITAAGLFA
LFVPFQHKDRQQYWNALPLEKAGAAKIIEQPQLSVDAVANTLAGMSRETLLTMAEBAR
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/translation="MSGQGKRLMVMAGGTGGHVFPGLAVAHHLMAQGWQVRWLGTADR
MEADLVPKHGIEIDFIRISGLRGKGIKALIAAPLRIFNAWRQABAIMKAYKPDVVLGM
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/protein_id="CAA36867.1"
/db_xref="plb:942055"
/db_xref="GI:42055"
                                                                                                           PLEPVNGKSGTAMLVDDYGHHPTEVDATIKAARAGWPDKNLVMLEQPHRETRTRDLYD
DFANVLTQVDTLLMLEVYPAGEAPIPGADSRSLCRTIRGRGKIDPILVPDPARVAEML
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/note="put. ribosome
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                                                                                      APVLTGNDLTLVQGAGNIGKIARSLAEIKLKPQTPEEEQHD'
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/db_xref="SWISS-PROT:P17952"
                                                                                                                                                                                                                                                                                                                                         /protein_id="CAA36868.1"
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/gene="murC"
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/protein_id="CAA36866.1"
/db_xref="PID:9809684"
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/db_xref="taxon:562"
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Haemophilus
Eubacteria;
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Submitted (27-SEP-1997) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
The H. influenzae sequence has been updated by R. Fleischmann. New database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. We
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A., Kirkness,E.F., Kerlavage,A.R., Bult,C.J., Tomb,J., Dougherty,B.A., Merrick,J.M., McKenney,K., Sutton,G.G., FitzHugh,W., Fields,C.A., Gocayne,J.D., Scott,J.D., Shirley,R., Liu,L.I., Glodek,A., Kelley,J.M., Weidman,J.F., Phillips,C.A., Spriggs,T., Hedblom,E., Cotton,M.D., Utterback,T., Hanna,M.C., Nguyen,D.T., Saudek,D.M., Brandon,R.C., Fine,L.D., Fritchman,J.L., Fuhrmann,J.L.,
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Haemophilus influenzae
                                                                                                                                                                                                                                    3 (bases 1 to 12085) White, O., Clayton, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geoghagen, N.S., Gnehm, C.L., McDonald, L.A., Small, K.V., Fraser, C.M., Smith, H.O. and Venter, J.C.
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                                                                                                       Direct Submission
                                                                                                                           White, O., Clayton, R.A.,
                                                                                                                                               Medical Center Dr, Rockville, MD 20850, (bases 1 to 12085)
                                                                                                                                                                                        Submitted (25-JUL-1995) The Institute for Genomic Research,
                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                96398784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 269 (5223), 496-512 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whole-genome random sequencing and assembly of Haemophilus
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1 (bases 1 to 12085)
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Similarity 42.48;
72; Conservation
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/translation="MTDKIAVLLGGTSAEREVSLNSGAAVLAGLREGGIDAYPVD"
676 c 858 g 639 t
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/protein_id="CAA36869.1"
/db_xref="pII:942057"
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influenzae
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Pred. No. 3.26e-08;
26; Mismatches 72;
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Rd
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Rd section
                                                                                                                           Kerlavage, A.R. and Fleischmann, R.D
                                                                                                                                                                                                                                       Kerlavage, A.R. and Fleischmann, R.D.
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109 of 163 of the complete
                                                                                                                                                                                                                                                                                                                                                                                   Brown, N.P., Hayes, W.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2793;
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REFERENCE
AUTHORS
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JOURNAL
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White,O., Clayton,R.A., Kerlavage,A.R.,
Peterson,J., Hickey,E., Dodson,R. and Gw
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Medical Center Dr, Rockville, MD 20850, USA
The whole genome was shifted by 588 nucleotides for a new start
On Oct 1, 1996 this sequence version replaced gi:1221895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gratefully acknowledge the work of Tatusov et. al. We have incorporated their annotation into the /notes fields of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (28-MAY-1998) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct
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/db_xref="taxon:71421"
99._.1526
                                                                                                                                                                                                                                                                  /note="similar to GB:D10483 SP:P06136 GB:K02668 GB:X02821
PID:145725 percent identity: 40.62; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                       /gene="I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKMLMKAFGLPVADMKVVTRETFSELDPQAVVAKLGLPLMVKPSLEGSSYGLTKVKAV
EELKSAVEYALKFDNTILIEEWLAGDELTVPVLDNQVLPAIRIVPEGEFYDYEAKYIS
DNTQYFCPAGLTPEREQALSTLVKRAYDAVGCRGWSRIDVMCDAKGNFRLVEVNTNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAHLGASRYLIAEADESDASFLHLQPMYSVYTNMEPDHMDTYEGDFEKMKATYVKFLH
NLPFYGLAVMCADDPYLMELVPKVGRQVITYGFSEQADYRIEDYEQTGFQGHYTVICP
NNERINVLLNYPGKHNALNATAALAVAKEEGIANEAILEALADFQGAGRREDQLGEFI
                   /translation="MNILKRKTPQNIREGEQKPKYYFHIRAFAVLLGVFFLLGVYFNW
QSILEKMDDKPISAFALVGQNTFTTADDIKESLLKMGELKGFWGQDVAPIQEQIEALP
WVKGAIVRKMMPNRLSIWVSEYQPVAFWNQNQFVTLDGIVFQLPSVRLTAKNLPYLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MNLKQEKIAVLLGGTSAEREVSLNSGKAVLEALLKQGYNAHPIDPKEYNVANLKKDGFNRAFNILHGRGGEDGTMQGLLEQIGLPYTGCGYMASALTMDKMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene-"HII140"
/note-"similar to GB:D10483 SP:P07862 GB:K02668 PID:145724
PID:146030 percent identity: 59.93; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MKHSHEEIRKIIPEMRRVQQIHFIGIGGAGMSGIAEILLNEGYQ
ISGSDIADGVVTQRLAQAGAKIYIGHAEEHIEGASVVVVSSAIKDDNPELVTSKQKRI
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/db_xref="GI:1574697"
                                                                                                                                                                                                                                                                                                                                                     2518. .3282
/gene="HI1141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTSHSLFPKSAATVGISFEQLVVKILELSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="D-alanine-D-alanine ligase (ddlB)"
/protein_id="AAC22795.1"
/db_xref="Fib:91574696"
/db_xref="GI:1574696"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="HI1140"
1598. .2518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="UDP-N-acetylmuramate--alanine ligase (murC)"
/protein_d="AAC22794.1"
/db_xref="PID:91574695"
/db_xref="GI:1574695"
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PDYQSLKVIETWNQIYINLKSNNIMAKGINIDDRGAWQVQLDNDIVLKLGRGDWKSKL
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PID:42056 percent identity: 68.16; identified by sequence
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                                                                                                                                                                                                                                                                                               sequence
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deacetylase (lpxc)

protein_id=AAC22799.1*

(protein_id=AAC22799.1*

(db_xref="plo:g1574700"

/db_xref="g1:1574700"

/db_xref="g1:1574700
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/product="cell division protein (ftsZ)"
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TFEGKKRMQFAELGIKDLSQYVDSMIIIPNQQIQKVLFKNAKLIDAFAAANDYLRNSV
MGISDMITSPGLINUDFADVRTVMSVGGQAMIGFGSAVGEPGAGRAEEAARLAVRNDL
LEKIDLSNAQGILVNITAGMDLVFEEENIIGETIGSFAGSFAEEMVVGGTSLVPBMSDEI
LEKIDLSNAQGILVNITAGMDLVFEEENIIGETIGSFAGSFAEDFAUVVGTSLVPBMSDEI
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                                                                                                                                                                                          /note-"similar to SP:Q02286 GB:M74134 GB:X60420 PID:148468 PID:43344 percent identity: 55.32; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="HI1145"
7010. .8167
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PID:216510 PID:40864 percent identity: 77.30; identity: 97.30; identity: 77.30; identity: 77.30; identity: 97.30; identity
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/DID:40863 percent identity: 67.53; identified by sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 4.8%;
Local Similarity 41.5%;
hes 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGGCTGGGGAGATAAACGTATTGTAATGATTTTCCAACCGCATCGTTATTCTCGCACTC 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARAARTAYCCNCAYAARGARGTNGTNGCNGTNTTYCARCCNCAYACNTTYWSNMGNACNC
submitted (13-0CT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
This sequence was determined by the E. coll Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and Hg01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coll K-12 strain MG1655. Predicted open reading
                                                                                                                                                                                                                                                         Direct Submission
Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoll@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoll@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia
                                                                                                                                                                                                                                                                                                                                                                                   Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The complete genome sequence of Escherichia coli K-12 Science 277 (5331), 1453-1474 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE000118.1 GI:1786262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome.
AE000118 U00096
                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                      Plunkett,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mau, B. and Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE000118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 21757)
                                                                                                                                                                                                                            (bases 1 to 21757)
                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 21757)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAC22800.1"
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FIHSLDRVHIEYCESSSHAMQLVASLNKPNIAALGNEDGGKLYGLSVLKTNIANQENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21757 bp
coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 264; DB 18;
Pred. No. 2.14e-08;
29; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
MG1655 section 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCT of '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 12085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1998 the complete
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CDS gene

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/note="b0076"

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/note="central position to predicted
/bound\_moiety="AraC predicted site"

protein\_bind

protein\_bind

complement (519.

/note="factor Sigma70; predicted +1 start at 84042"

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protein\_bind

460. .474

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promoter"

protein\_bind

protein\_bind

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/note="central position to leuABCD
/bound\_moiety="Lrp documented site"
complement(354. 368)

euaBCD promoter: .d site"

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protein_bind
                                                                                                                                               protein_bind
                                                                                                                                                                                                                                                                 promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [a-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web Site (http://www.genetics.wisc.edu). *** The E. coli K-12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene
                                         complement(201. .221
                                                                                                                                                   complement(201. .221)
                                                                                                                                                                                         at83735"
                                                                                                                                                                                                                                                                 complement(197.
                                                                                                                                                                                                                                                                                    /product="leu operon leader peptide"
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/db_xref="GI:1786263"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(77. .163)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(77. .163)
/note="b0075"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                    /note="central position to predicted
/bound_moiety="LexA predicted site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sub_strain="MG1655"
/db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="K-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Escherichia"
/note="No predicted promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="leader; Amino acid biosynthesis:
/note="f28; 100 pct identical to LPL_ECOLI ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="leuL'
                                                                                                                                                                                                                   'note="factor Sigma70; promoter leu; documented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="leuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'codon_start=1
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                                                                                                         promoter: -0.5"
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FEATURES

CDS

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protein_bind
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                                            IDPTSISKTYTADIFIYGDARQVLEQMLELLSQESAHQPLDEIRDWWQQIEQWRARQC
LKYDTHSEKIKPQAVIETLWRLIKGDAVYISDVGQIDKTALLYEPDKEPRWINSGGL
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VTXGTEDIPQVLKKAFWLAASGRPGPVVVDLFKDILNPANKLPYVWPESVSMRSYNPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1949.
NNRLVFVDVTVDGSEHVYPMQIRGGGMDEMWLSKTERT
                                                                                                                                                              TTGHKGQIKRALQTLVAAKKPVYYVGGGAITAGCHQQLKETVEALNLPVVCSLMGLGA
FPATHRQALGMLGMHGTYEANMTMHNADVIFAVGVRFDDRTTNNLAKYCPNATVLHID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QETEFVISYEDFHRPEFTSVPLFKDEMVLVASKNHPTIKGPLLKHDVYNEQHAAVSLD
RFASFSQPWYDTVDKQASIAYQGMAMMSVLSVVSQTHLVAIAPRWLAEEFAESLELQV
LPLPLKQNSRTCYLSWHEAAGRDKGHQWMEEQLVSICKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPIRERELSVTVELSMPEVQTDHPETAELSKPQLRMVDLNLLTVFDAVMQEQNITRAAHVLGMSQPAVSNAVARLKVMFNDELFVRYGRGIQPTARAFQLFGSVRQALQLVQNELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /bound_moiety="Lrp 1813. .1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1802.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contains 24 additional C-term residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-term residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="0373; 100 pct identical P10151(290 aa) but contains 59
                                                                                                                                                                                                                                                                                                                                                                                                                             /product="acetolactate synthase
large subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="o604; 98 pct identical (1 gap)
fromILVI_ECOLI SW: P00893 (566 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1995. .3809
/gene="ilvI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="central post/bound_moiety="Lrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="central position to predicted promoter:
/bound_mojety="Lrp predicted site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="PID:g1786264"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1978. .1992
/note="central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="central position to predicted promoter:107.5"
/bound_moiety="Lrp predicted site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="factor Sigma70; promoter ilvIHp3; documented+1 at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="central position to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="b0077"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bound_moiety="Lrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="factor Sigma70; promoter ilvIHp4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAC73187.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      function="enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EC_number="4.1.3.18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="ilvI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'function="putative regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sigma70; promoter ilvIHp2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      position to predicted promoter:136.5"
"Lrp predicted site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  position to predicted promoter:73.5"
"Lrp predicted site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pct identical to LEUO_ECOLI SW:
ut contains 59 additional N-ter aa and
100 pct identical to PIR: S40589 but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted promoter:
    predicted site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid biosynthesis: Isoleucine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid biosynthesis:
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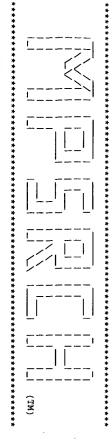
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Escherichia coli.
Escherichia coli.
             Henikoff,S., Haughn,G.W., Calvo,J.M. and Wallace,J.C. A large family of bacterial activator proteins Proc. Natl. Acad. Sci. U.S.A. 85 (18), 6602-6606 (198
                                                                                                       Haughn,G.W., Wessler,S.R., Gemmill,R.M. and Calvo,J.M. High A + T content conserved in DNA sequences upstream in Escherichia coli and Salmonella typhimurium J. Bacteriol. 166 (3), 1113-1117 (1986)
                                                                                                                                                                                                                                       3 (bases 1 to 306)
Wessler,S.R. and Calvo,J.M.
Control of leu operon expression in Escherichia
transcription attenuation mechanism
                                                                                                                                                                                                                                                                                                                                  Ayala, J.A., Regulation of transcription map of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (08-JAN-1991) Ayala J.A., Instituto de Biologia
Molecular, Centro de Biologia Molecular, Universidad Autor
Canto-Blanco 28049, Madrid, Spain
Proc. Natl. Acad.
88320486
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E. coli 2 minute region.
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72; Conservative
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/note="central position to predicted
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26; Mismatches 72;
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and Bacillus subtilis SpoVE protein, which function in cell division, cell elongation, and spore formation, respectively J. Bacteriol. 171 (11), 6375-6378 (1989) 90036736 17 (bases 16094 to 17806) Mengin-Lecreulx,D., Texier,L. and van Heijenoort,J. Nucleotide sequence of the cell-envelope murG gene of Escherichia coli	239 239 239	Nucleotide sequence of the murr gene encoding the UDF-MurNAc-pentapeptide synthetase of Escherichia coli Nucleotide Res. 17 (13), 5379 (1989) 89345095 14 (bases 12423 to 15030) 14 (bases 12423 to 15030) 1 Keda, M., Wachi, M., Ishino, F. and Matsuhashi, M. Nucleotide sequence involving murr and an open reading frame ORF-Y spacing murr and ftsw in Escherichia coli Nucleic Acids Res. 18 (4), 1058 (1990) 901020000	Can. J. Microbiol. 35 (11), 1051-1054 (1989) 90124047 10 (bases 1 to 28277) Michaud, C., Parquet, C., Flouret, B., Blanot, D. and van Heijenoort, J. Revised interpretation of the sequence containing the murE gene encoding the UDP-N-acetylmuramyl-tripeptide synthetase of Escherichia coli Escherichia coli Biochem. J. 269 (1), 277-278 (1990) 90328986 13 (bases 11142 to 12634) Darguet, C. Flouret, B. Magnin-Tagrault, D. and van Heijenoort I	s. 18 (9), 2813 (199) o 10074) uyama,I.N., Soma,M., f cellular division gene for penicillin- gene for penicillin- 191 (1), 1-9 (1983) 191 (1), 5.E. iguro,E.E. nce of the murE gene	eclerc,G., Noel,G olecular cloning, ew gene in the 2- oli . Bacteriol. 172 0330585 (bases 6088 to (bases 6088 to omez,M.J., Fluore ucleotide sequenc scherichia coli	6 (bases 1799 to 2187) 6 (bases 1799 to 2187) Haughn,G.W., Squires,C.H., DeFelice,M., Largo,C.T. and Calvo,J.M. Unusual organization of the ilvIH promoter of Escherichia coli J. Bacteriol. 163 (1), 186-198 (1985) 8 5234358 7 (bases 2101 to 4431) 7 (bases 2101 to 4431) 8 Squires,C.H., DeFelice,M., Devereux,J. and Calvo,J.M. Molecular structure of ilvIH and its evolutionary relationship to ilvG in Escherichia coli K12 8 Nucleic Acids Res. 11 (15), 5299-5313 (1983) 8 3272971 8 (bases 4274 to 6093)
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LIVIH J. Moll. Biol. 229 (2), 306-318 (1993)  NE 93156044  The Part of the State of	cell division gene, ftsA Mol. Microbiol. 2 (5), 581-588 (1988) 89039246 Erratum:[[published erratum appears in Mol Micr Feb;3(2):267]] 27 (bases 1 to 28277) Wang,Q. and Calvo,J.M. Lrp, a global regulatory protein of Escherichia co-operatively to multiple sites and activates	25 (bases 18619 to 19770) 25 (bases 18619 to 19770) 25 (bases 18619 to 19770) Robinson, A.C., Kenan, D.J., Sweeney, J. and Donachie, W.D. Further evidence for overlapping transcriptional units in a Escherichia coli cell envelope-cell division gene cluster: sequence and transcriptional organization of the ddl ftsQ r J. Bacteriol. 167 (3), 809-817 (1986) 86304170 26 (bases 20513 to 21772) Robinson, A.C., Begy, K.J., Sweeney, J., Condie, A. and Donachi		ORS Beall,B. and Lutkenhaus,S.  Sequence analysis, transcriptional organization, and insertional E Sequence analysis, transcriptional organization, and insertional mutagenesis of the envA gene of Escherichia coli  NAL J. Bacteriol. 169 (12), 5408-5415 (1987)  INE 88058745  NCE 22 (bases 23989 to 27799)  ORS Schmidt,M.G., Rollo,E.E., Grodberg,J. and Oliver,D.B.  ORS Nucleotide sequence of the secA gene and secA(Ts) mutations  preventing protein export in Escherichia coli  NAL J. Bacteriol. 170 (8), 3404-3414 (1988)	division genes ftsQ and ftsA of Escherichia coli: overlapping transcriptional units J. Bacteriol. 160 (2), 546-555 (1984) 85054557 20 (bases 21464 to 2333) YiQ.M. and Lutkenhaus,J. The nucleotide sequence of the essential cell-div Escherichia coli Gene 36 (3), 241-247 (1985) 86083166	Nucleic Acids Res. 18 (9), 2810 (1990) 90251461 18 (bases 16094 to 18886) 18 (bases 16094 to 18886) 1 keda, M., Wachi, M., Jung, H.K., Ishino, F. and Matsuhashi, M. Nucleotide sequence involving murG and murC in the mra gene region of Escherichia coli Nucleic Acids Res. 18 (13), 4014 (1990) 90326550 19 (bases 19464 to 21952) Robinson, A.C., Kenan, D.J., Hatfull, G.F., Sullivan, N.F., Spiegelberg, R. and Donachie, W.D.

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Location Qualifiers
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/db_xref="taxon:562"
/clone="pLC26-6, pLC4-14, pLC6-7"
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/note="leu mRNA"
/evidence=experimental
complement(<1. .63)
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Nov 24 00:43:15 1999; MasPar time 0.52 Seconds 326.236 Million cell updates/sec

Tabular output not generated.

>US-09-103-287-2 (1-437) from US09103287.pep 3121

Description: Perfect Score: Sequence:

1 MTHYHFVGIKGSGMSSLAQI.......GDIQKLQNAYLDKLGMKNAF 437

Scoring table: PAM 150 Gap 11

Searched: 1479 segs, 387401 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: HIV-AA8 1:ALL

Statistics: Mean 46.900; Variance 101.768; scale 0.461

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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2.89e+01	3.47e+01	4.15e+01	2.89e+01	3.47e+01	3.47e+01	2.89e+01	2.89e+01	4.15e+01	3.47e+01	1.63e+01	1.98e+01	1.63e+01	1.63e+01								

#### ALIGNMENTS

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92 ENV POLYPROTEIN	LT 3 ENVSFLDD9 PRELIMINARY: PRT: 112 AA	75 lkslfntvavlycvhgrievkdtkdaldkieeigkkskgkt 115  ::  : :  ::: :  :  : ::: : : : :   266 LNAL-AVIAISY-L-EKLDVTNIKEALETFGGVKRRFNETT 303	Query Match 2.5%; Score 78; DB 1; Length 489; Best Local Similarity 22.0%; Pred. No. 5.92e+00; Matches 9; Conservative 18; Mismatches 11; Indels 3; Gaps 3;	TRANSLATED USING PHASE 1 SEQUENCE 489 AA; 54331 MW;	20-APR-1993 HIVVI57, GAG POLYPROTEIN PEPT 1 >489 GAG POLYPROTEIN	LT 2 GAGSVI57 PRELIMINARY; PRT; 489 AA	91 vlgemnlprrwkpkm-iggiggfi-kvr-qydqiti-gicghkaigtvl 135 	34 grdnnslseageeagddrggp-v-sfsfpgitlwgrpivtikiggg-lkealldtgaddt 90	Query Match 2.8%; Score 88; DB 1; Length 1006; Best Local Similarity 18.3%; Pred. No. 6.31e-01; Matches 20; Conservative 35; Mismatches 47; Indels 7; Gaps 7;	PEPT 51 10061 10061 POLYPROTEIN TRANSLATED USING PHASE 1 SEQUENCE 1006 AA; 113750 MW;	-1989 POL POLYPROTEIN	LT 1 POLSMN PRELIMINARY; PRT; 1006 AA

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M90882
03-FEB-1992
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SEQUENCE 112
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M90881
10-MAR-1992
PEPT > 1 339
-i-5':N 3':N 1 339
-TRANSLATED USING PHASE 1
SEQUENCE 340 AA; 37290 MW;
                                                                  NEF$JB03
X57465
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TRANSLATED USING PHASE 1
SEQUENCE 116 AA; 12447 MW;
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TRANSLATED USING PHASE 1
SEQUENCE 115 AA; 12786 MW;
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                                           11-MAR-1991
HIVJB03, NEF
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Local Similarity 24.3%;
nes 18; Conservative
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Local Similarity 21.6%;
les 16; Conservative
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Local Similarity 24.0%;
nes 18; Conservative
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                                                                                                                                                                                    irsanfsdnaktiivqlnksvnitcvrpnnntresipigpgkafyatgeiigdirqahcn 67
                                                                                                                                                                                                                                                                                                                                                                                                lseakwnntlaqiv 77 .
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AA; 12460 MW;
                                                                              PRELIMINARY;
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                                                                                                                                                                                                                Score 74; DB 1; Length 116; Pred. No. 1.34e+01; 22; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76; DB 1; Length 115;
Pred. No. 8.96e+00;
27; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 74; DB 1; I
Pred. No. 1.34e+01;
27; Mismatches 25
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Best Local Similarity 26.9%;
Matches 14; Conservative
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Best Local Similarity 26.9%;
Matches 14; Conservative
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D10112; D00917
09-JUL-1991
HIVCAM1, POL POLYPROTEIN
PETTIDE 1 1003 POLYPROTEIN
POLSSE2 PRELIMIN
K02007
01-MAR-1989
HIVSF2, POL POLYPROTEIN
PEPT 51 100
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15-OCT-1991
HIVOXI, POL: POLYPROTEIN
4639
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SEQUENCE 1003 AA; 113718 MW;
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M26727
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11-MAR-1992
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                                                                                                 190 QEMAHNVKKGI-IAWGDDEHLRKIEADVPIYYYGFKDSDDI--YAQNIQITD 238
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Local Similarity 27.3%;
hes 12; Conservative
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Local Similarity 26.18;
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                                                  PRELIMINARY;
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Pred. No. 8.96e+00;
12; Mismatches 16
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Pred. No. 1.10e+01;
13; Mismatches 21;
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Pred. No. 8.96e+00;
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K03458
01-MAR-1989
                                                                                                                      L11790
20-APR-1993
HIVVI354, GAG POLYPROTEIN
1 >264
                                                                                           SEQUENCE
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SEQUENCE 148 AA; 16840 MW;
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03-FEB-1992
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266
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                                            y Match 2.3%;
Local Similarity 22.0%;
hes 11; Conservative
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Local Similarity 26.9%;
hes 14; Conservative
            75 lkslfntvatlycvhqkinvkdtkealdkieeignkskqktqqaaaaten 124
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Local Similarity 24.3%;
Les 18; Conservative
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                                                                                          TRANSLATED USING PHASE 1
QUENCE 264 AA; 29206 MW;
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LNAL-AVIAISY-L-EKLDYTNIKEALETFGGVKRRFNETTIANQVIVDD 312
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Pred. No. 1
22; Mismat
                                            Score 71; DB 1; I
Pred. No. 2.39e+01;
16; Mismatches 20
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Pred. No. 1.10e+01
13; Mismatches 2
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1.63e+01;
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GAGSVI32 PRELIMINA
L11788
20-APR-1993
HIVVI32, GAG POLYPROTEIN
1 >385
                                                                                                                           TRANSLATED (
SEQUENCE 486
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L11791
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SEQUENCE 385 AA; 42556 1
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HIVVI415, GAG
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                                                                             2.3%;
Local Similarity 30.8%;
es 8; Conservation
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Local Similarity 27.0%;
nes 10; Conservative
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AA; 53947 N
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1 >486
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Pred. No.
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Pred. No. 1.63e+01
15; Mismatches 1
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# ALIGNMENTS

BASE COUNT	source	FEATURES CDS	COMMENT		REFERENCE AUTHORS	MISM	RESULT 1 LOCUS DEFINITION ACCESSION SOURCE
/organism="Human immunodeficiency virus type 1" /isolate="B2167" /cell_type="lymphocyte" /proviral /sequenced_mol="DNA" /tissue_type="blood" 281 c 369 g 286 t	/gene="gag" //gene="gag" //codon_start=1 //cod	;	Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. The BZ167 gag sequence clusters with HIV-1 B subtype gag sequences.	Phylogenetic analysis of gag genes from seventy international HIV- isolates provides evidence for multiple genotypes AIDS 7, 769-780 (1993)	, Peeters,M n,G., Franse	(cocultivation on PBMCs).  immunodeficiency virus type 1  se; ss-RNA enveloped viruses; Positive strand RNA	HIVB2167 1480 bp ss-RNA VRL 20-APR-1993 Human immunodeficiency virus type 1, Brazilian isolate B2167, gag region L11752 Human immunodeficiency virus type 1 (HTV-1). Brazilian isolate

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                                                                                                                                                                                                                                  833 ARAARYINGAYGINACNAAYATHAARGARGCNYINGARACNITYGGNGGNGINAARMGNM 892
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                                                                                                                                                                                                                                                                                                                            / Match 2.4%;
Local Similarity 41.7%;
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This sample has been taken from patient M, one of the seven patients (A,M,L,F,C,V,R), in the study(1). All patients had acute, self-limited symptomatic illness with measurable viremia followed by seroconversion. Patient M was a chronically infected male who subsequently transmitted the virus to patient F. The authors report that the sequences in this study are found to be uniformly macrophage-tropic and non-syncytium-inducing. The sequence for sample M clone 2, along with other patient M clones 1, 3-9, 11, and 12, is shown in alignment following the printed text entry. These gag sequences cluster with HIV-1 B subtype sequences. See also L21224-L21591 and L24161, L24162.
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                                                    HIVF10S1 309 bp ss-RNA
Human immunodeficiency virus
gag cds, pl7 region.
                                     gag cds, p17
L21375
   Human
                                                                                                                                                                                                                                                                                                                                                                              190 bp downstream from beginning of gag cds
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Science 261, 1179-1181 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhu,T., Mo,H., Wang,N., Nam,D.S., Cao,Y., Genotypic and phenotypic characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1 (HIV-1), Human immunodeficiency virus type 1
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L21492
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Similarity 43.1%;
31; Conservative
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/gene="gag"
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/sequenced_mol="RNA"
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Pred. No. 2.65e-01;
14; Mismatches 28; Indels
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Pred. No. 2.69e-02;
14; Mismatches 27;
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Best Local Similarity 41.7%;
Matches 30; Conservative
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This sample has been taken from patient F, one of the seven
This sample has been taken from patient F, one of the seven
patients (A,M,L,F,C,V,R), in the study(1). All patients had acute,
self-limited symptomatic illness with measurable viremia followed
by seroconversion. Patient F was infected by patient M via sexual
transmission. The authors report that the sequences in this study
are found to be uniformly macrophage-tropic and nonsyncytium-
inducing. The sequence for sample F clone 10, along with other
patient F clones 1-9, 11, and 12, is shown in alignment following the
printed text entry. These gag sequences cluster with HIV-1 B subtype
sequences. See also L21224-L21591 and L24161, L24162.
                                                                                                                                                            Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. The PH136 gag sequence clusters with HIV-1 B subtype sequences.
                                                                                                                                                                                                                                                                   1 (bases 1 to 1474)
Louwagie, J.J., McCutchan, F., Brennan, T., Peeters, M., Brennan, T., Sanders-Buell, E., Eddy, G., van der Groen, G., Fransen, K., Gershy-Damet, M., Deleys, R. and Burke, D. Phylogenetic analysis of gag genes from seventy international HIV-1 isolates provides evidence for multiple genotypes
AIDS 7, 769-780 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PH136.
Human immunodeficiency virus type 1
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
Retroviridae; Lentivirinae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 309)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp downstream from beginning of gag cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunodeficiency virus type 1 (HIV-1), Philippines isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunodeficiency virus type 1
                                                       /product="gag protein"
/gene="gag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sequenced_mol="RNA"
                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNKSKKKAQQATAAADTANSSQVSQNYPIVQNIQGQMVHQPISPRTLNAWVKVVEEKA
translation="MGARASVLSGGELDRWERIRLRPGGKKKYKLKHIVWASRELERF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Human immunodeficiency virus type 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="LQPSLQTGSEELRSLYNTIAVLYCVHQKIDVKDTKEALEKIEEE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 131; DB 3; Pred. No. 2.65e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
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                 GC_signal
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                                                                                                                                    misc_signal
                                                                                                                                                                                        misc_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 aaaagatagatgtaaaaagacaccaaggaagctttagagaagatagaggaagaggcaaaaca 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARAARYINGAYGINACNAAYAIHAARGARGCNYINGARACNIIYGGNGGNGINAARMGNM 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kindly provided in computer-readable form by Dr. Alison McIntosh, Sir William Dunn School of Pathology, University of Oxford, South Sir William Dunn School of Pathology, University of Oxford, South Sir William Dunn School OXI 3RE, United Kingdom. CAM-1 sequences clust Parks Rd., Oxford OXI 3RE, United Kingdom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           England, complete genome. D10112 D00917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIVCAM1 9591 bp ss-RNA VRL Human immunodeficiency virus type 1, isolate CAM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thesis (1991) Cambridge University, U.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of a Cambridge isolate immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 9591)
McIntosh,A. and Karpas,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cambridge, England
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1 (HIV-1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retroviridae; Lentivirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.48; Similarity 41.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     551
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EKAFSPEVIPMESALSBGATPODLNTMLNTVGGHQAAWQMLKETINEBAAEWDBLHPV
HAGBVVAPGQMEAPGRISGTSTLDEOGGWFUNNPIPVGETYKRWIINGLNKIVKW
YSPTSILDIKQGPKEPPRDYVDRFYKTLRAEQASQEVKNWMTETLLVQNANPDCKTIL
                                                                                                                                                                                        /note="5'LTR U3 351..360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRPEPTAPPEESFRFGEETTTPSQKQEPIDKELYPLASLKSX"
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                                                                                                                                                                                                                                                                      WRERQRHIRAISNWILSTHLGRPAEPVPLQLPPLERLTLDCSKDCGTSGTQGVGSPQI
LVESPAVLESGTKE"
                                                                                                                                                                                                                                                                                                                                                                              join(5832..6046,8380..8470)
/product="tat protein"
/product="tat protein"
/codon_start=1
/translation="MEPVDPRLEPWKHPGSQPRTACTNCYCKQCCFHCQVCFITKGLG
/translation="MEPVDPRLEPWKHPGSQPRTACTNCYCKQCCFHCQVCFITKGLG
/SYRKKRRQRRRTPOSSKTHQASSLSKQPASQFQGDPTGPKESKKKVEGETETHPGD"
/product="rev_protein"
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278 c 365 g
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/isolate="PH136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNCGKEGHIAKNCRAPRKKGCWKCGREGHQMKDCTERQANFLGKIWPSHKGRPGNFLQ
                                                                                                          note-"NF-kB
                                                                                                                                                              'note="NF-kB related site"
                                                                                                                                                                                                                                                                                                                             translation="MAGRSGDSDEELLKAVRLIKLLYQSNPLPSSKGTRQARRNRRRR"
                                                                                                                                                                                                                                                                                                                                                             'codon_start•1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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Pred. No. 2.65e-01
14; Mismatches 2
                                                                                                       related site"
                                                                                                                                                                                                                  region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAM-1 sequences cluster
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from Cambrige,
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KIEEEDKIKKKKKAQQAAAGTGKSQVSQNYFIYQRQQQWYHGLPT
EKAFSPEVIFWSALSEGATFPOLNTWLNTVGGQWYHGLGQWYHGLFT INEEARAWKKYPU
EKAFSPEVIFWSALSEGATFPOLNTWLNTVGGGDAHAMAMKETINEEARAWKHYPU
HAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKRWILLGLNKIVRM
YSPTSLIDIRGGFKEPFRDYVDRFYKTLRAEQASQEVKNWMTETLLVQNANPDCKTIL
KALGPAATLEBMMTAQQVGGFGHKARVLAEARAYAPAATAMAGRGHERQRKTVKC
ENCGKVGHIAKNCRAPRKKGCWKCGKEGHQMKDCNERQANFLGKIWPSHKGRPGNFLQ
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KEATTTLFCASDAKALDTEVHNVWATHACVPIDPNPQEVVLENVTENFNMWKNNVVEQ
MHEDDIISLWDQSLKPCVKLTPLCVTLICTNVNITRTNSSDWDRREGEKNKGEIKNCSF
NVTTSIRNKVRKEYALFYKLDVVPIDKANTSYTLIHCNTSVITQACPKVSFEPIPIHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="menrwqvm1vwqvDrmr1rTwKSLvKHHmy1SGKnKKwSYRHHY
ESTHPR1SSEVH1PLGEARLVVTTYWGLHTGERDWHLGQGVS1EWRTKGYNTQVDPDL
ADQLIHLYYFDCFSESA1RKA1VGRLVSPRCEYQAGHNKVGSLQYLALTAL1APKK1K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEWEFVNTPPLVKLWYQLEKEPIVGAETFYVDGAANRETRLGKAGYVTDRGRQKVVPL
TDTTNOKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAQPKSSELVSQIIEELIK
KEKVYLAWVPAHKGIGGNEGVVKLVSAGIRKYLFLDGIDKAQEBHEK YHSQNIRAWASGY
FNLPPVYAKEIVASCDKCQLKGEAMHGQVDCSPGIWQLDCTHLEGKVILVAVHVASGY
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IGGIGGFIKVRQYDQIPIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFPISPI
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PYNPQSQGVVESMNNELKKIIGQVRDQAEHLKTAVQMAVFIHNFKRKGGIGGYSAGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KWTYQPIMLPEKDSWTYNDIQKLYGKLNWASQIYAGIKVKQLCKLLRGIKALTEYVPL
TEBAELELAENREILKEPVHGVYYDPSKDLIAELQKQGQGQWTYQIYQEPFKNLKTGK
YAKMRGTHTNDVKQLTEAVQKIATESIVIWGKTPKFKLPIQKETWDAWWIDYWQATWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRPEPTAPPEESFRFGEEKTTPSQKQEPIDKELYPLASLRSLFGNDPSSQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETVPVKLKPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAI
CTPAGFAILKCNDKKFNGKGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEKEVVIRSE
                                                                                                                                                         /product="envelope polyprotein"
                                                                                                                                                                                                                                                                                                                             6063..6308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLPSVRKLTEDRWNKPQKTKGHRGSHTMNGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIDIIATDIQTKELQKQITKIQNFRVYYRDSRDPLWKGPAKLLWKGEGAVVIQDNSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYQYMDDLYVGSDLEIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="start codon missing. it starts right after TAA."
/product="pol_polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2087..5098
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                                                                                                                                                                                                                                            /product="vpu
                                                                                                                                                                                                                                                                                                                                                                                                              'number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product-"vpr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product="vif polyprotein"
                                                                                                                               codon_start=
                                                                                                                                                                                                                                      product="vpu protein"
                                                                                                                                                                                                                                                                                                   'pseudo
                                                                                                                                                                                                                                                                                                                                                                                    /product="rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product="tat protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           893 GNTTYAAYGARA 904
                                                                                                                                                                                                                                                                                                                                                                                                        Louwagie, J.J., McCutchan, F., Brennan, T., Peeters, M., Brennan, T., Sanders Buell, E., Eddy, G., van der Groen, G., Fransen, K., Gershy-Damet, M., Deleys, R. and Burke, D. Phylogenetic analysis of gag genes from seventy international HTV-1 isolates provides evidence for multiple genotypes AIDS 7, 769-780 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolate CI59 (cocultivation on PBMCs).
Human immunodeficiency virus type 1
Viridae; ss-RNA enveloped viruses; Positive strand
                                                                                                                                                                                                                                                                                                                 Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1, isolate CI59 from Abidjan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retroviridae; Lentivirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1 (HIV-1), Abidjan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ivory Coast, gag region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.48;
Similarity 41.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 1459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3405
                                                                                                                                                                                                                               s sequence contains a premature stop codon at position 913 CI59 gag sequence clusters with HIV-1 A subtype sequences Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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KRAVGAIGALFIGFLGAAGSTMGAVALTLTVOTROLLSGIVQCONNLLRAIEAQOHLI
OLTVWGIKQLQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSIKKSLDKIWL
NMTWMEWERELDNYTHLIELGQQLQEKNEKDLLELDTWASLMNNFDITNWLWYI
KIFIMIIGGLIGLRIVFTILSLVNRVRQGYSPLSFQTRPPVPRGDDRPEGIEEEGGGR
DRDTSGRLVTGFLALIWDDLRSLCLFSYHRLRDLLLIVARIVELLGRRGWEALKYWWN
ALNPGLLETADGCQQLMEQLQSALRTGSEELKSLFNAIAVLWCVHQRIDIKDTKEALD
KLEEVQNKSKQKTQQAAAATGSGSQNYPIVQNAQGQMTHQPMSPRTLNAWVKVIEEKA
FSPEVIPMFTALSEGATPQDLNMMLNIVGGHQAAMQMLKDTINEEAAEWDRVHPVQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFTNNAKTIIVQLKEPVEINCTRLNNNTRKSIAIGPGRTVYATDRIIGDIRQAHCNLS
STKWNNTLKQIVTKLKEQFGNKTIIFNQSSGGDPEIVMHSFNCGGEFFYCNTTQLENT
TWLFNGTWNDTEGLNNTERNITLPCRIKQIINRWQEVGKAMYAPPITGTISCSSNITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAITSSNTAATNADCAWLEAQEEEEVGFPVRPQVPLRPMTYKAALDISHFLKEKGGLE
GIIYSQRRQDILDLWIYHTQGYFPDWQNYTPGPGIRYPLTFGWCFKLVPVEPEQVEEA
                                                                                       translation="MGARASVLSGGKLDAWEKIRLRPGGKKKYRLKHLVWASRELERF"
                                                                                                                  /codon_start=
                                                                                                                                                 /product="gag protein"
                                                                                                                                                                      note-"premature termination at 913'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="3'LTR U3 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKRENASLLHPMSQHGMDDPEKEVLMWKFDSRLAFHHMAREKHPEFYKDC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8798..9430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'codon_start=
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Pred. No. 2.65e-01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 agagcaaacaaaagac 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 833 ARAARYTNGAYGTNACNAAYATHAARGARGCNYTNGARACNTTYGGNGGNGTNAARMGNM 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 aaaggatagacataaaagacaccaaagaagccttagataaattagaggaagtacaaaata 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Louwagie, J. J., McCutchan, F., Brennan, T., Peeters, M., Brennan, T., Sanders-Buell, E., Eddy, G., van der Groen, G., Fransen, K., Gershy-Damet, M., Deleys, R. and Burke, D. Phylogenetic analysis of gag genes from seventy international HIV-1 isolates: provides evidence for multiple genotypes AIDS 7, 769-780 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. The LBV23-10 gag sequence clusters with HIV-1 A subtype sequences. "Location/Qualifiers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gabonese national residing in Libreville, gag region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIVLBV2310 1459 bp ss-RNA VRL 20-APR-195 Human immunodeficiency virus type 1, isolate LBV23-10 taken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retroviridae; Lentivirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viridae; ss-RNA enveloped viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1 (HIV-1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 2.3%;
Similarity 42.1%;
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolate LBV23-1
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                                                                                                                                                                                                                                           ·/translation="MGARASVLSGGKLDSWEKIRLRPGGKKKYRLKHLVWASRELERF ALNEGLETAEGCQLMEQDQSALRTGSEELKSLENTIATHCVHQRIDYKDTKEALD KLEEIQNKSKQKTQQAAAATGSSSQNYF1VQNAQQQMTHQPMSPRTLNAWKVIEEKA FSPEVIPMESALSEGATPQDLNMMLNIVGGHQAAMQMLKDTINEEAAEWDRVHPVHAG PIPPGQMREPRGSDIAGTTSNLQEQIGWMTSNPPIPVGEIYKRWIVLGLNKIVRMYSP
                                                                                                                                                                                              VSILDIRQGPKEPFRDYVDRFFKVLRAEQATQEVKNWMTETLLVQNANPDCKSILRAL
GPAATLEEMMTACQGVGGPGHKARVLAEAMSQVQQTNIMMQRGNFRGQRTIKCFNCGK
                                                                                                                                                 TAPPAESFGMGEEITSSPKQEPRDKGLYPPLTSLKSX"
                                                                             ∵isolate="LBV23-1
                                                                                                                                                                       EGHLARNCKAPRKRGCWKCGKEGHQMKDCTERQANFLGKIWPSSKGRPGNFPQSRPEP
                                             /cell_type="lymphocyte"
                                                                                                 /organism="Human immunodeficiency virus type 1"
                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                         /product="gag protein"
/gene="gag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="blood" 276 c 377 g
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VSILDIRQGPKEPFRDYVDRFFKTLRAE"
/sequenced_mol="DNA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="gag protein"
/gene="gag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Human immunodeficiency virus type 1"
/isolate="CI59"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequenced_mol="DNA"
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Pred. No. 7.75e-01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Positive strand RNA virus,
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                                                                                                                                                                                        Query Match
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    893
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    GNTTYAAYGARACNAC 908
                                                                                                      agaggatagatgtaaaagacaccaaagaagctttagataaaatagagggaaataaaaaata 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaaggatagacgtaaaagacaccaaggaagccttagataaattagaggaaatacaaaata 328
                                      agaacaagcaaaagac 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNTTYAAYGARACNAC 908
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                                                                                 ARAARYTNGAYGTNACNAAYATHAARGARGCNYTNGARACNTTYGGNGGNGTNAARMGNM 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. The VI415 gag sequence clusters with HIV-1 A subtype sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Louwagie, J.J., McCutchan, F., Brennan, T., Peeters, M., Brennan, T., Sanders-Buell, E., Eddy, G., van der Groen, G., Fransen, K., Gershy-Damet, M., Deleys, R. and Burke, D. Phylogenetic analysis of gag genes from seventy international HTV-1 isolates provides evidence for multiple genotypes AIDS 7, 769-780 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1 (HIV-1), Rwandan isolate VI415.
Human immunodeficiency virus type 1
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIVVI415 1459 bp ss-RNA
Human immunodeficiency virus
Rwandan national residing in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gag
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Similarity 42.1%;
32; Conservative
                                                                                                                                                                  Similarity 32; Conser
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cds
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ilarity 42.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MGARASVLSGGKLDAWEKIRLRPGGRKKYRMKHLVWASRELDRFALDRFALDETAECCQCILEQLQALKTGTEEIKSLLGTVATLYCVHQRIDVKDTKEALDKIALRGTKUSKOLTQLAAGCQMIHQAISPRTLAWTWKTLEEKIEEKKKKYROKTQQAAAGTGNSSNVEJOKOLTQAAGCQMIHQAISPRTLAWTWKTLEEKAFSPEVIPMFSALSEGATPQDLMMLNIVGGHQAAMQMLKDTINEEAAEWDRLHPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RALGTGATLEEMYTACOGVGGPGHKARVLAEAMSQVQHTNIMMQRGNFKGQRRIKCFN
CGKEGHLARNCRAPRKKGCWKCGKEGHQMKDCTERQANFLGKIWSSSKGRPGNFPQSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAGPIPPGQMREPRGSDIAGTTSTTQEQIAWMTGNPPNPVGDIYKRWIILGLNKIVRM
YSPTSILDVKQGPKEPFRDYVDRFFKILRAEQATQEVKGWMTETLLVQNANPDCKTIL
                                                                                                                                                                                                                                                                   /tissue_type="blood"
278 c 366 g
                                                                                                                                                                                                                                                                                                                                                                            /organism="Human immunodeficiency /isolate="VI415"
                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTAPPAEIVGMGGEISPPKQEQREQAPPLVSLKSX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="gag protein"
/gene="gag"
                                                                                                                                                                                                                                                                                                                                                  cell_type="lymphocyte"
                                                                                                                                                                                                                                                                                                            'sequenced_mol="DNA"
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                                                                                                                                                              Score 126; DB 3;
Pred. No. 7.75e-01;
13; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 126; DB 3; Pred. No. 7.75e-01 13; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369
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Belgium,
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                                                                                                                                                                                                                                                                       273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gag region.
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                                                                                                                                                                                                       Length 1459;
                                                                                                                                                                                                                                                                                                                                                                                             virus type 1"
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                                                                                                                                                                  Indels
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STANDARD
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                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                        410 gaaggatgcaccccctatgatattaatcagatgttaaattgtgtagg 456
                                                                                                                                                            y Match 2.2%;
Local Similarity 46.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up to now, HIV-2 sequences have been derived almost solely from cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA) from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the Patient 60667K was a heterosexual 37-year old female from Sierra Leone, who was living in the Washington, D.C. area. Originally she lived in an urban area in West Africa before traveling extensively and coming to the United States. After seeking medical care for a STD, patient 60667K was identified as HIV-2 positive. She had children were seronegative. Western blot analysis of patient 60667K was blood cells showed HIV dual reactivity. Virus isolation was successfully performed at the University of Alabama at Birmingham. Sample 60667K clusters with the subtype B viruses.
RAANSWNGCNCCNCCDATYTTRTCDATNARRTCYTGDATNGTNARNG 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag sequence, sample 60667K, clone 1, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Virol. 68, 743;
full staff_review
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 2 Viridae; ss-RNA enveloped viruses; Positive strand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biology
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                                                                                                                                                                                                                                                         275 a 160 c 187 g 144 t bp downstream from the start of gag
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                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                            /note="NCB1 gi: 532134"
/rodon_start=2
/codon_start=2
/translation="NUBLERFGLAENLLGSKEGCHKILAVLEPLVPTGSENLKSLENT
/translation="NUBLERFGLAENLLGSKEGCHKILAVLEPLVPTGSENLKSLENT
VCVIYCLHAGEKVKDYEEAKKIAQRHLVGNTEKMPATGRPTAPSSGGNYPVQQIAGNY
SHLPLSPRTLNAWVKLVEEKKFGENVVPGFQALSEGCTPYDINQMLNCVGDHQAAIEI
IREIINEEAAEMDQQHPSPGFWPAGQLREPRGSDIAGTTSTVEEQIQMMCRAQNPVPV
                                                                                                                                                                                                                                                                                                                     GNIYRRWIQIGLQKCVRMYNPTNILDIKQGPKEPFQN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="gag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /partial
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                                                                                                                                                            Score 119; DB 3;
Pred. No. 3.19e+00;
                                                                                                                                                                                                                                                                                       187 g
                                                                                                                              Mismatches
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                                                                                                                                                                                                                                   PH153.
Human immunodeficiency virus type 1
Human immunodeficiency viruses; Positive strand RNA
Viridae; ss-RNA enveloped viruses;
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L11793
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Human immunodeficiency virus
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Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850.
                                                                                                                                                                                                                                                                                                                                                      gag region
L11781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2%;
Similarity 46.6%;
27; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1 (HIV-1), Zairean isolate VI557 Human immunodeficiency virus type 1 Human immunodeficiency virus type 1 Viridae; ss-RNA enveloped viruses; Positive strand RNA virus; Retroviridae; Lentivirinae.
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                                                                                                                                                                                                         (bases 1 to 1492)
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SRPEPTAPPAESFGFGEEMTPPPKQERKDAESPLTSLKSX"
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YSPVSILDIRQGPKEPFRDYVDRFFKALRAEQATQEVKGWMTDTLLVQNANPDCKTIL
RALGQGASIEEMMTACQGVGGPGHKAKVLAEAMSQVNTNAVMMMQKGNFKGQRRIIKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALNPDLLDTAEGCLQLIEQLQPALKTGTEELQSLFNLLATLYCVHQRIDVKDTKEALE
KLKEAQNKSQNRTQQATGDKGNGNKISQNYPIVQNAQGQPVHQAISPRTLNAWVKVVE
EKAFSPEVIPMFSALSEGATPQDLNAMLNIVGGHQAAMQMLKDTINEEAAEWDRVHPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="blood"
277 c 363 g
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/isolate="VI557"
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Pred. No. 1.76e+00;
13; Mismatches 17
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isolate VI557, gag
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isolate PH153,
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                                                                                                    Kindly provided prior to publication by Henry M. Jackson Foun and the Walter Reed Army Institute of Research, Rockville, MD The 132 sequence clusters with HIV-1 B subtype gag sequences. from to/span description 1 > 1492 gag (AA at 1) 559 a 286 c 362 g 285 t
                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1492)
MCCutchan, F.E., Hegerich, P.A., Brennan, T.P., Phanuphak, P.,
Singharaj, P., Jugsudee, A., Berman, P.W., Gray, A.M., Fowler, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
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Human immunodeficiency virus type 1, sample BK132 from Bangkok,
                                                                                                                                                                                                                                                                                                     Burke, D.S
                                                                                                                                                                                                                                                                                                                                                                                 Retroviridae; Lentivirinae.
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Similarity 41.7%;
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2.28;
llarity 41.78;
Conservative
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KIEEEQNKSNKKAQQAAADTGSCSQVSQNYE IVQNIGGMYHAAL SE PRILNAWYKVVE
EKAFSEPVIPMESALSEGATPQDLINTMLNTVGGHQAAMQMLKETINEEXAEURALHPY
HAGPIAFOQMREPRGSDLAGTTSTLQEQIGWMTNNPPIPVGEIYKRWIILGLNKIVRM
YSPTSILDIRGGPKEPFRDYUDRFYKTLRAEQASQDVKNWMTETLLVQUANPDCKTIL
KALGPAATLEEMMTACQGVGGPGHKARVTLRAEQASQDVKNWMTETLLVQUANPDCKTIL
KALGPAATLEEMMTACQGVGGPGHKARVTLRAEDASQATNASTMMLQRGNFRNTRKTVKC
ENGKEGHIARNCKAPRKKGCWKCGREGHQMKDCTERQANFLCKIWPSHKGRPGNFLQ
SRPEPTAPPEESFRFREETTTPPQKQEPIDKELYPSASLKLX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sequenced_mol="DNA"
/tissue_type="blood"
295 c 357 g
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/isolate="PH153"
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Pred. No. 2.15e+00;
13; Mismatches 29;
Score 121; DB 3; Le
Pred. No. 2.15e+00;
13; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                 HIV2D194 9472 bp ss-RNA
Human immunodeficiency virus type 2 (HTV-2),
a Gambian person; complete proviral genome.
J04542 X52223
                Biesert,L., Kreutz,R., Immelmann,A., Henco,K., Meichsner,C.,
Andreesen,R., Gelderblom,H. and Rubsamen-Waigmann,H.
Molecular cloning of two West African human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.28;
Similarity 40.38;
29; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human and chimp lymphocytes. This sequence clusters with HIV-1 subtype B sequences. SG3 is T-cell tropic as opposed to mono-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kindly provided in computer-readable form by Dr. Beatrice Hahn, CFAR, University of Alabama at Birmingham, Birmingham AL. This represents one of the most cytopathic variants that the authors of [1] have encountered. The BC virus is cytopathic in both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virology 194, 858-864 (1993) full staff_review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A molecular clone of HIV-1 tropic and cytopathic for human and chimpanzee lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ghosh, S.K., Fultz, P.N., Keddie, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone SG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SG3, complete genome.
L02317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                              Human immunodeficiency virus type 2, isolate D194, clone 10; derived from circular proviral DNA; biologically active clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hahn, B.H. and Shaw, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1 (HIV-1),
                                                                       Kuhnel, H., von Briesen, H., Dietrich, U., Adamski, M., Mix, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
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3291 a 1633 c 2225 g 2019 t
beginning of R region of the 5' LTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 9168)
                                                                                              (bases 1 to 9399)
2 isolates that replicate well in macrophages: a Gambian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="entire sequence was obtained
competent plasmid clone pSG3.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_line="immortalized T-cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="SG3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /isolate="BC"
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Pred. No. 2.15e+00;
14; Mismatches 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9168;
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isolate D194 from
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STANDARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation in gag and a premature stop in er
original copy of the sequence.
The D194 isolate was taken from a Gambian
patient: suffered from severe neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IULL STAIT_review
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                                                                                                                                                                                                                                                                                                                                                               GLAESILLESKEGCQKIIKVLEPLVPTGSENLKSLFNTVCVIWCLHAEEKVKDTEEAKK LAQRHLVAETGTAEKMENISRETAPPSGKGGNFVQQAGGNYIVLSPRTLNAWVKL VEEKKFGAEVYDGFQALSGGTTYDINQMLNCVGDHQAAMQIIREIINEEAADWDAA PIPGPLPAGQLRDPRGSDIAGTTSTVDEQIQMYRQPNPVPVGNIYRRWIQIGLQKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="METPLKEPESSLESYNEPSSCTSERDVTAQERAKQGEELLAQLH RPLEACTNSCYCGKSYHCQLCFLKKGGIWYARQGRRRRTPRKTKTHPPPASDKSIS TRTGDSQPTKKQKTPETVVSACGLCH" join(6069...6138,8275..8516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(5843..6138,8275..8371)
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DGPTGKAAPQLPRGPSSSGADTNSTPNRSSSGPVGEIYAAREKAERAEGETIQGGDGG
LTAPRAGRDAPQRGDRGLATPQFSLWKRPVVTAFIEDQPVEVLLDTGADDSIVAGIEL
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/gene="tat"
                                                                                                                                                           1716..4937
                                                                                                                                                                                                                                                                                     RMYNPTNILDVKQGPKESFQSYVDRFYKSLRAEQTDPAVKNWMTQTLLIQNANPDCKL
VLKGLGMNPTLEEMLTACQGVGGPSQKARLMAEALKEALTPAPIPFAAAQQRRAIRCW
NCGKEGHSAKQCRAPRRQGCWKCGKSGHIMANCPERQAGFLGMGPRGKQPRNFPAAQA
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                                                                                                                                                                                                                                  DLLHLNSLFGKDQ"
                                                                                                                                                                                                                                                             PQGLIPTAPPIDPAVDLLEKYMQQGRKQREQRERPYKEVTEDLLHLEQGETPHRGATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="primer (Lys-tRNA) binding site"
/evidence=EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <6069..6138
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/translatklhtipppptdspldraiqqlqgltiqelpdpptdlpesnsnqglae
                                                                                                       /evidence=EXPERIMENTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="aggtagagcctgggtgttccctgctagactctcaccagtgcttggccggca
stgggcagacg in [2] revises ag in [1]"
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/evidence=EXPERIMENTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MGARNSVLRGKKADELEKVRLRPNGKKRYRLKHVVWAANELDRF"
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                                                                                                                                                                                   in [1]"
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LNWVENKTNOTHGNYAPCHIROI INTWHKVGT NVYLPPREGELTCNSTVSI IANIDS
DGNOTNITESABVAELY RLEIGDYKLIEVTPIPFAPTKEKRYSSAPVRKKGYBYLGE
LGFLATAGSAMGGASLTLSAQSRTLLAGIVQQQQQLLDVVKRQQEMLRLTVWGTKNLQ
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PGFALLRCNDTNYSGFEPKCSKVVAASCTRMMETQTSTWEGFNGTRAENRTYIYWHGK
DNRTIISLNKYYNLTMHCKRPGNKTVVPITLMSGRRFHSRPVYNKKPGQAWCWFQGNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARVTAIEKYLKDQAQLNSWGCAFRQVCHTTVPWVNDSLTPDWNNMTWQEWEKRVHYLE
ANISQSLEQAQIQQEKNMYELQKLNSWDVFGNWFDLTSWIKYIQYGVYIVVGIIGLRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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RPQRKGAARKOWRRDHWRGLRVARQDYRSLKQGGSEPSAPRAHFPGVAKVLGILA"
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DMTPAERLINMITTEQEIQFLQRKNSNFKKFQVYYREGRDQLWKGPGELLWKGDGAVI
VKVGADIKVVPRRKAKIIRDYGGRQELDSSSHLEGAREDGEVA"
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LNLPVAKLDPIKVTLKPGKDGPRLKQWPLTKEKIEALKEICEKMEREGQLEEAPPTNP
YNTPTFAIKKKDKNKWRMLIDERELNRVTQDFTEIQLGIPHPAGLAKKKRITVLDVGD
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IALGNYIYNRHGDTLEGARELIRVLQRALFVHIRAGCDRSRKGQTRRRAPCPAAPTPR
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                                                                                                                                                                                                                                                                                                                                                                   J. Virol. (1992) In press simple staff_entry
                                                                                                                                                                                                                                                                                                                                                                                                                         Complete nucleotide sequence, genome organization, and biological properties of HIV-1 in vivo: Evidence for limited defectiveness a
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,Y., Hui,H., Burgess,C.J., Price,R.W., Sharp,P.M., Hahn,B.H. Shaw,G.M.
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MPRVPLREMTYKLAIDMSHFIKEKGGLEGIFYSRERHBILDLFLEKEEGIIPDMONTH
HGPGTRYPMYFGWLWKLVPVDISQEAEEVETNCLVHPAQTSRYDDEHGETLVWRFDPM
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LTR 9077 > 9706 3' LTR BASE COUNT 3427 a 1759 c 2362 g ORIGIN  Query Match Best Local Similarity 41.7%; Pred. No Matches 30; Conservative 13; Miss  Db 1056 aaaagatagaggtaaaagacaccaaggaagc:  :  :	LTR 9077 > 9706  BASE COUNT  3427 a 1759 c 2362 g 2158 t  ORIGIN  Query Match Query Match Sest Local Similarity 41.7%; pred. No. 2.15e+00; Matches 30; Conservative 13; Mismatches 29;  Db 1056 aaaagatagaggtaaaagacaccaaggaagctttagagaagatag  : : :  : : : :  :  :  :  Qy 833 ARAARYTNGAYGTNACNAAYATHAARGARGCNYTNGARACNTTY  Db 1116 aaagtaagaaaa 1127 :    :   :  Qy 893 GNTTYAAYGARA 904  Search completed: Sat Nov 27 09:30:35 1999  Job time: 12 secs.	LTR 9077 > 9706 3' LTR COUNT 3427 a 1759 c 2362 g 2158 t  IN 2.2%; Score 121; DB 3; Length 9706; st Local Similarity 41.7%; Pred. No. 2.15e+00; tches 30; Conservative 13; Mismatches 29; Indels 0 1056 aaaagatagaggtaaaagacaccaaggaagctttagagaagatagaggaagacca	> 9706 a 1759 c 2.2%; rity 41.7%; conservative aggtamaagacacc	Sear Job	Оу	дь	V	Db	Qu Be	BASE CORIGIN
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#### ALIGNMENTS

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EP-889123-A2.
07-JAN-1999.
26-JUN-1998; 305064.
03-JUL-1997; US-052720.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
BURDHAM MKR, Wallis NG;
WPI; 99-062655/06.
New isolated Murc polypeptide from Staphylococcus aureus and related nucleic acid - useful in diagnosis, treatment and prevention of bacterial infections

Claim 2; Pages 3-4; 39pp; English.

Claim 2; Pages 3-4; 39pp; English.

The present sequence represents a MurC gene encoding a Staphylococcus aureus UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide). Host cell containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC polypeptide are used to treat conditions requiring increased activity or
                                                                                                                                                                                                                                                                                                                                                                                                                  V99650; standard; DNA; 1351 BP.
V99650;
17-MAR-1999 (first entry)
17-MAR-1999 (first entry)
UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoding DNA.
MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide;
bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine;
lammunogen; drug; genetic immunisation; ds.
Staphylococcus aureus.
Location/Qualifiers
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/product= "UDP-N-acetylmuramate:L-alanine ligase
/product= (MurC polypeptide)"
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Matches
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anti-S.aureus vaccines claim 1; Page 1287-1288; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The
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07-JAN-1997; 100117.
05-JAN-1996; US-009861.
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Barash SC, Choi GH, Dillon
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                                                                  ATHGCNTGGGGNGAYGAYGARCAYYTNMGNAARATHGARGCNGAYGTNCCNATHTAYTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              757;
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57.7%;
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 G;
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PS Claim 2; Pages 4-5; 39pp; English.

CC The invention relates to a UDP-N-acetylmuramate:L-alanine ligase CC (MurC polypeptide) encoded by the S. aureus MurC gene. Host cells CC containing an expression system comprising the MurC gene can be used for CC crecombinant production of the polypeptide. Agonists or the MurC CC polypeptide are used to treat conditions requiring increased activity or CC expression of the polypeptide Antagonists, inhibitory nucleic acid or CC competitive polypeptide are useful for inhibiting the polypeptide e.g. CC bacterial (especially S. aureus) infections. They are also useful against CC The antibacterial agents are useful to treat in-dwelling devices for CC infection prevention or generally as wound treatments to prevent adhesion CC infection prevention or generally as wound treatments also useful for Alannosing or producing (susceptibility to) disease, for radising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide; bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine; immunogen; drug; genetic immunisation; ds.
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drug design and as an immunogen for vaccines. useful in antisense/ribozyme therapeutics; to
                                                                                                                                                                                                                                    nucleic acid -, useful
bacterial infections
                                                                                                                                                                                                                                                                                         Burnham MKR, Wallis NG; WPI; 99-062655/06.
                                                                                                                                                                                                                                                                                                                                             26-JUN-1998;
03-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                           EP-889123-A2.
07-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Partial nucleotide sequence of the MurC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V80065 standard;
V80065;
                                                                                                                                                                                                                                                              New isolated MurC
                                                                                                                                                                                                                                                                              P-PSDB; W89199.
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SMITHKLINE BEECHAM
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US-052720.
                                                                                                                                                                                                                                                 MurC polypeptide from Staphylococcus aureus and -. useful in diagnosis, treatment and prevention
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 The MurC gene sequences are detect mutant MurC gene;
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Best Local
                                                                                                                                                                                                          DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; cardiac infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
(SMIK ) SMITHKLINE BEECHAM CORE (SMIK ) SMITHKLINE BEECHAM PLC. Black MT, Burnham MKR, Hodgson
                                                               13-MAY-1998.
24-SEP-1997; 307485.
24-SEP-1996; US-027032
                                                                                                                                                                                                                                                                                                                                                   V53479 standard; DNA; 619
V53479;
30-OCT-1998 (first entry)
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                                                                                                                                           EP-841394-A2.
                                                                                                                                                                 Staphylococcus aureus.
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larity 60.5%; Pred
Conservative 159;
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natches 96;
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V52194 s V52194;

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11864

23-OCT-1998 Streptococcus

pneumoniae

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This sequence encodes a Staphylococcus aureus protein of unknown function, and represents a DNA Sequence of the invention. The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection. Sequence 619 BP; 208 A; 117 C; 79 G; 215 T;
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ttctgcaaattcatttaaaaatgcttgtgttctagagaaagtgtgttgttgaaatactg
                                                            KNCKYTTNACNCCNCCRAANGTYTCNARNGCYTCYTTDATRTTNGTNACRTCNARYTTYT
                                                                                                                                      KNGGRTGRTGNGCRTARTCRTCNACDATNACYTGRTTNGCDATNGTNGTYTCRTTRAANC
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L Similarity 60.1%;
356; Conservative
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Pred. No. 2.01e-186;
143; Mismatches 92;
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CC by a process comprising: (a) screening a genomic DNA library using as a CC probe a target sequence defined by any of the sequences in SEQ ID NO:1 CC to 391, identifying members of the library which contain sequences CC that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced CC from an organism, amplifying nucleic acid molecules whose nucleotide CC sequence is homologous to amplification primers derived from the CC fragment of the S. pneumoniae genome to prime the amplification and CC isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present compositions and vaccines for S. pneumoniae.

So Sequence 11864 BP; 3440 A; 2668 C; 2183 G; 3573 T;
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Matches 550; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1219
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Claim 1; Page 524-530;
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Kunsch CA, Rosen CA;
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(HUMA-) HUMAN GENOME SCI INC.
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31-OCT-1996; US-029960
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                                                                                                                                             tcactgtatcattgacaattttctcagtgaaacgacgtttaacaccggcaaatgttttca
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                                                                                                                                                                                                                                                                                                                                        GNGTNCKNSWRAANGTRTGNGGYTGRAANACNGCNACNACYTCYTTRTGNGGRTAYTTYT
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Enterococcus faecalis genome contig SEQ ID NO:780. Enterococcus faecalis; contig; detection; Enterococuscus faecalis; computer readable medium; ds Enterococcus faecalis.

infection;

04-MAY-1998; 14-NOV-1997; 06-MAY-1997;

U08985. US-066009. US-044031.

WO9850555-A2. 12-NOV-1998.

ILT 6 X13717 standard; X13717; 19-MAR-1999 (fir

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Claim 1; Page 1983; 2084pp; English.

Claim 1; Page 1983; 2084pp; English.

A computer readable medium has been developed which has recorded on it

Search and the sequences isolated from the Enterococcus faecalis genome.

Callos to X13919 represent these nucleotide sequences which are primary concleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence cof Enterococcus faecalis in samples. They can also be used for commercial importance infection in an animal and monitoring comparession of disease, and for identifying agents which can be used to mobilate the growth or pathogenicity of Enterococcus faecalis, or can other related organism, in vivo or in vitro. In particular the collypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
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Matches
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                 catttacacgaacattgccttaatggatgaatttgctgaagcactggatttggcagatg
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                                                               THGAYACNGCNMGNAARAARTAYCCNCAYAARGARGTNGTNGCNGTNTTYCARCCNCAYA
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HUMAN GENOME SO
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ilarity 49.0%;
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Pred. No. 2.62e-131;
144; Mismatches 199;
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So Sequence 1267 BP;. 365 A; 269 C; 261 G; 372 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis claim 1; Page 72; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi GH, Hromockyj A, Johnson WPI; 98-272224/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae SP0070 nucleotide. Streptococcus pneumoniae; antigen; vaccine; infection;
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31-OCT-1996; US-029
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07-MAY-1998.
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NCAYGTNATGAAYGGNGAYAARAARACNWSNTTYYTNATHGGNGAYGGNACNGGNATGGG
                                                             RTAYACNWSNGTNGCNGTNACNGGNGCNCAYGGNAARACNWSNACNACNGGNYTNYTNWS
                                                                            ctttgttagcatgggagtagcaggagcacatggaaaaaacttcaacgacaggtatgttgtc
                                                                                                                       NCAYCARYTNAARYTNGAYGTNGTNWSNTAYAAYGAYTTYYTNGGNCARATHATHGAYCA
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llarity 42.4%;
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Pred. No. 1.28e-126;
220; Mismatches 476;
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vaccine; attenuation; c
Enterococcus faecalis.
WO9850555-A2.
12-NOV-1998.
04-MAY-1998; U08985.
                                            x13228;
19-MAR-1999 (first entry)
Enterococcus faecalis genome contig SEQ ID NO:291.
Enterococcus faecalis; contig; detection; Enteroco
                                                                                     X13228
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titlgtctatggtgaagatgctgaattgcgtaagatttacgtctgatgcaccaatttatta
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                                                                                    standard;
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Claim 1; Page 1327-1330; 2084pp; English.

A computer readable medium has been developed which has recorded on it

Ba nucleotide sequences isolated from the Enterococcus faecalis genome.

CX 12938 to X13919 represent these nucleotide sequences which are primary

CX nucleotide sequences, also known as contigs. The computer based system

CX can identify fragments of the Enterococcus faecalis genome with

CX commercial importance. The products can be used to detect the presence

CX of Enterococcus faecalis in samples. They can also be used for

CX diagnosing Enterococcal infection in an animal and monitoring

CX progression of disease, and for identifying agents which can be used to

CX modulate the growth or pathogenicity of Enterococcus faecalis, or

CX canother related organism, in vivo or in vitro. In particular the

CX polypeptides encoded by the Enterococcus faecalis nucleotide sequences

CX can be used in vaccines to prevent or attenuate an Enterococcal
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Best Local :
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Barash SC, Dillon PJ, Kunsch
WPI; 99-045171/04.
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06-MAY-1997; US-044031
16-MAY-1997; US-046655
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                                                                                                        GAYTAYGCNATHATGACNAAYATHGAYTTYGAYCAYCCNGAYTAYTTYAARGAYATHAAY
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llarity 48.8%;
Conservative
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Best Local S
Matches 43
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04-UU-1998; U21976.
24-NOV-1997; U21976.
27-NOV-1996; US-031879.
(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
Black MT, Hodgson JE, Knowles DJC, LA
Reid RH, Zarfos PN;
WPI; 98-32265428.
P-PSDB; W62754, W63755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g pneumonia, bacteremia, meningitis or endocarditis Claim 1; Page 151-152; 181pp; English.

The sequence is that of a Streptococcal polypeptide coding region. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially Sp infection. It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleumempyema, endocarditis or infection of the cerebrospinal fluid. Sequence 1825 Bp; 550 A; 385 C; 366 G; 524 T;
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V43027 standard; DNA;
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l Similarity 42.4%;
434; Conservative
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ading frame; infection; be
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Pred. No. 3.30e-104;
185; Mismatches 395;
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19-DEC-1996.
06-JUN-1996. U0912:
07-JUN-1995. US-48:
01-APR-1996. US-63
(ASTR ) ASTRA AB.
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28-JUL-1997 (first entry)
H. pylori cytoplasmic protein ORF 11253.aa.
Cytoplasmic; vaccine; prevention; treatment;
identification; binding compound; bacterium;
bacteria; inhibitor; duodenal ulcer disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T67723;
     Berglindh OT, Smith D, WPI; 97-052306/05.
                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis;
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US-630405.
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(pos: 397..399, a
(pos: 496..498, a
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life cycle; activato
chronic gastritis;
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Note: This DNA sequence is not reproduced in the specification and the related specification, w09719098.
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Best Local
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29-MAY-1997.
15-NOV-1996; U18542.
17-NOV-1995; US-561469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisense; inhibition; ds.
used for diagnostics and therapeutics Claim 1; Page 77; 235pp; English.
This sequence encodes an H. pylori cytoplasmic protein involved in outer membrane or cell wall biosynthesis. This sequence showed homology to N-acetylmuramate-Alanine ligase. Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention
                                                                                                                                                                                                      P-PSDB; W24585.
Helicobacter pylori nucleic acid sequences
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T77403;
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(pos:397..399, aa:
(pos:496..498, aa:
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                                                                                                                                                                                                                   and related proteins
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Best Local S
Matches
                                                                                                                                                                                                                                                                                            06-JUN-1996;
07-JUN-1995;
01-APR-1996;
              Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter claim 9; Page 752; 1481pp; English.

The present sequence encodes a Helicobacter pylori cytoplasmic protein involved outer membrane or cell wall biosynthesis. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pMPX vectors to construct a series of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are used to evaluate compounds, especially activators or in bacterial life cycle, for the ability to bind an H. pylori sequence. The nucleic acid sequences, and corresponding pralso useful for generating vaccines for immunising subjects
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytoplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori cytoplasmic protein ORF 01ep30520orf27
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   nucleotides, and
                                                                                                                                                                                                                          P-PSDB; W20606
                                                                                                                                                                                                                                                            Berglindh
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                                                                                                                                                                                                                                                                                                                                                                    WO9640893-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The ORF/protein reference the related specification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             861.BP;
                                                                                                                                                                                                                                                                                              US-487032.
US-630405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     outer membrane;
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/note= "no stop codon given"
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1..1365
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 predicted coding
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Pred. No. 1.44e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sease; chronic gastritis; diagnosis;
cell wall; biosynthesis; ds.
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 regions defined
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at least 18
by computer
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The present invention describes a computer readable medium which has CC the nucleotide sequences SEQ ID NO:1 to 391 (Y52134 to Y52524) recorded CC on it, or a representative fragment or a sequence at least 95% identical CC to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391 (Y52134 to Y52524) are genomic fragments from Streptococcus CC pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae CC genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a CC probe a target sequence defined by any of the sequences in SEQ ID NO: 1 to 391, identifying members of the library which contain sequences CC that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced CC molecules from the members; or (b) isolating primers derived from the sequences is homologous to amplification primers derived from the computer based system for identifying fragments of the S. pneumoniae genome to prime the amplification and CC isolating the amplified sequences. The computer readable medium can be CS. pneumoniae genome of commercial importance, or expression modulating CC sequents of the S. pneumoniae genome. Products from the present
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                     Query Match
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30-CCT-1997; U19588.
31-CCT-1996; US-029960
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Barash SC, Choi GH, I
Kunsch CA, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various were analysed for significant homology to other known or expo
                                                               compositions and vaccines 
Sequence 843 BP; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae
Claim 1; Page 1370-1371; 1409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae. WO9818931-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae; computer readable medium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae genome fragment SEQ ID NO:356. Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 evaluation. development,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical compositions and vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V52489 standard; DNA; 843
                                                                                               fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998 (first entry)
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60; Conser
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larity 36.4%;
Conservative
  3.4%;
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Dillon PJ, Dougherty BA,
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Score 183; DB 47;
Pred. No. 6.50e-02;
                                                                                  ß
                                                            pneumoniae.
202 C; 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for Streptococcus
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                                                               <u>ი</u>
                   Length 843
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on; ds.
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodies a protein from Streptococcus pneumoniae.

The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for Inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or camplification methods), also for isolating Streptococcus genes or their callelic variants: The protein can be used similarly to detect specific menitodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive climmunisation (optionally coupled to a toxin). Vaccines are administered, c.g. by injection, orally or through the skin, typically at 0.01-1000 cc (especially 10-300) mu g/ml per dose.

Sequence 1003 BP; 282 A; 211 C; 243 G; 267 T;
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Best Local S
Matches 4
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                                                                T89154 :
   Streptococcus
                                   06-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis Claim 1; Page 71-72; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
Choi GH, Hromockyj A, Johnson LS, Kunsch CA;
WPI; 98-272224/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9818930-A2.
07-MAY-1998.
30-OCT-1997; U19422.
31-OCT-1996; US-029960.
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                                                                                                                                                                                                                                                                      544 tcaaaccatcaaggaaactctttcagccttcggtggtgtcaaacaccgtctc
                                                                                                                                                                                                                                                                                                                                                                          484 ccacaatgtggaaaatgcccttgcgactattgctgtagccaagcttcgtgatgtggacaa 543
                                                                                                                                                                                                                846 NACNAAYATHAARGARGCNYTNGARACNTTYGGNGGNGTNAARMGNMGNTTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                          YCAYACNGTNYTNAAYGCNYTNGCNGTNATHGCNATHWSNTAYYTNGARAARYTNGAYGT
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                                                                                            standard;
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/note= "this codon has an apparent 2 nucleotide deletion
which alters the reading frame; no stop codon
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MurD gene
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Pred. No. 6
20; Mismat
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No. 6.50e-02;
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Best Local Similarity 40.2%;
Matches 45; Conservative
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28-OCT 1997.
18-JUN-1996; US-665435.
18-JUN-1996; US-665435.
(ELIL ) LILLY & CO ELI.
HOSKINS JA, PEETY RB, S
WPI: 97-535046/49.
                                                                                                                                                                                              drug screening
Example 1; Columns 1-4; 13pp; English.
The present sequence represents DNA encoding Streptococcus pneumoniae
MurD protein (uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate
ligase). The murD protein is useful in a method for identifying compounds
that inhibit Streptococcus pneumoniae murD activity. Compounds
identified are potentially useful as antibacterial agents.
Sequence 1350 BP; 384 A; 272 C; 328 G; 366 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae.
Key Location/
CDS 1..1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MurD gene; antibacterial agent; drug screening;
uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligase;
                               786
                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae MurD protein - useful for antibacterial
                                                                                                                                                                                                                                                                                                                             P-PSDB; W29454.
                                                                                                     YCAYACNGTNYTNAAYGCNYTNGCNGTNATHGCNATHWSNTAYYTNGARAARYTNGAYGT 845
                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= MurD protein
/note= "no stop codon included"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       Skatrud PL,
                                                                                                                                          Score 183; DB 36; 1
Pred. No. 6.50e-02;
20; Mismatches 47;
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Search completed: Sat Nov 27 09:38:03 1999 Job time: 312 secs.

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P. Tobb	<u></u>
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MPsrch\_tpn n.a. - n.a. Smith-Waterman search, using a protein query which has been backtranslated into n.a. using IUPAC symbols

Tabular output not generated. Run on: Sat Nov 27 09:30:52 1999; MasPar time 96.53 Seconds 1174.641 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-09-103-287-2 (1-437) from US09103287.pep 5451

1 ATGACNCAYTAYCAYTTYGT......TNGGNATGAARAAYGCNTTY 1311
TACTGNGTRATRGTRAARCA.....ANCCNTACTTYTTRCGNAAR

Scoring table: TABLE bktranslate2 Gap 30

Nmatch

STD:

Dbase 0; Query 0

Searched: 165359 seqs, 43243793 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-issued 1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1

Statistics: Mean 51.193; Variance 211.724; scale 0.242

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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	÷			1.95e+01		2.28e+01	•	•	•	•	•		2.28e+01	2	N	N	N						1.42e+01		0.000

## ALIGNMENTS

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INFORMATION: )836-9300 83-4109 ID NO: 14:	NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMMU	YAGENT	TION NU	APPLICATION NUMBER: US/07/935,313	TION: 435	5	CATION DATA:	PatentIn	OPERATING SYSTEM: PC-DOS/MS-DOS	COMPUTERS: TRM DC COMPS+;}}	BLE FORM:	31	ĸ	CIT: ALEXANDILA STATE: VA	T: 180	ardner	33	R OF SEQUENCES: 52	TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS	SCHEIFLINGER	DORNER, F.	AL INFORM	atent No. 5670367	Sequence 14, Application US/08232463	equence 14. Application US/08232	XXXXXXX	1

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Best Local
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US-08-665-435a-3 STANDARD; DNA; UNC; 1350
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                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08665435A Sequence 3, Application US/08665435A
                                                                                                                                                                                                                                                                                                                           XXXXXX
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                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213
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                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                           APPLICANT: Hoskins, Joann
APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: Biosynthetic Gene MurD of
TITLE OF INVENTION: pneumoniae
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                             APPLICANT:
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LENGTH: 7218 base pair
                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                           STREET: Lilly C
CITY: Indianapo
STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTTRTANSWNACNACRTCNARYTTNARYTGRTGNGCNCKNACDATYTCYTCRTGNSWNSW 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAANSWNGTYTTYTTRTCNCCRTTCATNACRTGNSWNARNARNCCNGTNGTNSWNGTYTT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGCRAANGCRTTNCCYTGDATNACNACCATRTCYTCYTTDATRTTRTTNGCNCCRAANGG 154
FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCCRTGNGCNCCNGTNACNGCNACNSWNGTRTAYTGRTCDATDATYTGNCCNARRAARTC 274
                      APPLICATION NUMBER:
                                                                                                               COUNTRY:
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                                                                                                                                      Indianapolis
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Lilly Corporate Center
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                                                                                                                                                                                                                                             Peery, Robert
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Matches
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ANTI-SENSE: NO
SEQUENCE 1350 BP; 384 A; 272 C; 328 G; 0 T; 366 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXX
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                                  TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         891 UCAAACCAUCAAGGAAACUCUUUCAGCCUUCGGUGGUGUCAAACACCGUCUC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   831 CCACAAUGUGGAAAAUGCCCUUGCGACUAUUGCUGUAGCCAAGCUUCGUGAUGUGGACAA 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             846 NACNAAYATHAARGARGCNYINGARACNTTYGGNGGNGINAARMGNMGNTTY 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          786 YCAYACNGTNYTNAAYGCNYTNGCNGTNATHGCNATHWSNTAYYTNGARAARYTNGAYGT 845
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                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                     SEQUENCE CHARACTERISTICS
                                                          REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D
                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS: ADDRESSEE: Eli Lilly
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Biosynthetic Gene TITLE OF INVENTION: pneumoniae NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Skatrud, Paul
APPLICANT: Peery, Robert
APPLICANT: Hoskins, JoAn
APPLICANT: Wu, Chyun-Yeh
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                                                                                                                                              FILING DATE:
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                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                           COUNTRY:
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           LENGTH:
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Similarity 29.5%;
33; Conservati
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nucleic acid
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Lilly Corporate Center
           1350 base pairs
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Pred. No. 1.41e-03;
32; Mismatches 47
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Query Match
Best Local Similarity
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                                   SEQUENCE
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LOCATION: 1..1350
SEQUENCE 1350 BP; 384 A; 272 C; 328 G;
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                                                                                                              TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1350 base pair
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Local Similarity 40.2%;
nes 45; Conservative
                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 46285
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floppy disk
                                 ANTI-SENSE: NO DENCE 1350 BP;
                                           MOLECULE N
HYPOTHETICAL: N
                                                                                                                                                          REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: Biosynthetic Gene Mur D of Streptococcus
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Webster, Thomas D
                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                               NAME: Webster, Thomas REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                               TOPOLOGY:
                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                  nucleic acid
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                                                                                                             1350 base pairs
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Lilly Corporate Center
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                                  384 A; 272 C;
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3.4%;
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US/08843309
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 Score 183;
Pred. No. :
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Pred. No. 1.41e-03
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                                 328 G;
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1.41e-03;
                                  0 T; 366 OTHER
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           Length 1350;
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Best Local
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LOCATION: 1..1353
SEQUENCE 1353 BP; 386 A; 272 C; 328 G; 367 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08843309 Sequence 1, Application US/08843309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5834270 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXXXX
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                                                              831 CCACAATGTGGAAAATGCCCTTTGCGACTATTGCTGTAGCCAAGCTTCGTGATGTGGACAA 890
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846 NACNAAYATHAARGARGCNYTNGARACNTTYGGNGGNGTNAARMGNMGNTTY 897
                       891 TCAAACCATCAAGGAAACTCTTTCAGCCTTCGGTGGTGTCAAACACCGTCTC 942
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NAME: Webster, Thomas D
REGISTRATION NUMBER: 39,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Hoskins, JoAnn
APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: Biosynthetic Gene Mur D of Streptococcus
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL:
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CLASSIFICATION:
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                                              YCAYACNGTNYTNAAYGCNYTNGCNGTNATHGCNATHWSNTAYYTNGARAARYTNGAYGT 845
                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                LENGTH:
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Similarity 40.2%;
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Lilly Corporate Center
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                                                                                                       Score 183; DB 3;
Pred. No. 1.41e-03;
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Best Local
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Patent No. 5521093
APPLICANT: LEMOINE, Y
TITLE OF INVENTION: Y
GENE FUSIONS LINKED VIA K
TRUNCATED KEX2 GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:4:
                                                                                                                                                                                                                                                                                   Sequence 3, Sequence 3, Patent No. 5
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Sequence 5127 BP;
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  ZIP: 20005-3918
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
                                                                                                                                                                       APPLICANT: KEELING, PETER I.
APPLICANT: KNIGHT, MARY E.
APPLICANT: GUAN, HANDING
TITLE OF INVENTION: MODIFICATION OF STARCH
TITLE OF INVENTION: SYNTHESIS IN PLANTS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
CURRENT APPLICATION DATA:
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                                                                                                         STREET: Lluu New CITY: Washington
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                                                                                     COUNTRY:
                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 26,121
FILING DATE: 04-MAR-1993
APPLICATION NUMBER: 500,885
                                                                                                                                        ADDRESSEE: Pillsbury Madison &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 191,354 FILING DATE: 07-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23-FEB-1995
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Similarity 39.2%;
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Application US/08572951
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                                                                                                                            1100 New York Avenue, N.W.
                                                                                       USA
                                                                                                                                                   Intellectual Property Group of
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Pred. No. 1.18e-01;
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                                                                                                                                        Sutro LLP
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                   US-08-676-974-2 STANDARD; DNA; UNC; 2277
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                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: COLLINS.
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       512 ATRITNGTCATDAINGCRIARTCNGGYTTRIANSWNARRAARIGNCKNCK 463
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Local Similarity 14.5%;
hes 16; Conserva+:..-
REFERENCE/DOCKET NUMBER: UC:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                         COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                            CITY: San Francisco
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                                                                                      APPLICATION NUMBER: FILING DATE:
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                                                                         CLASSIFICATION: 530
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DEDNESS: both
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                                                                                                                                                                                                                                    E: Science & Technology Law Group 268 Bush Street, Suite 3200
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Pred. No. 7.64e-01;
43: Mismatches 50;
                           UCB96-055
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SEQUENCE 2277 BP; 511 A; 212 C; 395 G; 216 T; 943 OTHER.
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                                                                                        TELEFAX: (415)343-434
INFORMATION FOR SEQ ID NO:
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Local Similarity 14.4%;
                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,967
                                                                                                                REFERENCE/DOCKET NUMBER: UC TELECOMMUNICATION INFORMATION: TELEPHONE: (415)343-4341
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LENGTH: 2277 base pairs
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NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
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MEDIUM TYPE: Floppy
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MOLECULE TYPE: cDNA
UENCE 2277 BP; 511 A; 212 C;
                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
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STATE: CA
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                           TOPOLOGY:
                                    STRANDEDNESS:
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268 Bush Street, Suite 3200
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                                                                                                    (415)343-4342
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US/08676967
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Pred. No. 1.48e+00;
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  395 G;
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  216 T; 943
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Query Match 2.6%;
Best Local Similarity 37.9%;
Matches 33; Conservative
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Best Local (
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                                                    TOPOLOGY: linear SEQUENCE 2588 BP; 550 A; 743 C; 800 G; 495 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XXXXXX
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                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Local Similarity 14.4%;
les 27; Conservation
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                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ROSA, MARGARET D.
APPLICANT: STOSSEL, THOMAS P.
TITLE OF INVENTION: MULTIMERIC GELSOLIN FUSION CONSTRUCTS
                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: B1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                     TELEFAX: (***)
TELEFAX: 14-8367
TEX: 14-8367
                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 04-MAY-1990
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                       TOPOLOGY: 1i
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PC/TUS9102954
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Score 142; DB 4;
Pred. No. 1.75e+00;
18; Mismatches 36
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Pred. No. 1.48e+00;
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                         Length 2588;
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US-08-137-252-3 STANDARD; DNA; UNC; 401 BP
                                               1018 ANACNGCNACNACYTCYTTRTGNGGRT
                                                                         2120 CACCTGGGACCAGGTCTTTGTCTGGGT 2146
                                                                                                                           2060 AGAGGTTCCTGGTGAGCTCATGCAGGAAGACCTGGCAACGGATGACGTCATGCTTCTGGA 2119
                                                                                                                                                                                                       SEQUENCE 2608 BP; 557 A; 750 C; 804 G; 497 T; 0 OTHER
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US-07-725-083-1 STANDARD; DNA; UNC; 2608 BP
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                                                                                                                                                   Match 2.6%;
Local Similarity 37.9%;
es 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03-JUL-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/353,432
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Breakefield, Xandra O.
APPLICANT: Ozelius, Laurie J.
TITLE OF INVENTION: Genetic Diagnosis of Torsion Dystonia
                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                    ANARNSWYTCNGCRAAYTCRTTNARRAANGCYTGNGTNCKNSWRAANGTRTGNGGYTGRA 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANARNSWYTCNGCRAAYTCRTTNARRAANGCYTGNGTNCKNSWRAANGTRTGNGGYTGRA 1019
                                                                                                                                                                                                                                                                                                                                                                          NAME: Goldstein, Jorge A. REGISTRATION NUMBER: 29,021 REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANACNGCNACNACYTCYTTRTGNGGRT 992
                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 15..2363
                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                                                                                                CENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Sterne, Kessler, Goldstein &
1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                             2608 base pairs
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                                                                                                                                                                                                                                                           both
                                                                                                                                                                                                                                                                                                                                     (202) 371-2600
202) 371-2540
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US/07725083
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                                                                                                                                                      18;
                                                                                                                                                                 Score 142; DB 1;
Pred. No. 1.75e+00;
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Best Local :
                                                                     Matches
                                                                                                           OTHER INFORMATION: /standard_name= "5' SEQUENCE 401 BP; 100 A; 93 C; 89 G; 119 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08137252
Sequence 3, Application US/08137252
Patent No. 5480774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XXXXXX
                                             232 GTTATTACTATTATTGTTTATTGATCAAGACTGGTCTCGAGAAAGTCCTGGTGACTTAGA 291
292 ACATGCACATTAAAATGTGTCACTATAACCTATTCTTCTTGTC 334
                       320 GTNACNGCNACNSWNGTRTAYTGRTCDATDATYTGNCCNARRAARTCRTTRTANSWNACN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 543-504 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hew, Choy
APPLICANT: Du, Shoa J
TITLE OF INVENTION: E
TITLE OF INVENTION: S
NUMBER OF SEQUENCES:
                                                                               Match 2.5%;
Local Similarity 40.8%;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 401 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
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CITY: San Francisco
                                                                                                                                                                         LOCATION: 125..339
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/137,252
FILING DATE: 14-OCT-1993
CLASSIFICATION: 436
                                                                                                                                        NAME/KEY: misc_feature LOCATION: 340..401
                                                                                                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TORNEY/AGENT TORNEY/AGENT Kenneth A.
NAME: Weber, Kenneth A.
31,677
                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: 125..339
                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                NAME/KEY: .. misc_feature
                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                    Conservative
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                                                                                                                                                                                                                                      misc_feature
1..124
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415) 543-5043
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                                                                                                                                                                                                                                                                     /Standard_name= "Partial DNA
Sequence of Chinook Salmon GH-II Gene"
/note= "Sequence spans from the 3' end
intron 5 and 5' end of exon 6."
                                                                                                                                                                            /standard_name=
                                                                                                                                                                                                                         /standard_name=
                                                                   Score 139; DB 1;
Pred. No. 2.86e+00;
17; Mismatches 44
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Best Local S
Matches 1
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                                      1636 TCNAARTCNAARGCNAARYT 1655
                                                                              1576 ACNGGNAARATHGAYACNMGNAARATHAARGARATHYTNATHAARGCNCARAARGGNAAR 1635
                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-231-729B-2 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 119050/1993
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rose, Herbert C.
REGISTRATION NUMBER: 20846
REFERENCE/DOCKET NUMBER: 60130/No. 5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-6770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: ZENNO, Shuhei
                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity nes 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ZENNO, Shunei
APPLICANT: SHIRAISHI, Shinji
APPLICANT: INOUYE, Satoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                       NAME/KEY: CDS
NAME/KEY: CDS
LOCATION: 1..1659
OTHER INFORMATION: f
OTHER INFORMATION: n
OTHER INFORMATION: n
OTHER INFORMATION: n
                                                                                                                                                                                                                         MOLECULE TYPE:
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                     TNTAYGTNGAYGGNGARTTY 753
                                                           AYWSNGAYGAYATHTAYGCNCARAAYATHCARATHACNGAYAARGGNACNGCNTTYGAYG 733
                                                                                                                                                                                                                                                                                   TELEPHONE: Zuz ... 7576776
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CLASSIFICATION:
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                  nucleic acid
                                                                                                  2.5%;
llarity 21.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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SAIGO, Kaoru
                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                            single
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                                                                                                                                       for codons 28, 32, 112, 130, 142, 190, 212, 212, 265, 329, 336, 386, 436, 512, and 532, if the nucleotide is Tor C, then the 5' nucleotide is C; and i nucleotide is A, then the 3' nucleotide is A or G 193 C; 268 G; 265 T; 612 OTHER.
                                                                                                  Score 137; DB 1; Le
Pred. No. 3.97e+00;
30; Mismatches 33;
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                                                                                                                   Length 1659;
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Sequence 10,
                    XXXXX
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                                                                   734 THTAYGTHGAYGGHGARTTY
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                                                                                                                                                   Local Similarity 21.3%; nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 1
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: INOUYE, Satos
APPLICANT: SAIGO, KAOTU
TITLE OF INVENTION: FIRE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ZENNO, Shuhei APPLICANT: SHIRAISHI, Sh
                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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Application PC/TUS930726:
                                                                                                                                                                                                                                                                                                     1659 base pairs
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                                                                                                                                                                                                                                  1..1659
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                                                                                                                                                                                                                                                                                 single
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OTHER INFORMATION: "Xaa" at codon 409 is either Glu or Asp: OTHER INFORMATION: "Xaa" at codons 28, 32, 112, 130, 142, 190, OTHER INFORMATION: 329, 336, 386, 512, and 532 is either a SEQUENCE 1659 Bp; 321 A; 193 C; 268 G; 265 T; 612 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08231729B Sequence 1, Application US/08231729B Patent No. 5618722
                                                                                                                                                                                                                               1576 ACNGGNAARATHGAYACNMGNAARATHAARGARATHYTNATHAARGCNCARAARGGNAAR 1635
PCT-US93-07261-10 STANDARD; DNA; UNC; 4766
                                                                                                                                                                                  674 AYWSNGAYGAYATHTAYGCNCARAAYATHCARATHACNGAYAARGGNACNGCNTTYGAYG 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-737-6776
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: ROSE, Herbert C.
REGISTRATION NUMBER: 29846
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-6770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: LEYDIG, VOIT & MAYER 700 Thirteenth Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
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30; 1
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Pred. No. 3.97e+00;
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                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                                                                                                   Length 1659;
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Search completed: Sat Nov 27 09:32:33 1999 Job time: 101 secs.
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Best Local Similarity 37.0%;
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 3..4766
SEQUENCE 4766 BP; 2403 A; 508 C; 863 G; 992 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application PC/TUS9307261
GENERAL INFORMATION: PfEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US93/07261
FILING DATE: 19930805
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/927,531
FILING DATE: 07-AUG-1992
ATTORNEY/ACENT INFORWATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31.895
REFERENCE/DOCKET NUMBER: DX0288K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7398
TELEPHONE: 201-822-7039
                                                                                   740 TNGAYGGNGARTTYTAYG 757
                                                                                                                                                                 680 AYGAYATHTAYGCNCARAAYATHCARATHACNGAYAARGGNACNGCNTTYGAYGTNTAYG 739
                                                                                                                                                                                                                                                                               620 ARCAYYINMGNAARATHGARGCNGAYGTNCCNATHTAYTAYTAYGGNTTYAARGAYWSNG 679
                                                                                                                           703 TTGAAACCAAATTTTATG 720
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IMMEDIATE SOURCE:
CLONE: p2b1;p12-1
FEATURE:
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ADDRESSEE: John H. C. Blasdale
STREET: One Giralda Farms
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ORIGINAL SOURCE:
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STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                      Score 135; DB 4; Length 4766; Pred. No. 5.48e+00; 26; Mismatches 61; Indels
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed Nov 24 00:36:34 1999; MasPar time 19.53 Seconds 896.452 Million cell updates/sec

Description: Perfect Score: Sequence: Title: >US-09-103-287-2 (1-437) from US09103287.pep 3121

1 MTHYHFVGIKGSGMSSLAQI......GDIQKLQNAYLDKLGMKNAF 437

Scoring table: PAM 150 Gap 11

Searched:

122810 seqs, 40068593 residues

ORGANISM DATE TITLE RESULT ENTRY

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pirl 2:pir2 3:pir3 4:pir4

Mean 50.576; Variance 122.235; scale 0.414

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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	449	445	508	450	682	505	445	457	494	494	449	449	457	453	505	491	475	803	468	495	481	454	432	Length
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	JC6560	G70371	A70125	B69198	A69170	<b>S75968</b>	A71699	I64184	B47691	D70579	B71917	G64597	S56459	B64002	S76722	CEECAM	E64185	A71475	H70201	C71679	C71338	B70418	C69662	ID
,	<pre>UDP-N-acetylmuramoyla</pre>	UDP-MURNAC-pentapepti	UDP-N-acetylmuramoyla	UDP-N-acetylmuramyl t	<pre>UDP-N-acetylmuramyl t</pre>	UDP-N-acetylmuramoyla	UDP-n-acetylmuramoyla	<pre>UDP-N-acetylmuramoyla</pre>	<pre>UDP-N-acetylmuramoyla</pre>	probable murC protein	udp-n-acetylmuramate-	=		hypothetical protein	<pre>UDP-N-acetylmuramoyla</pre>	UDP-N-acetylmuramate-	<pre>UDP-N-acetylmuramate-</pre>	probable muramate-Ala	UDP-N-acetylmuramate-	<pre>UDP-n-acetylmuramate-</pre>	probable UDP-N-acetyl	<pre>UDP-N-acetylmuramate-</pre>	UDP-N-acetylmuramate-	Description
		2.23e-02	5.11e-04	1.27e-04	1.73e-05	5.45e-06	. 05e	1.93e-08	7.76e-09	.52e		4	2.39e-45	σ.	9.98e-53	8.97e-57		1.53e-68	7.56e-71		2.58e-74	2.69e-77	0.00e+00	Pred. No.

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758	447	447	416	374	227	1670	1558	585	452	143	493	432	320	121	437	598	482	451	464	856	457	
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S37855	F64706	D71812	E69599	S75646	H64336	S71551	в71603	C70330	F64730	E69065	D64612	H64383	S33172	S18067	B64185	D71127	E70450	D47691	H70137	A64699	F69662	
hypothetical protein 6	UDP-MurNac-tripeptide 5	1-t 5	<u>α</u>			N	2	conserved hypothetica 2	N	•		Na+ transporter - Met 1		thyroid hormone recep 1	co Co				muramoyla	0	UDP-N-acetylmuramoyla 2	
5.65e+00	5.28e+00	5.28e+00	5.28e+00	5.28e+00	6.65e+00	2.05e+00	2.05e+00	2.61e+00	2.61e+00	3.30e+00	1.62e+00	L.62e+00	9.96e-01	1.62e+00	4.77e-01	l.75e-01	2.26e-01	2.90e-01	1.36e-01	5.32e-02	2.23e-02	

## ALIGNMENTS

#journal #title			#autnors	ACCESSIONS	ORGANISM DATE	ENTRY
Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, Y.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenegger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Nature (1997) 390:249-256 The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.	Y: Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazaravic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Woestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Porwollk, S.; Prescott, A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Seroror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;	Bolotin, A.; Borchert, S.; Boriss, R.; Boursler, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Choi, S.K.; Codani, J.J.; Connerton, K.M.; Duesterhoeft, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Ehrlich, S.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,	<pre>kunst, r.; ogasawara, n.; moszer, 1.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;</pre>	17-Mar-1999 C69662; S71002 A69580	<pre>#formal_name Bacillus subtilis 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change</pre>	C69662 #type complete UDP-N-acetylmuramatealanine ligase (EC 6.3.2.8) murC -Bacillus subtilis

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ENTRY
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#title Bacillus subtills operon under the dual control of general stress transcription factor sigma(B) and sporulation transcription factor sigma(H).
#cross-references MUID:96310371
#accession S71002
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#accession C69662
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##cross-references GB:Z99119; GB:AL009126; NID:g2635411;
PID:g2635463
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                                                                                                                                                                                                                                                               h 63.3%;
Similarity 63.9%;
                           B70418 #type complete
UDP-N-acetylmuramate-alanine ligase -
#formal_name Aquitex acolicus
08-May-1998 #sequence_revision 08-May-
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translation not shown
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                             08-May-1998 #text_change
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Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, G.J.; Swanson, R.V.

#journal Nature (1998) 392:353-358
#title The complete genome of the hyperthermophilic bacterium
#cross_references_MUID:98196666
                                                                                   #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKKFHFIGIGGIGMSGIAQILLEMGYKVSGSDISENKNTKL-LKQKGAKIYIGHRPENLG: :||:|| | || || : |: :||: :||: :||:
                                                                                                                                                                                                                                                                                                                                                                                                                                SRTQAFLNEFAESLCKADRVFLCEIFGSIRENSGALTIQDLIDKIGGASFI-N-EDLIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAKNLYLKEGRYEFGVEFKGKELGRIHLGIA-GIHNVYNALAATGVA-LE-LGVSFEVIK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DHPDYFKDINDVFDAFQEMAHNVKK-GI-IAWGDDEHLRK-IE-ADVPIYYYGFKDSDDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHVM-NGDKKTSFLIGD-----GTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTHYHFYGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFGANNIK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EALETFGGVKRRFNETTI-ANQVIVDDYAHHPREISATIDTARKKYPHKEVVAVFQPHTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
139; Conser
Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, M.; Hickey, E.K.; Clayto R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod, M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A70300
Deckert,
                                                                                                                                                                 #formal_name Treponema
syphilis spirochete
24-Jul-1998 #sequence_;
                                                                                                                                                                                                                                            C71338 #type complete probable UDP-N-acetylmuramate--alanine ligase (murC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.9%;
larity 30.8%;
Conservative
                                                                                                      A71250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily UDP-N-acetylmuramate--alanine liga: #length 454 #molecular-weight 50893 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B70418
                                                                                                                                                                                                                           syphilis spirochete
                                                                                                                                              17-Mar-1999
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                                                                                                                                                                 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 620; DB 2; Le
Pred. No. 2.69e-77;
125; Mismatches 164;
                                                                                                                                                                                                    pallidum subsp. pallidum #common_name
                                                                                                                                                                 24-Jul-1998
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      McDonald,
                                                              Clayton,
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                                                                                                                                                                                                                                                               #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                          ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##experimental_source strain Nichols
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##cross-references GB:AE001213; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
##cross-references
                        ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QMVKELRLDASVLVGSAVSGNNDSCVVLNGDTFFIAETCEYRRHFLHFHPQKIVLTSVEH 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAVFQPHTFSRTQAFLNEFAESLCKADRVFLCEIFGSIRE-NSGALTIQDLID 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLD-VTNIKEALETFGGVKRRFNE-TTIANQVIVDDYAHHPREISATIDTARKKYPHKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVEHLTALRKVLALFQGCRRRSEVLGEVRGILFMDDYGHHPTAIKKTLRGLKTFFPERRI 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSDDIYAQNIQ-ITDKGTAFDVYV-DGEFYDHFLSPQYG-DHT-VLN-ALAVIAISYLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AWGD-YGVSIHGVQDRKISFSLRGFAGEFYVALPGEHSVLNATGALALALSLVKKQYGEV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHPDYFKDINDVFDA-FQEMAHNVKKGIIAW-GDDEHLRKI-E-A--DVP--IYY-YGFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHQDYYSSYEDILAAYFHYIDRLPQFGELFYCVDDQGVREVVQLAFFSRPDLVYVPYGER 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HVMNGDK-KTSFLIGDG-TGM--G-LP-ESD-YFAFEACEYRRHFLSYKPDYAIMINIDF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVIQGNAFASS-HEEIVRAHQLKLDVVSYNDFLGQII-DQYTSVAVTGAHGKTSTTGLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVIHSAAYVPEENDELAEAYRRGIPTLTYPEALGDISCARFSC-GIAGVHGKTTTTAMIA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFGANNIKEDM- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMIGIKGTGMSALAELLCARGARVSGSDVADVFYTDRILARLGVPVRTPFSCQNLADAPD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126;
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Similarity 30.5%;
                                                                                                                               Nature (1998) 396:133-140
The genome sequence of Rickettsia prowazekii and of mitochondria.
                                                                                                                                                                                                                                                                                                                                                                    C71679 #type complete
UDP-n-acetylmuramate--alanine ligase (murC) RP247
Rickettsia prowazekii
#formal_name Rickettsia prowazekii
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                                                                                                                                                                                                                Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.; Sicheritz-Ponten, T.; Alsmark, U.C.M.; Podowski, Naeslund, A.K.; Eriksson, A.S.; Winkler, H.H.; K
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                                                                                                                                                                                                                                                                                                                                              21-Nov-1998 #sequence_revision 21-Nov-1998
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1-495 ##label AND
es GB:AJ235271; G
                                                                 preliminary; nucleic acid
  translation not shown
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Pred. No. 2.58e-74
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  GB:AJ235269;
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                                                                                  sequence
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  NID:g3860788;
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  PID:e1342553;
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Best Local S
Matches 14
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                                                                                                                                                                                 #cross-references MUID:98065943
#accession H70201
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                                        ##molecule_type DNA
##residues 1-468 ##label KLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 ANFLAELDDVVSIIIDNA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 AIKNGFNNFKGVKRRFTKVAEYNKAVIIDDYAHHPEEIKATLATAKNIANQQNGKVIAIF
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##cross-references GB:AE001180; GB:AE000783; NID:g2688755; PID:g2688761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 VVIQGNAFASSHEEIVRAHQIKLDVVSYNDFLGQIIDQYTSVAVIGAHGKTSTIGLLSHV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 HFIGIGGVGMSGIAEILHNLGYKVQGSDLVENYN-TK-RLESYGIKIFLGQAKQNIKNVS
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Similarity 33.6%;
147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Arttach, P.; Bowman, C.; Galland, S.; Fujii, C.; Cotton, M.D.; Horst, F.; McDonald, M.D.; McDonald, M.D.; Horst, F.; McDonald, M.D.; Horst, F.; McDonald, M.D.; Horst, F.; McDonald, M.D.; Horst, F.; McDonald, M.D.; McD
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                                                                                                                                                                                                                                                                                 K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C.
Nature (1997) 390:580-586
Genomic sequence of a Lyme disease spirochaete, Borreli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #formal_name Borrelia
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Pred. No. 2.42e-71;
111; Mismatches 151
                                                                                                              not shown
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                                                                                                                                            sequence
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TIGR: BB0817

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REFERENCE
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SUMMARY #length 468 #molecul
                                                                                       Query Match 18.2%;
Best Local Similarity 29.9%;
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                        #authors Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marat R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov, R.L.; Zhao, Q.; Koonin, E.V.; Davis, R.W.

#journal Science (1998) 282:754-759

#title Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.

#cross-references MUID:99000809
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                                                                                                                                                                                                #gene
                                                                                                                                                                                                                                ##residues 1-803 ##label ARN 1-803 ##cross-references GB:AE001348; GB:AE001273; NID:g3329216; PID:g3329224 ##experimental_source serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 AS-FINE--DLINVLEQFDNAVVLF--MGAGDIQKLQNAYL 428
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YHFIGIGGIGMSALAHVLLDRGYSVSGSDLSEGKVVE-KLKNKGAEFFLGNQEEHIPEGA 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOHPDYFKDINDVFDAFQEMAHNVKK-GI-IAWGDDEHL-R-K--IEA-DVPIYYYGFKD 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVLFNKLGLNPNVIVGSSVKDFKDNSAIAGISNIFIVETCEYKKHFLNFSPNMLILTNVD 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 18.6%; Score 581; DB 2; Length 468; Similarity 32.3%; Pred. No. 7.56e-71; 149; Conservative 125; Mismatches 144; Indels 43;
                                                                                                                                                                         murC/ddlA
#length 803
                                                                                                                                                                                                                                                                                                                                           A71475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A71475 #type complete
probable muramate-Ala ligase and D-Ala-D-Ala ligase -
Chlamydia trachomatis (serotype D, strain UW3/Cx)
#formal_name Chlamydia trachomatis
13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A71570
                                                                                                                                                                                                                                                                                                                      preliminary
                                                                                                                                                                         #molecular-weight 89229 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #molecular-weight 53480 #checksum
                                                                                            106;
                                                                                                        Score 567; DB 2;
Pred. No. 1.53e-68
                                                                                         Mismatches
                                                                                                           .53e-68;
                                                                                                                                Length 803;
                                                                                       Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.; Marathe
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          62
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                                                                                       13;
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#pathway
CLASSIFICATION
                                                                                                 SUMMARY
                                                                                                                     FEATURE
125-130
                                                                                                                                                                                           KEYWORDS
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REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
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  Best Loc
Matches
                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #title Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. #cross-references MUID:95350630 #accession E64185
                                                                                                                                                                                                                                                                                                           #description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
##residues 1-475 ##label TIGR
##cross-references GB:U32794; GB:L42023; NID:g1574694; PID:g1574695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 AESLCKADRVFLCEIFGSIRENSGALTIQDLIDKIGGASFIN 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 PSAFKDADEVLLTEVYSAG-EEAEDISYOKLAEAISQESIVK 402 : :: || | :: | :: | :: | :: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302
                        y Match 16.9%;
Local Similarity 30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRLQRKNSSETFLFLEDYAHHPSEISCTLRAVRTAVGQRRILAIYQPHRFSRLRECIDSF 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKGTAFDV-YVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GWRLYFTAKYQDVV-YADIEVQLVGMHNVLNAAAAMGIALSLGIDEGAIRNAFRGFSGVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FKDINDVF-DAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEGDRELLLASLKDFA--LKTQQICWYNGDCPR-LRSCLQGHTFGLDSSCDLHILSYYQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNGDKKT-SFLIGD-GT-GM-GLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVVYSSSISKKNPEFLSAKSRGNRVVHRAELLAELAQDQISIFVTGSHGKTTVSSLITAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.; Science (1955) 269:496-512
                                                                                                                                                                                  peptidoglycan biosynthesis
#superfamily UDP-N-acetylmuramate--alanine ligase
#TP; cell division; cell wall; ligase; P-loop; peptidoglycan
                                                                                                                                                                                                                                                                                   one of the ligases responsible for the synthesis of UPD-N-acetylmuramyl pentapeptide, an intermediate
                                                                                          #region nucleotide-binding motif A (P-loop)
#length 475 #molecular-weight 51994 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UDP-N-acetylmuramate--alanine ligase (EC Haemophilus influenzae (Strain Rd KW20) #formal_name Haemophilus influenzae 18-aug-1995 #sequence_revision 18-aug-199
  Conservative
                                                                                                                                                                biosynthesis
                                                                                                                                                                                                                                                           cell-wall biosynthesis
                                                                                                                                                                                                                                                                                 UPD-N-acetylmuramyl pentapeptide,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                          TIGR: HI1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #type complete
  104; Mismatches 145;
                     Score 529; DB 2;
Pred. No. 2.60e-62;
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                                           Length 475
  Indels
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  22;
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Gaps
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ALTERNATE_NAMES ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                      *Juurnal Eur. J. Biochem. (1995) 230:80-87

*title Over production, purification and properties of the uridine-diphosphate-N-acetylmuramate:L-alanine lig Escherichia coli.

*cross-references MUID:95324553

*accession S65354
                                                                                                                                                                                                                                                                                                                                                                                                                                                   #accession S40001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Ikeda, M.; Wachi, M.; Jung, H.K.; Ishino, F.; Matsuhashi, M.
#journal Nucleic Acids Res. (1990) 18.4014
#title Nucleotide sequence involving murG and murC in the mra gene
cluster region of Escherichia coli.
#journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #accession JQU545
##molecule_type DNA
                                                                                                           #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors
                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-491 ##label YUR
##cross-references EMBL:D10483; NID:g216434; PID:d1001828; PID:g216505
#MCE 565354
                                                                                                                                                  ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-491 ##label IKE
##cross-references EMBL:X52644; NID:g42053; PID:g42056
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                                                                                                                                                                        ##molecule_type protein
                                                                                                                                                                                               ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFSRTQAFLNEFAESLCKADRVFLCEIFGS 37:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIYTQAKLDPTFVNGGLVKSAGKNAHLGASRYLIAEADESDASFLHLQPMVSVVTNMEPD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYT-SVAVTGAHGKTSTTGLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVVVVSSAIKDDNPELVTSKQKRIPVIQRAQMLAEIM-RFRHGIAVAGTHGKTTTTAMIS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LETFGGVKRRFNE-TT-I-AN-QV-IVDDYAHHPREISATIDTARKKYPHKEVVAVFQPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFGANNIKED
                      Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shac Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, Fujita, N.; Isono, K.; Mizobuchi, K.; Nakata, A. submitted to the EMBL Data Library, December 1992 $40601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UDP-N-acetylmuramoyl-L-alanine synthetase
#formal_name Escherichia coli
31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change
  Science
                                                                                                                                  A64720
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JQ0544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-Jul-1998
                                                                                                                                                                                             preliminary
                                                                                                                                                      .-14 ##label LIG
  (1997)
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  277:1453-1462
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#authors
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126-131
                                                                                          ACCESSIONS
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Best Local
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#cross-references MUID:97426617
#accession C64731
                                                                                                                                            #variety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #description
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                                                                                                                                                                                                                                                                                                                                         378 LFQPHRETRTRDLYDDFANVLTQVDTLLMLEVY 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##cross-references GB:AE000118; GB:U00096;
UWGP:b0091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues
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                                                                                                                                                                                                                                                                                                          339 VFQPHTFSRTQAFLNEFAESLCKADRVFLCEIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##experimental_source strain K-12, substrain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVEDYQQIGPQGHFTLLRQDKEPMRVTLNAP-GRHNALNAAAAVAVATEEGIDDEAILRA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYT-SVAVTGAHGKTSTTGLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVVVVSSAISADNPEIVAAHEARIPVIRRAEMLAELM-RFRHGIAIAGTHGKTTTTAMVS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIHFVGIGGAGMGGIAEVLANEGYQISGSDLAPNPVTQ-QLMNLGATIYFNHRPENVRDA
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                                                                                                                                                                                                                                                                                                                                                                                                              LESFQGTGRRFDFLGEFPLEPVNGKSGTAMLVDDYGHHPTEVDATIKAARAGWPDKNLVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HMDTYQGDFENLKQTFINFLHNLPFYGRAVMCVDDPVIRELLPRVGRQTTTYGFSEDADV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV-MNGDKKTSFLIGD----GTGM-G-LPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIYAEAGLDPTFVNGGLVKAAGVHARLGHGRYLIAEADESDASFLHLQPMVAIVTNIEAD 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYHFYGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFGANNIKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPDYFK-DINDVFDAFQEMAHNVKK-G-IIAWGDDEHLRKIEADV--PIYYYGFKDSDDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123;
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Similarity 31.3%;
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2 min
                                                                                                                                                               protein slr1423
#formal_name Sy
                                                                                                                                                                                             S76722 #type complete
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC
murC - Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             one of the ligases responsible for the UPD-N-acetylmuramyl pentapeptide, an
Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M. Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Sh
                                                                                          S76722
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#length 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptidoglycan biosynthesis
                                                                                                                          25-Apr-1997 #sequence_revision
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                                                                                                         21-Aug-1998
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                                                                                                                                                           _name Synechocystis
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#molecular-weight 53626 #checksum
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Pred. No. 8.97e-57;
105; Mismatches 138;
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                                                                                                                          25-Apr-1997
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#cross-references MUID: 97061201

#accession S76722
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PID:g1653723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type DNA
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Local Similarity 31.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLAAAKQKVTHGKYERVVAIFQPHRYSRTHTFMAEFATAFKDADLVVLTDIYSAGEQNPY 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDINDVFDAFQEMAHNVKKGIIAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVMN-GDKKTSFLIG-D-GT--GMG-LPES 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NISNALAAVAVGRLLGLDFPVIAQAIASFNGAKRRFECKGYCNGITFIDDYAHHPSELLA 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDEHLRKIEADVPIYYYGFKDSDDIY-AQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYLVAEVDESDGSLTKHHPEIGIVTNIELDHPDHYSTLAEVVEIFRTFESHCQT-LIGCL 265
                                    Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Euhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.;
Science (1995) 269:496-512
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GTG
Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.
                                                                                                                                                                                                                                                                                                                                                    #formal_name Haemophilus influenzae
18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
10-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein HI0121 - Rd KW20)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 122; Indels 13;
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#title Analysis of the Escherichia coli genome VI:
the region from 92.8 through 100 minutes.
#cross-references_MUID:95334362
#accession S56459
                                                                                                                          #authors
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##residues 1-457 ##label BUR
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                                                                                                                                                                                                                                                               ##cross-references EMBL:U14003; NID:g1263172; PID:g537075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
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TIGR:HI0121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 G-FKDSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKL
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Local Similarity 29.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKHIHILGICGTFMGGVAMIAKQMGYHVTGSDTNVYPPMSTFLEEQGIEIIPNYDVAQLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILP-FGANNIK 59
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shackirkpatrick, Goeden, M.A.; Rose, D.J.; Mau, Goeden, M.A.; Rose, Goeden, M.A.; Rose, D.J.; Mau, Goeden, M.A.; Rose, Goeden, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 0457
#formal_name Escherichia coli
28-Oct-1995 #sequence_revision 03-Nov-1995
__14-Nov-1997
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S56314
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hypothetical 48.5K protein (fbp-pmba intergenic
Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #length 453 #molecular-weight 50074 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blattner, F.R.
                                                                                                                                                                                          the nucleotide sequence was
Library, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                preliminary; nucleic acid sequence
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Pred. No. 6.64e-48;
92; Mismatches 156; Indels 26;
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ACCESSIONS
REFERENCE
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#cross-references MUID:97426617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##experimental_source strain K-12, substrain MG1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFSRTQAF-LNEFAESLCKADRVFL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNTMKMGICKDDLAPSLGRADEVFL 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNNLEFDHADIFDDLKAIQKQFHHLVRIVPGQGRIIWPENDINLKQTMA-MGCWSEQELV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HVMNG-DKKTSFLIGD--GT-GMG--LPESDYFAFEA----CEY--RR-HFLSYKPDYAI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WILEQCGYKPGFVIGGVPGNFEVSAHLGESDFFVIEADEYDCAFFDKRSKFVHYCPRTLI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HILGICGTFMGGLAMLARQLGHEVTGSDANVYPPMSTLLEKQGIELIQGYDASQLEPQPD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEALETFGGVKRRFNETTIANQVIV-DDYAHHPREISATIDTARKKYPHKE-VVAVFQPH 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNI 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEQGHWQAKKLTTDASEWEVLLDGEKVGEVKWSLVGEHNMHNGLMAIAAARHVGVAPADA 301
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                                                                                                                     Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Kichardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Addams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Uterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujil, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
Nature (1997) 388:539-547
                        The complete genome sequence Helicobacter pylori. noes MUID:97394467 G64597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 0
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#length 457 #molecular-weight 49874 #checksum
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    translation not shown
preliminary; nucleic
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acid
                                                                                                     of.
sequence
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                                                                                                     the
                                                                                                  gastric pathogen
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not shown;
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                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                #authors Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.;
Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge,
B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.;
Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.;
Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
Merberg, D.; Mils, D.M.; Mils, Mils, D.M.; Mils, Mils, Mils, D.M.; Mils,                                                                                                                                                                 #gene
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1-449 ##label TOM
                                                                                                                                                                                                                            ##experimental_source strain J99
                                                                                                                                                                                                                                                             ##cross-references GB:AE001489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354
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TIGR:HP0623
#length 449 #molecular-weight 50793 #checksum 3884
                                                                                                                                                                                                                                                                                              ##residues
                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
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Local Similarity 28.9%;
nes 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MN-GDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYA-IMTNIDFDHPDYF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HFIGIGGIGISGLAKYLKAQGATISGSDIA--ISPSVKYLKALGVEINIPHDPKAINNQD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFAESLCKA-DRVFLCEIFGS
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                              13.1%;
Similarity 29.2%;
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udp-n-acetylmuramate--alanine ligase -
(strain J99)
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12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
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Pred. No. 4.98e-45;
95; Mismatches 151;
Score 409; DB 2;
Pred. No. 5.81e-43;
90; Mismatches 156
                                                                                                                                                                                                                                                             GB:AE001439; NID:g4155102; PID:g4155106
                                                               Length 449
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                                                                                                                                                                                                                                                                          ##cross-references GB:Z95388; GB:AL123456; NID:g3261759; PID:e315954; PID:g2104326
                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
##residues 1-49
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                                                                                                                                                                                                                                                    ##experimental_source strain H37Rv
                                                                                                              y Match 11.2%;
Local Similarity 28.9%;
                     14 HMVGIGGAGMSGIARILLDRGGLVSGSDAKESRGVH-ALRARGALIRIGHDASSLDLLPG 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQ-ITD 238
HFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKG--IKILPFGAN-NI-KE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDILOKNNLILIDDYAHHPTEIGATLKSARIYANLLNTOEKIIVIWQAHKYSRLMDNLEE 365
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                                                                                              136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
Nature (1998) 393:537-544
Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
                                                                                                                                                                                murC #length 494 #molecular-weight 51176 #checksum
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17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1998
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                                                                                           Conservative
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                                                                                         107; Mismatches 185;
                                                                                                              Score 349; DB 2;
Pred. No. 1.52e-33;
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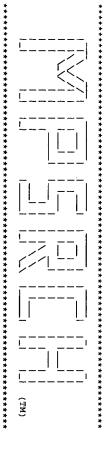
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                                                                                                                                                                                                                                                                                                       #journal J. Mol. Biol. (1994) 235:209-220
#title The Bacillus subtilis spoVD gene encodes a mother-cell-specific penicillin-binding #cross-references MUID:94118264
#accession S43864
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#title
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                                                                                                                                                                                                                           ##molecule_type DNA
##residues 1-16 ##label DA2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-494 ##label DAN
##cross-references EMBL:Z15056; NID:g40160; PID:g40162
##note sequence extracted from NCBI backbone
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                                                                                                                                                        ##cross-references EMBL:Z25865; NID:g397893; PID:g397896
##note the nucleotide sequence was submitted to
Library, September 1993
                                                                                                                                                                                                                                                                                                 ##status
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Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Br; A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.
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Daniel, R.A.; Drake, S.; Buchanan, C.E.; Scholle,
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J. Gen. Microbiol. (1993) 139:361-370
DNA sequence of the murE-murD region of
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UDP-N-acetylnuramoylalanyl-D-glutamate--2,6-diaminopimelate
ligase (EC 6.3.2.13) murE - Bacillus subtilis
#formal_name Bacillus subtilis
19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
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#dene murE
#map_position 133 (degrees)
KEYWORDS ligase; peptidoglycan biosynthesis
SUMMARY #length 494 #molecular-weight 54325 #checksum 6945
Search completed: Wed Nov 24 00:38:32 1999 Job time : 118 secs.
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Best Local Similarity 32.3%;
Matches 42; Conservative
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#accession E69662
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1.494 ##label KUN
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##cross-references GB:299111; GB:AL009126; NID:g2633699; PID:e1185108;
##cross-references GB:29913889
##experimental_source strain 168
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Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;

Maueel, C.; Medique, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott,
A.M.; Presccan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scaldon, E.;
Schleich, S.; Schroeter, R.; Scoffone, F.; Scklguchi, J.;
Sekowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo,
B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;
Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.;
Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.;
Winters, P.; Wipat, A.; Yanamorto, H.; Yamane, K.; Yasumoto,
K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.;
The complete genome sequence of the Gram-positive bacterium
Bacillus subtilis.
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translation not shown
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Pred. No. 7.76e-09;
22; Mismatches 63; Indels
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Nov 24 00:31:14 1999; MasPar time 13.64 Seconds 905.767 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score:

Sequence: >US-09-103-287-2 (1-437) from US09103287.pep 3121 1 MTHYHEYGIKGSGMSSLAQI......GDIQKLQNAYLDKLGMKNAF 437

Scoring table: PAM 150 Gap 11

Searched:

77977 segs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 51.864; Variance 106.076; scale 0.489

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	5	v	4	w	2	_	Result	•
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UDP-N-ACETYLMURAMOYLAL	UDP-N-ACETYLMURAMOYLAL	UDP-N-ACETYLMURAMOYLAL	UDP-N-ACETYLMURAMOYLAL	UDP-N-ACETYLMURAMOYLAL	UDP-N-ACETYLMURAMOYLAL	UDP-N-ACETYLMURAMOYLAL	UDP-N-ACETYLMURAMOYLAL	UDP-N-ACETYLMURAMOYLAL	UDP-N-ACETYLMURAMATE	UDP-N-ACETYLMURAMATE	UDP-N-ACETYLMURAMATE	UDP-N-ACETYLMURAMATE:L	UDP-N-ACETYLMURAMATE:L	UDP-N-ACETYLMURAMATE	Description									
1.96e-02	2.44e-03	2.44e-03	3.07e-05	1.58e-07	2.05e-08	2.21e-10	7.63e-11	4.90e-13	1.29e-37	.50e-4	2.66e-53	1.12e-53	1.10e-56	2.33e-62	1.09e-63	1.50e-66	4.02e-67	1.21e-73	1.07e-83	8.82e-88	0.00e+00	0.00e+00	Pred. No.	

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61 DMVVIQGNAFASSHEEKARAHQMKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120

Query Match 97.2%; Best Local Similarity 97.5%; Matches 426; Conservative

Score 3035; DB 1; Length 437; Pred. No. 0.00e+00; 5; Mismatches 6; Indels

0;

Gaps

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45	44	43	42	41	40	39	38	37	36	<u>ა</u>	34	ယ	32	31	30	29	28	27	26	25	24
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(E)	ALPHA ENOLASE (EC 4.2.	TRANSCRIPTIONAL ACTIVA	HYPOTHETICAL PROTEIN M	DNA POLYMERASE III (EC	PENICILLIN-BINDING PRO	OUTER MEMBRANE PROTEIN	THYROID HORMONE RECEPT	ALPHA ENOLASE (EC 4.2.	MINOR EXTRACELLULAR PR	HYPOTHETICAL 87.9 KD P	PUTATIVE COMPETENCE-DA	ENOLASE (EC 4.2.1.11)	PHOSPHOGLYCERATE KINAS	TRANSCRIPTIONAL ACTIVA	HYPOTHETICAL PROTEIN M	UDP-N-ACETYLMURAMOYLAL	PROBABLE ADENINE PHOSP	HYPOTHETICAL PROTEIN M	ORNITHINE CYCLODEAMINA	UDP-N-ACETYLMURAMOYLAL	UDP-N-ACETYLMURAMOYLAL
6.28e+00	4.866+00	6.28e+00	4.86e+00	2.90e+00	3.76e+00	3.76e+00	2.90e+00	2.90e+00	1.72e+00	1.72e+00	1.32e+00	1.72e+00	1.72e+00	1.72e+00	1.72e+00	5.86e-01	5.86e-01	3.39e-01	1.94e-01	8.33e-02	4.70e-02

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p40778:
p40778:
01-FEB-1995 (REL. 31, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8)
                           EMBL;
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                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAPIDUS A., GALLERON N., SOROKIN A., "Sequencing and functional annotation in the 200 kb rrnB-dnaB region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 98048467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MICROBIOLOGY 143:3431-3441(1997).
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                                                                                                                                                                                                                                                                                                      FUNCTION: CELL WALL FORMATION.

CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALF
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

PATHWAY: PEPPILOGLYCAN BIOSYNTHESIS.

SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).

SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MICROBIOL. 20:339-350(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKLQNAYLDKLGMKNAF
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                                                                                                   s requires a license agreement (
an email to license@isb-sib.ch)
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                           0; G2293216;
G556014; -.
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Best Local :
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MURC_TREPA
083361;
15-DEC-1998
15-DEC-1998
15-DEC-1998
                                                                                                                                             FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
DODSON R., GWINN.M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
DODSON R., GWINN.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T
MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND
MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND
MCDONALD L., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.
                                                                                       "Complete genome sequence spirochete."; SCIENCE 281:375-388(1998).
                                                                                                                                                                                                                                     STRAIN-NICHOLS;
MEDLINE; 98332770
                                                                                                                                                                                                                                                                                                                              ACETYLMURANOYL-L-ALANINE SYNTHETASE).
MURC OR TP0341.
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15-DEC-1998 (REL. 37, LAST ANNOTATION
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (
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ATP-BINDING.
NP_BIND 108 114
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                                                                                                                                                                                                                                                                                                 BACTERIA;
                                                                                                                                  VENTER J.C.;
                                                                                                                                                                                                                                                                                                               TREPONEMA PALLIDUM
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FUNCTION: CELL WALL FORMATION.

CATALTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

PATHWAY: PEPTIDOSLYCAN BIOSYNTHESIS.

SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).

SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
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273; Conser
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432;AA;
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Pred. No. 0.00e+00;
60; Mismatches 94;
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                                                                                                                  Treponema
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Best Local S
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                                                                                                                                                                                                                                                                                                          MURC_BORBU
051757;
15-DEC-1998
15-DEC-1998
           FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A. LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GIDOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D., PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANS VAN VUGT R., PALMER N., ADAMS M.D., GOCAYLE J.D., WEIDMAN J., UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C., GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH SMITH H.O., VENTER J.C.;
                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
MEDLINE; 98065943.
                                                                                                                                                                                                                                            ACETYLMURANOYL-L-ALANINE SYNTHETASE) MURC OR BB0817.
                                                                                                                                                                                                                                                                        15-DEC 1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001213; G3322616; -. TIGR; TP0341; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HVMNGDX-KTSFLIGDG-TGM--G-LP-ESD-YFAFEACEYRRHFLSYKPDYAIMINIDF
                                                                                                                                                                                                                                                                                                                                                                                                                                           VVDFMSHTYSRTAALLTEFAESFQDADVVILHEIYASAREVYQGEVNGEHLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHQDYYSSYEDILAAYFHYIDRLPQFGELFYCVDDQGVREVVQLAFFSRPDLVYVPYGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSDDIYAQNIQ-ITDKGTAFDVYV-DGEFYDHFLSPQYG-DHT-VLN-ALAVIAISYLE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHPDYFKDINDVFDA-FQEMAHNVKKGIIAW-GDDEHLRKI-E-A--DVP--IYY-YGFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QMVKELRLDASVLVGSAVSGNNDSCVVLNGDTFFIAETCEYRRHFLHFHPQKIVLTSVEH 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVIQGNAFASS-HEEIVRAHQLKLDVVSYNDFLGQII-DQYTSVAVTGAHGKTSTTGLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVIHSAAYVPEENDELAEAYRRGIPTLTYPEALGDISCARFSC-GIAGVHGKTTTTAMIA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLD-VTNIKEALETFGGVKRRFNE-TTIANQVIVDDYAHHPREISATIDTARKKYPHKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
126; Conser
 sequence of a Lyme disease
                                                                                                                                                                                                              SPIROCHAETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 AA;
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                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 602;
; Pred. No. 8
117; Mismat
                                                                                                                                                                                                            SPIROCHAETACEAE; BOR
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spirochaete,
                                                                                                                                                                                                                                                                                                                                                            468
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 Borrelia
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                                                                                                            E.K., GWINN M.,
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                                                                                HANSON
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Best Local
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                                                                            MURC_HAEIN STANDARD; PRT; 475 AA. P45066; P45066; P10-NOV-1995 (REL. 32, CREATED) 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                burgdorfer1.";
NATURE 390:580-586(1997).
-!- FUNCTION: CELL WALL F
                                                  MURC OR HI1139
                                                                 ACETYLMURANOYL-L-ALANINE SYNTHETASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
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-i- CATALUTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANINE.
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
-i- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-i- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                BACTERIA; PROTEOBACTERIA;
                            HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                             NTYFFKDVKDSINFIKSLLISGDLFITMGAGNNFILHD-FL 468
                                                                                                                                                                                                                                                                                                                                      ILDEMPHTETRTKEFFADEVEVLSAADILILHNIYLSNRENENPDELSVKLFLNIKKINK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLN-ALAVIAIS-YLE---K-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDHPDYFKDINDVFDAFQEMAHNVKK-GI-IANGDDEHL-R-K--IEA-DVPIYYYGFKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDLIVYSSAYNKDGLQVLLEAKELNIPILSYPEALGELSRKYYSIGIAGSHGKTTTTAFL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRN-K-GI--KILPFGANNIKED
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                                                                                                                                                                                                                                                                                                                                                                                                                   IFDFEEAIKRIAKNYSGIKRRVEVVKEENGVIYMDDYAHHPREIKNTLFGIKNFYKNKRI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVLFNKLGLNPNVIVGSSVKDFKDNSAIAGISNIFIVETCEYKKHFLNFSPNMLILTNVD 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 18.6%;
Similarity 32.3%;
149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
468 AA;
                                  INFLUENZAE
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53480 MW;
              GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 581; DB 1; Le
Pred. No. 1.07e-83;
125; Mismatches 144;
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09511A39 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.
KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M.
MCKENNEY K., SUTTON G., FITZHIGH W., FIELDS C.A., GOCAYNE J.D.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whole-genome random sequencing and assembly of Haemophilus
 344
                                     377
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                                                                                                                                                                                                                     175
                                                                                                                                                                                                                                                         198
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FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
SUBGELLULAR IOCATTON: CYTOPLASMIC (PROBABLE).
SUBGELLULAR IOCATTON: CYTOPLASMIC (PROBABLE).
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                                                                                                         LADFOGAGRRFDQLGEFIRPNGKVRLVDDYGHHPTEVGVTIKAAREGWGDKRIVMIFQPH
                                                                                                                                            YAQNIQITDKGTAFDV-YVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEA
                                                                                                                                                                                RIEDYEQTGFQGHYTVICPNNERINVLLNVP-GKHNALNATAALAVAKEEGIANEAILEA
                                                                                                                                                                                                                     HPDYFK-DINDVFDAFQEMAHNVKK-GI-IAWGDDEHLRKIEADV--PIYYYGFKDSDDI
                                                                                                                                                                                                                                                         HMDTYEGDFEKMKATYVKFLHNLPFYGLAVMCADDPVLMELVPKVGRQVITYGFSEQADY
                                                                                                                                                                                                                                                                                             HVMNGDK-KTSFLIGD---GTGM-G-LPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFD
                                                                                                                                                                                                                                                                                                                             MIYTQAKLDPTFVNGGLVKSAGKNAHLGASRYLIAEADESDASFLHLQPMVSVVTNMEPD
                                                                                                                                                                                                                                                                                                                                                                MVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYT-SVAVTGAHGKTSTTGLLS
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                                                                         LETFGGVKRRFNE-TT-I-AN-QV-IVDDYAHHPREISATIDTARKKYPHKEVVAVFQPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 16.9%;
1 Similarity 30.5%;
119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 529; DB 1;
Pred. No. 1.21e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 145;
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RESULT M

MURC\_ECOLI

PRT;

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X52644; G42056; -. X55034; G40859; -. D10483; G216505; -

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MEDLINE; 97309380.

EVELAND S.S., POMPLIANO D.L., ANDERSON M.S.;

"Conditionally lethal Escherichia coli murein mutants contain defects that map to regions conserved among murein and folyl poly-gamma-glutamate ligases: identification of a ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P17952; 007099;

01-NOV-1990 (REL. 16, CREATED)

01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)

15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

UDP-N-ACETYLMURAMATE--ALANIE LIGASE (EC 6.3.2.8) (UDP-N-
                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                       -I- FUNCTION: CELL WALL FORMATIÓN.
-I- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
-I- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-I- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                                                                                                                                                    LIGER D., MASSON A., BLANOT D., VAN HEIJENOORT J., P. "Over-production, purification and properties of the uridine-diphosphate-N-acetylmuramate:L-alanine ligase
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-14, AND CHARACTERIZATION. MEDLINE; 95324553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE MAU B., SHAO Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "NUCLEIC ACIDS RES. 18:4014-4014(1990).
                                                                                                                                                                                                                                                                                      Escherichia coli.";
EUR. J. BIOCHEM. 230:80-87(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURI
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12 / MG1655;
MEDLINE; 97426617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YURA T., MORI H., NAGAI H., NAGATA T., ISHIHAMA A., ISONO K., MIZOBUCHI K., NAKATA A.; "Systematic sequencing of the Escherichia coli genor the 0-2.4 min region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACTERIA;
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                                                             or send an
                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                    BIOCHEMISTRY 36:6223-6229(1997).
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NUCLEIC ACIDS
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                                                                                                                                                                                          SIMILARITY; BELONGS TO THE MURCDEF FAMILY.
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                                                             email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                     MURC_PORGI
Q51831;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.

-: FUNCTION: CELL WALL FORMATION (BY SIMILARITY).

-: CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

-!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                                                                                                                                          15-JUL-1998 (REL. 36, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE-ALANINE LIGASE (EC 6.3.2.8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U67892; G2177094
PIR; JQ0545; CEECAM.
PIR; S40601; S40601.
ECOGENE; EG10619; MURC
                                                                                       STRAIN=381;
ANSAI T.;
                                                                                                                                                                                 MEDLINE; 96118684.
ANSAI T., YAMASHIT
                                                                                                                                                                                                                                                      PORPHYROMONAS GINGIVALIS (BACTEROIDES GINGIVALIS) BACTERIA; CYTOPHAGALES; BACTEROIDACEAE; PORPHYROM
                                                                                                              REVISIONS
                                                                                                                                          "A murC gene in Porphyromonas gingivalis 381.";
MICROBIOLOGY 141:2047-2052(1995).
                                                                                                                                                                      TAKEHARA T.;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                ACETYLMURANOYL-L-ALANINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259
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                                                                                                                                                                                                                                                                                                                                                                                                                                            VFQPHTFSRTQAFLNEFAESLCKADRVFLCEIF 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LESFOGTGRRFDFLGEFPLEPVNGKSGTAMLVDDYGHHPTEVDATIKAARAGWPDKNLVM
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344
491 AA;
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344 G
53626 MW;
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Y.,
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Pred. No. 4.02e-67
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D: IN MURC3.
                                                                                                                                                                                 SHIBATA Y., WACHI
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               -i- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-AL-
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE
-i- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                               "Characterization of ftsZ, the cell division gene of aphidicola (endosymbiont of aphids) and detection of CURR. MICROBIOL. 36:85-89(1998).
                                                                                                                                                                                                                                                               UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC ACETYLMURANOYL-L-ALANINE SYNTHETASE).
                                                                                                                                                                                                                                                                            15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.
                                                                                                                                                                                                                                                                                                                                051926;
15-DEC-1998 (REL. 37, CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D84504;
                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 98087557.
                                                                                                                                                                                                                BACTERIA;
                                                                                                                                                                                                                                BUCHNERA APHIDICOLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                 BAUMANN L., BAUMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-BINDING.
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Local Similarity 31.7%;
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   SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                                                                                                  BUCAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIMTNIDFDHPD-YFKDIN--DVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTSTLLAHLLKQSHVDCNAFLGGISNNYQSNLLLSDKSDLVVVEADEFDRSFHHLKPFM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOPHLYSRTADFYQDFAKSLSMLDQVVLLDIYPA-RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KE----DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFGAN-N-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126;
                                                                                                                                                                                                                  PROTEOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114
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                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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   TO THE
                                                                                                                                                                                                                  GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.50e-66;
96; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 492; DB 1;
Pred. No. 1.50e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL)
 MURCDEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38C4714B CRC32;
                                                                                                                                                                                                                SUBDIVISION;
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                                                                  + L-ALANINE
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                                                                                                               the product.";
                                                                                                                                  Buchnera
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                           NAMENO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y., MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T., HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.
                                                                                                                                                                                                                                                                                                       MURC
   Synechocystis
                                                                                          SEQUENCE FROM N.A.
MEDLINE; 97061201.
KANEKO T., SATO S.,
                                                                                                                                                                            MURC OR SLR1423
SYNECHOCYSTIS SI
                                                                                                                                                                                                        ACETYLMURANOYL-L-ALANINE SYNTHETASE).
                                                                                                                                                                                                                   15-JUL 1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                                                                                                                     P74528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF012886; G2738586;
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                Sequence analysis of the
                                                                                                                                                                                                                                                                                                                                                                    395
                                                                                                                                                                                                                                                                                                                                                                                                   437
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                                                                                                                                                                                                                                                                                                                                                                    FI-NEDLI-N-VLEQFD-NAVVLFMGAGDIQKLQN 425
                                                                                                                                                                                                                                                                                                                                                                                                  LVTNRNLILNYLLPHLNGNDIILIQGAGDIDTIIN 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKNFKGTSRRFEYVGKLFIKKKSIQNKSVMLINDYGHHPTELSETIKTIRKSWPKKNLIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAQNIQITDKGTAFDVYVDGEFYD-HFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVMNGDKKTSFLIGDG--TGM---G-LPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                 VFQPHTFSRTQAFLNEFAESLCKADRVFLCEIFGSIRE-NSGA--LTIQDLIDKIG-GAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFQPHRYTRTRNLYFDFIKILSQVDSLLILNVYSANESFISGADSFSLYSDIKKIKKNVI 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LETF-GGVKR----R-F-NETTIANQ-VI-VDDYAHHPREISATIDTARKKYPHKEVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RITSYKQSDFISNFTLIRKKQLNNLEIILNLPGEHNALNATAAIAFATYQKIPDEKIYQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPDYFKDINDVFD-AFQEMAHNVKK-GI-IAWGDDEHLRKIEADVP--IYYYGFKDSDDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138;
                                                                                                                                                            CYANOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
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   ري
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                                                                                                                                                                                                                                                                                                       STANDARD;
   strain
                                                                                                                                                                          (STRAIN PCC 6803)
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genome of the unicell PCC6803. II. Sequence
                                                                                                                                                            CHROOCOCCALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
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Pred. No. 1.09e-63;
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                                                                                                                                                                                                                                                                                                      505
              unicellular cyanobacterium
                                                                                                                                                            SYNECHOCYSTIS
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                                                                                                                                                                                                                                                                                                    B
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determination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
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MEDLINE: 9530000.

FLEISCHMANN R.D., ADAMS M.D., WHITE U., CLARLEY B.A., MER KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MER MCKENEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., SCOTT J.D., SHIRLEY R., END L.-I., GLODEK A., KELLEY J.M., SCOTT J.D., SHIRLEY R., END L.-I., GLODEK A., KELLEY J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPL_HAEIN
P43948;
01-NOV-1995
                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=RD / KW20; MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                           HAEMOPHILUS INFLUENZAE.
BACTERIA; PROTEOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANOTATION UPDATE)
UDP-N-ACETYLMURAMATE:L-ALANYL-GAMMA-D-GLUTAMYL-MESO-DIAMINOPIMELATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALA DP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

-!- PATHMAY: PEPTIDOGLYCAN BIOSYNTHESIS.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                  LIGASE (EC 6.3.2.-).
MPL OR HI0121.
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P37773; P76804;
01-OCT-1994 (REL. 30, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE:L-ALANYL-GAMMA-D-GLUTAMYL-MESO-DIAMINOPIMELATE
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BACTERIA; PROTEOBACTERIA;
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     SEQUENCE FROM
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                                                                                                                                                                  (EC 6.3.2.-).
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ilarity 29.7%;
Conservative
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  N.A.
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50074 MW;
                                                                              GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
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Pred. No.
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; 72A96638 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     367
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SEQUENCE
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"Identification of the mpl gene encoding UDP-N-acetylmuramate:
L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase in Esche
coli and its role in recycling of cell wall peptidoglycan.";
J. BACTERIOL. 178:5347-5352(1996).
-i- EUNCTION: INVOLVED IN.CELL WALL FORMATION. REUTILIZES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U14003; G537075; -. EMBL; AE000494; G1790680; EMBL; X12545; -; NOT_ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
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-!- SIMILARITY: BELLONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-K12 / MG1655;
MEDLINE; 95334362.
BURLAND V.D., PLUNKETT G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Intrinsic and extrinsic bacterial genome.";
NUCLEIC ACIDS RES. 22:475
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PEPTIDOGLYCAN SYNTHESIS; CELL DIVISION; CELL WALL;
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                                                GEQGHWQAKKLTTDASEWEVLLDGEKVGEVKWSLVGEHNMHNGLMAIAAARHVGVAPADA 301
                                                                                                                                             LNNLEFDHADIFDDLKAIQKQFHHLVRIVPGQGRIIWPENDINLKQTMA-MGCWSEQELV
                                                                                                                                                                                                                                               WILEQCGYKPGFVIGGVPGNFEVSAHLGESDFFVIEADEYDCAFFDKRSKFVHYCPRTLI
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                                                                                                 MTNIDEDHPDYFKDINDVFDAFQEMAHNVK-KGIIAWGDDE-HLRKIEADVPIYYYGFKD
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  SDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNI
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the Escherichia coli fructose-1,6-bisphosphatase gene.";
S RES. 16:8707-8707(1988).
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49874 MW;
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102; |
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Pred. No. 1.12e-53;
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A2BF8001 CRC32;
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025340;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A., NELSON K., QUACKENBUGSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., BERG D.E., GOCANNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M., COTTON M.D., WELDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E. HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000576; G2313743; TIGR; HP0623; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATURE 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 97394467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLMURANOYL-L-ALANINE SYNTHETASE).
136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HELICOBACTER
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CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.

SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).

SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
CPSFGAIIGAHSKEFDSNVRESANDSLVFEADESDSSFL-FSNPYAAIVPNTEPEHLEHY
                                                                                           VIIHSAIIKEDNKEIQRAKELEIPILŚRKDALYSILKDKRVFSVCGAHGKSSITAMLSAI
                                                                                                                                                                                                                                    HFIGIGGIGISGLAKYLKAQGATISGSDIA--ISPSVKYLKALGVEINIPHDPKAINNQD
                                                     VVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHV 122
                                                                                                                                                                           HFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVA-LRNKGIKI-LPFGANNIKEDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANALGSFINARRRLELRGEANGVTVYDDFAHHPTAILATLAALRGKVGGTARIIAVLEPR 361
                                                                                                                                                                                                                                                                                                      110;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               449 AA;
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8 (REL. 36,
8 (REL. 36,
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50793 MW;
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                                                                                                                                                                                                                                                                                                Score 422; DB 1;
Pred. No. 2.66e-53;
95; Mismatches 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                               EC3E4D2A CRC32;
                                                                                                                                                                                                                                                                                                   Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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194
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                                                                                                                                                                                                                                         Query Match
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-!- FÜNCTION: CELL WALL FORMATION (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE.
-!- ROP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
-!- PATHMAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-!- PATHMAY: PEPTIDOGLYCAN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       006225;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.
MURC OR MTCY270:16.
                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                            or send
                                                                                                                                                                                                                                                                                                                                                                                        the European Bjoinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
                                                                                                                                                                                                                                                                                              NP_BIND
                                                                                                                                                                                                                                                                                                           ATP-BINDING.
                                                                                                                                                                                                                                                                                                                           PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MURC_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: .BELONGS TO THE MURCDEF FAMILY.
                                 133 LIVALQHCGLDPSFAVGGELGEAGTNAHHGSGDCFVAEADESDGSLLQYTPHVAVITNIE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 -MN-GDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYA-IMTNIDFDHPDYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 GHDLERFFFAYEYFLDHAQKRVI-YKEDPFLKNYSKN-AI---VL-EKKDIY--NIQYIL
                                                                   61
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                                                                                                                                                                      14 HMVGTGGAGMSGIARILLDRGGLVSGSDAKESRGVH-ALRARGALIRIGHDASSLDLLPG
                                                                                                                                                                                                                       Local
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 LSHVM-NGDKKTSFLIG-D-G-TGMGLPE-S-DYFAFEACEYRRHFLSYKPDYAIMTNID
                                                                   D-MVVIQGNA-FASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGL
                                                                                                   GATAVVTTHAAIPKTNPELVEARRRGIPVVLRPAVLAKLMAGRTTLMVTGTHGKTTTTSM 132
                                                                                                                                      HFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKG--IKILPFGAN-NI-KE
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                                                                                                                                                                                                         136;
                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Swiss
                                                                                                                                                                                                                                                                           494 AA;
                                                                                                                                                                                                                                                                                              122
                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                           128
                                                                                                                                                                                                                       11.2%;
28.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute of Bioinformatics
                                                                                                                                                                                                                                                                       51176 MW;
                                                                                                                                                                                                      ; Score 349; DB 1;
; Pred. No. 8.50e-40;
107; Mismatches 185
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                                                                                                                                                                                                       Mismatches 185;
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                                                                                                                                                                                                                                                                           CRC32;
                                                                                                                                                                                                                                       Length 494;
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                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                       42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collaboration
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                                                                   118
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIRZNER S., KAPLAN A.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNECHOCOCCUS SP.
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P95836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MURC
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U86147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACETYLMURANOYL-L-ALANINE SYNTHETASE) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                 ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                     PEPTIDOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432
294 GVKRRENETTIANQV-IVDDYAHHPREISATIDTAR-K----
                                                                                                                                                     176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313
                                     118
                                                                           235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 IGGA-SFINE-DLIN--VLEQFD-NAVVLFMGAGDIQKLQNAYLDKLGMK 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193
                                                                                                               59
                                                                                                                                                                                                                             Local Similarity nes 78; Conser
                                                                                                                                                                                     1 PDHYCDLEAVISTFKTFSDNCSQLIANW-DCPTVRDRLPGTIS-YSFDPARGADYTVDQV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAPADEVLDGLAGFEGVRRRFELVGTCGVGKASVRVFDDYAHHPTEISATLAAARMVLEQ
                                                                                               SFRGSGTQARIWERGELLGRIHLPLMEAHNLSNALAAIAACRHLG-MDFASIREGLAGFE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTVPMRYVPDFSAVAQQVAAAASPGDVIVTMGAGDVTLLGPEILTALRVR 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEV---VAVFQPHTFSRTQAFLNEFAESLCKADRVFLCEIFGSIRENS-GALTIQDLIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDGGRCMVVFQPHLYSRTKAFAAEFGRALNAADEVFVLDVYGA-REQPLAGVSGASVAEH 431
                                   GARRRFEFRGSAQGIQFVDDYAHHPSELAATLAAARLQIDSGCSRLPEVPKRLVAIFQPH 177
                                                                                                                                                 PDYFKDINDVFDAFQEMAHNVKKGIIAWGDDEHLR-KIEADVPIYYYGFKDSDDIYAQNI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLDVTNIKEALETFGGVKRRFN--ET-TIANQ-VIV-DDYAHHPREISATIDTARKKYPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDDIYAQNI--QITDKGTAFDVYVDGEF-YDH---FLSPQY-GDHTVLNALAVIAISYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GETMAATLVSWQQQGVGAVAHIRLASELATAQGPRVMRLSVPGRHMALNALGALLAAVQI 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDHLDFYGSVEAYVAVFDSFVERIVPGGALVVCTDDPGGAALAQRATELGIRVLRYGSVP
                                                                       QITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAIS-YLEKLDVTNIKEALETFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDHPDYFKDINDVFDAFQE-MAHNVKKG-IIAWGDD---EHL--RKIEADVPIYYYGFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYANOBACTERIA; CHROOCOCCALES; SYNECHOCOCCUS
                                                                                                                                                                                                                                                                                                           280 AA;
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                 SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE
                                                                                                                                                                                                                                                                                                                                                                                     G1841788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (STRAIN PCC 7942) (ANACYSTIS NIDULANS
                                                                                                                                                                                                                                                   10.8%;
                                                                                                                                                                                                                                                                                                           30753 MW;
                                                                                                                                                                                                                             Pred.
50; N
                                                                                                                                                                                                                                                 Score 337; DB 1;
Pred. No. 1.29e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                         AE03BF51 CRC32;
                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2.8) (UDP-N-
                                                                                                                                                                                                                                                                   Length 280;
 --KYPH--KEVVAVFQPH
                                                                                                                                                                                                                             Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R2)
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252
 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278
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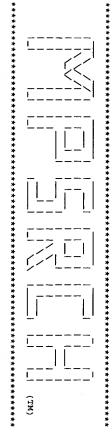
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                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MURD_ENTFA
007108;
15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: CELL WALL FORMATION. CATALYZES THE ADDI-
GLUTAMATE TO THE NUCLEOTIDE PRECURSOR UDP-N- ACET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U94707; G2149905; -. HSSP; P14900; lUAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACTERIA; FII
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MURD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURANOYLALANINE--D-GLUTAMATE LIGASE
ACETYLMURANOYL-L-ALANYL-D-GLUTAMATE SYNTHETASE)
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALANINE (UMA) (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOUGHERTY T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUCCI M.J., THANASSI J.A., DISCOTTO L.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-A24836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENTEROCOCCUS FAECALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDING ENZYME)..
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION;
     238
                                                                   182
                                                                                                     188
                                                                                                                                      122
                                                                                                                                                                 133 LLNADRTAGEARLAGN-IGFPAST-VAQEATA-KDDLVMELSSFQLMGIETF-HPQ-IAV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 TFSRTQAFLNEFAESLCKADRVFLCEIFGSIRENSGALTIQDLIDKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
                                                                                                                                                                                                    63 -VVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSH 121
                                                                                                                                                                                                                                                                                                        15
                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D-GLUTAMATE = ADP + ORTHOPHOSPHATE + UDP-N-ACETYLM
L-ALANYL-D-GLUTAMATE.
PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
DKGTAFDYYV-DGE-FY-DHFLSP--QYG---DHTVLNALAVIAISYLEKLDVTNIKEAL
                                  TKEAVEGAYLLDGKLYFNEEYIMPADELGIPGSHNIENALAAICVPKLKNVSNAQIKQSL 306
                                                                                                                                                                                                                                                                                                      LGLAKSGVSA-AKLLHELGALVTVNDAKQFDQNPDAQDLLTLGIRVVTGGHPIELLDEEF 73
                                                                                                   ITNIFEAHLDY-HGSRKEYVAAKWAIQKNMTAEDTLILNWNQVELQTLAKTTAANVLPFS
                                                                                                                                    VMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKD
                                                                                                                                                                                                                                  ELIVKNPGILYTNPLVAEALTRKIPIITEVELAGQIAE-CPIVGITGTNGKTTTTTMIGL 132
                                                                                                                                                                                                                                                                     VGIKGSGMSSLAQIMHDLGHEVQGSDIENYV-FTEV-ALRNKGIKILPFG-ANNI-KEDM 62
                                                                  INDVFDAFQEMAHNVKKG-IIA-WGDDEHLRKIEADVPIYY-YGFKDSDDIYAQNI-QIT
                                                                                                                                                                                                                                                                                                                                     6.2%;
Similarity 22.7%;
70; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                           119
456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20,00
                                                                                                                                                                                                                                                                                                                                                                                                                            125
                                                                                                                                                                                                                                                                                                                                                                                                           49758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACILLUS/CLOSTRIDIUM GROUP; ENTEROCOCCACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STREPTOCOCCUS FAECALIS)
                                                                                                                                                                                                                                                                                                                                         Pred.
91; 1
                                                                                                                                                                                                                                                                                                                                                       Score 194; DB 1;
Pred. No. 4.90e-13;
                                                                                                                                                                                                                                                                                                                                                                                                           ATP (POTENTIAL).
C469660E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                         Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UDP-N-ACETYLMURAMOYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZES THE ADDITION OF D-
UDP-N- ACETYLMURAMOYL-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KESSLER
                                                                                                                                                                                                                                                                                                                                                                          Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EC 6.3.2.9) (UDP-N-
(D-GLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                         Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                  237
                                                                                                                                                                                                                                                                                                                                         22;
```

δÃ Search completed: Wed Nov 24 00:32:46 1999 Job time : 92 secs. 307 TNFSGVPHR 315 |:|| :| 290 ETFGGVKRR 298

S. H

B

j.



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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Wed Nov 24 00:33:03 1999; MasPar time 27.28 Seconds 874.409 Million cell updates/sec

Title:

Description: Perfect Score: Sequence:

>US-09-103-287-2 (1-437) from US09103287.pep 3121 1 MTHYHFYGIKGSGMSSLAQI......GDIQKLQNAYLDKLGMKNAF 437

Scoring table: PAM 150 Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Mean 49.820; Variance 102.447; scale 0.486

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Query   Query   Query   Query   Query   Query   Pred. No.
Description
DB ID  Description  Pre  067373  UDP-N-ACETYLMURAWATE-A  084767  UDP-N-ACETYLMURAWATE-A  1.026630  UDP-N-ACETYLMURAWATE-A  1.026630  UDP-N-ACETYLMURAWATE-A  1.026630  UDP-N-ACETYLMURAWATE-A  1.026630  UDP-N-ACETYLMURAWATE-A  1.026630  UDP-N-WIRNAC-TRIPEPTID  2.067631  UDP-MURNAC-TRIPEPTIDE  3.067631  UDP-MURNAC-TRIPEPTICA  2.067641  2.064991  2.064991  2.084691  2.084691  2.084691  2.084691  2.084691  3.091003  THYROID HORNONE RECEPT  3.097681  3.091003  THYROID HORNONE RECEPT  3.007681  TRANSCRIPTIONAL ACTIVA  2.069554  UDP-N-ACETYLMURAMOYLAL  3.069554  UDP-N-ACETYLMURAMOYLAL  3.069556
Description Pre- O67373 UDP-N-ACETYLMURAMATE-A 3. O84767 UDP-N-ACETYLMURAMATE-A 3. O69551 UDP-N-ACETYLMURAMATE-A 1. O26630 UDP-MURNAC-PENTAPEPTID 2. O67002 UDP-MURNAC-PENTAPEPTID 3. O67631 UDP-MURNAC-TRIPEPTIDE 3. O58475 598AA LONG HYPOTHETICA 2. O84991 42 KDA TRANSPOSASE. 8. O94991 42 KDA PROTEIN. 1. O86491 UDP-N-ACETYLMURAMYL-TR 6. O84898 DEOXYRIBODLPYRIMIDINE 1. O86491 UDP-N-ACETYLMURAMOYLAL 3. O69554 UDP-N-ACETYLMURAMOYLAL 3. O69554 UDP-N-ACETYLMURAMOYLAL 3. O69554 UDP-N-ACETYLMURAMOYLAL 3. O69554 UDP-N-ACETYLMURAMOYLAL 3. O69555 UDP-N-ACETYLMURAMOYLAL 3. O69556 UDP-N-ACETYLMURAMOYLAL 3.
Description Pre- UDP-N-ACETYLMURAMATE-A 3. UDP-N-ACETYLMURAMATE-A 1. UDP-N-ACETYLMURAMATE-A 1. UDP-N-ACETYLMURAMATE-A 1. UDP-MURNAC-PENTAPETID 2. HYPOTHETICAL 99.3 KD 9 7. UDP-MURNAC-TRIPETIDE 2. HYPOTHETICA 2. 42 KDA TRANSPOSASE. 8. 42 KDA PROTEIN. 1. UDP-N-ACETYLMURAMYL-TR 6. DEOXYRIBODIPYRIMIDINE 1. THYROID HORMONE RECEPT 3. TRANSCRIPTIONAL ACTIVA 3. UDP-N-ACETYLMURAMOYLAL 3. UDP-N-ACETYLMURAMOYLAL 3. UDP-MURNAC-PENTAPETID 3.
Pre
Pred. No. 1.62e-91 1.62e-91 1.62e-91 3.19e-81 1.01e-03 5.01e-03 5.30e-03 3.58e-03 3.58e-03 2.63e-02 2.63e-02 2.63e-02 1.52e-01 6.37e-02 1.52e-01 6.37e-02 1.52e-01 3.59e-01

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125 AEILINAGLEPTVIIGGRLKRLGTNAKLGRGELLVSEADESDGSFLKLQPAVAVITNVDK 184

45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26	. 25	24	23	22	21
102	104	103	103	104	104	102	102	103	106	106	106	107	106	106	107	105	110	110	108	108	108	108	108	109
	•	ω .ω			ω ω		ω .ω	w		3. <b>4</b> .	3.4	3.4	ω 4	3.4			٠					ω .5		
	2919	2412	1928	1014	540	468	436	429	2457	447	374	371	354	325	321	245	1671	1661	1198	1198	1193	1161	1161	585
G	14	4	4	ν	ب	N	Ν	N	σ	N	Ν	2	IJ	ហ	N	۳	4	σı	N	N	N	N	N	N
Q26031	085431	Q92616	Q99736	Q47107	033398	Q59822	052187	051747	077375	026027	P74121	050503	P90561	002304	Q56873	028187	P77933	045497	Q45893	069277	Q45880	Q45891	069276	066671
VARIANT-SPECIFIC SURFA	RNA POLYMERASE.	MYELOBLAST KIAA0219 (F	HSGCN1 (FRAGMENT).	CYTOTOXIC NECROTIZING	MINOR STRUCTURAL GAS V	DIHYDROLIPOAMIDE DEHYD	IGG-BINDING PROTEIN SB	CONSERVED HYPOTHETICAL	MAL3P6.20 PROTEIN.	UDP-MURNAC-TRIPEPTIDE	HYPOTHETICAL 42.9 KD P	PERIPLASMIC SOLUTE-BIN	42 KDA 'D, D35E' TRANSP	T09E11.1 PROTEIN.	WBCJ PROTEIN (ORF14.8)	HYPOTHETICAL 28.6 KD P	DNA-DEPENDENT DNA POLY	SUR-2 PROTEIN.	NTNH PROTEIN.	NONTOXIC-NONHAEMAGGLUT	NTNHA.	NTNH PROTEIN.	NONTOXIC-NONHAEMAGGLUT	HYPOTHETICAL 68.4 KD P
	2.49e+00	3.27e+00			2.49e+00				1.45e+00	1.45e+00	1.45e+00	1.10e+00	1.45e+00	1.45e+00	1.10e+00	1.90e+00	4.76e-01	4.76e-01		.33e-		8.33e-01	8.33e-01	6.31e-01

### ALIGNMENTS

DO 067373  PRELIMINARY; PRT; 454 AA.  AC 067373; DT 01-AUG-1998 (TREMBLREL 07, CREATED) DT 01-AUG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE) DT 01-AVG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE) DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE) DE UDP-N-ACETYLMURAMATE-ALANINE LIGASE.  GN MUDC. OS AQUIFEX ABOLICUS. OS AQUIFEX ABOLICUS. OC BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX. RN SEQUENCE FROM N.A. RC STRAIN-VF5; RC STRAIN-VF5; RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GELLOMAN R.A., SHORT J.M., OLSON G.J., SYANSON R.V.; RT "The complete genome of the hyperthermophilic bacterium Aquifex RELDMAN B.C., COVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R. SEQUENCE FROM N.A. RL NATURE 392:353-358(1998). RP SEQUENCE FROM N.A. RC STRAIN-VF5; RR SEQUENCE FROM N.A. RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER RA GRAHAM D.E.,
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UDP-N-ACETYLMURAMATE-ALANINE LIGASE AND D-ALA-D-ALA LIGASE.
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                 FKDINDVF-DAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQIT 237
                                                                                                                                                                                                                                                                                  VVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHV 122
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                                                                                                                                              MNGDKKT-SFLIGD-GT-GM-GLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDY 178
                                                                                                                                                                                        LQEAKKNPSFAIGGLNQEGINGGSGSEYFVAEADESDGSIRCYTPEFSVITNIDDEHLSN 185
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MEDLINE; 93188700.
EIGLMEIER K., HONORE N., WOODS S.A.
"Use of an ordered cosmid library
of Mycobacterium leprae.";
MOL. MICROBIOL. 7:197-206(1993).
EMBL; ALO22602; E1287791;
026630;
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01-JAN-1998
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BROWN D., CHURCHER C.M.;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ
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069551;
01-AUG-1998 (TREMBLREL 07, CREATED)
01-AUG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE-ALANINE LIGASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARKHILL J., BARRELL B.G., RAJANDREAM M.A. SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. PARKHILL J., BARRE
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                                                                                                                                                                                                       173
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Similarity 32.7%;
66; Conservative
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235
235 -AA;
8 (TREMBLREL.
8 (TREMBLREL.
                                                                                                     PRELIMINARY;
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235
24350 MW;
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05, CREATED)
05, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDAT
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                                                                                                                                                                                                       191
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Pred. No. 1.81e-14;
47; Mismatches 73;
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J. BACTERIOL. 179:7135-7155(197).
                                                                                                                                                                                                                                                                                       DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LE GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AE000709; G2983375; -. SEQUENCE 445 AA; 49581 MW; 51EEC831 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 98196666.

DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.
GRAHAM D.E., OVERBREEK R., SNEAD M.A., KELLER M., AUJAY M., HUBE
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aguifex
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MEDLINE; 98037514.
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METHANOBACTERIUM THERMOAUTOTROE
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GFKDSDDIYAQNIQITDKGTAFDVYVDGE-FYDHFLSPQYGDHTVLNALAVIAISYLEKL 280
                                                                    SFGERGELQAQNVEVSEKGVSFEV--EGEKFFISVPSLGLVEN-ILACFCVLKV--LG-F 288
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28; Conser
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. 08, LAST AN
E SYTHETASE.
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Pred.
33; M
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LAST ANNOTATION UPDATE)
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No. 5.01e-07;
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                                                                                                                                             Mismatches
                                                                                                                                                                                   128; DB 2;
No. 2.31e-03;
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Best Local S
Matches 3
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067631;
01-AUG-1998 (TREMBLREL. 0
01-AUG-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
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O25974:
O1-JAN-1998 (TREMBLREL. O
01-JAN-1998 (TREMBLREL. O
01-NOV-1998 (TREMBLREL. O
MEDLINE; 98196666.

DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AU. FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; "The complete genome of the hyperthermophilic bacte:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOMB J. F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., FLEISCHMANN R.D., KETCHUM K.A., KLENK K.-P., GILL S., DOUGHERTY B.A NELSON K., OUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., MCKENNEY K., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M. BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M. HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL PROTEIN. SEQUENCE 856 AA; 9
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                                                                         STRAIN-VF5
                                                                                      SEQUENCE FROM N.A.
                                                                                                                  BACTERIA; AQUIFICALES;
                                                                                                                                AQUIFEX AEOLICUS.
                                                                                                                                               MURE
                                                                                                                                                          UDP-MURNAC-TRIPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of pylori[published erratum appears 25;389(6649):412].";
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                                                                                                                                                                                                                                                                                   TTIANQVIVDDYAHHP-REISATI
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AE000643; G2314608;
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Similarity 26.4%;
38; Conservative
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                                                                                                                  AQUIFICACEAE;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 7.88e-03;
35; Mismatches 61
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     bacterium
                                         W.G.,
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Best Local Similarity
P90564;
P90564;
01-MAY-1997
Q1-MAY-1997
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058475
058475;
01-AUG-1998
01-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete Sequence and Gene Organization of the Genome of Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii DNA RES. 5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y., YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y., SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHEUKU Y., FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA
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01-JAN-1999 (TREMBLREL.
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NATURE 392:353-358(1998).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYROCOCCUS HORIKOSHII.
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                                                                                                                                                                          223 FKDSDDIYAQNIQITDK-GTAFDVYVDGEFYDHF-LSPQYGD-HTVLNALAVIAISYL
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                                                                                                                                                                                                                             FSTSESFDRIEIRISGKKGRALEIYLDGEFIKRYEFKTEYGDERIVLKVRVDPGMHYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAISY-LEK-LDVTNIKEALETFGGVKRRFNETTIANQVIVDDYAHHPREISATIDTARK
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                                                                                                                                                                                                                                                                                                                                                                             AP000003; D1
WCE 598 AA;
                                                                                                                                                                                                                                                                               Similarity
19; Conser
       (TREMBLREL.
                                                                                                                                                                                                                                                                             3.8%;
larity 32.8%;
Conservative
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A; 68436 MW;
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       03,
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07, LAST SEQUENCE UPDATE)
09, LAST ANNOTATION UPDATE)
PROTEIN.
       CREATED)
                                                                                                                                                                                                                                                                          Score 120; DB 1; Lo
Pred. No. 2.63e-02;
17; Mismatches 19;
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Pred. No. 3.53e-02;
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          SEQUENCE UPDATE)
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Matches 20; Conservative
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Q94991;
O1-FEB-1997 (TREMBLREL. (
O1-FEB-1997 (TREMBLREL. (
O1-NOV-1998 (TREMBLREL. (
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WILLIAMS K., DOAK T.G., HERRICK G.;
"Developmental precise excision of Oxytricha trifallax telomere-bearing elements and formation of circles clos of the flanking target duplication.";
EMBO J. 12:4593-4601(1993).
                                                                 HERRICK G., CARTINHOUR S.W.,
"Multiple sequence versions processing family.";
                                                                                                                                     STRAIN-SUBKARYONIDE 3.5;
MEDLINE; 88118409'.
                                                                                                                                                                                                                                                           OXYTRICHA FALLAX.
EUKARYOTA; ALVEOLATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TRANSPOSON=TBE1' FAL4; MEDLINE; 86079559.
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EUKARYOTA; ALVEOLATA;
  SEQUENCE FROM
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   OXYTRICHIDAE;
                                                                                                                                                                                                                                                                                                         42 KDA PROTEIN
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SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA
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DOAK T.G., DOERDER F.P., JAHN C.L., HERRICK G.;

Pa proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common "D35E" motif.";

PROC. NATL. ACAD. SCI. U.S.A. 91:942-946(1994).
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42 KDA TRANSPOSASE.
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fallax.";
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TRANSPOSON-TBE1 FAL4;
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
  N.A.
                                             34:429-434(1987)
                                                                                                                                                                                                                                     OXYTRICHA
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                                                                                                                                                                                                                                                         CILIOPHORA;
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LAST ANNOTATION UPDATE)
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Pred. No. 8.53e-02;
27; Mismatches 33
                                                                                           of the Oxytricha
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la fallax 8
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"Internal eliminated sequences interrupting the Oxytricha 8: allelic divergence, conservation, conversions, and possible transposon origins.";
LUDOVICE A.M., WU S., DE LENCASTRE H.;

"Molecular cloning and DNA sequencing of the Staphylococcus aureus
UDP-N-acetylmuramyl tripeptide synthetase (murE) gene, essential fo
the optimal expression of methicillin resistance.";
                                                                                                                                                                                          STAPHYLOCOCCUS.
                                                                                                                                                                                                                STAPHYLOCOCCUS AUREUS. BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                             01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMYL-TRIPEPTIDE SYNTHETASE.
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DOAK T.G., WILLIAMS K., HERRICK G.;
SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
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"A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common "D35E" motif."; PROC. NATL. ACAD. SCI. U.S.A. 91:942-946(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADVPIYYYGFKDSDDIYAQNIQI
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24.1%;
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                                                                                                                                                                                                                   BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
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Pred. No. 1.52e-01;
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O84898 PRELIMINARY; PRT;
O84898;
O1.NOV-1998 (TREMBLREL. 08, CREATED);
O1.NOV-1998 (TREMBLREL. 08, LAST SET
O1.NOV-1998 (TREMBLREL. 08, LAST AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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EMBL; Y14370;
SEQUENCE 492
                                                                                                                                                                           JT 13

OPELIMINARY; PRT; 121 AA.

O91003;
O1-NOV-1996 (TREMBLREL. 01, CREATED)
O1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
THYROLD HORMONE RECEPTOR BETA 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **Species identification of Mycoplasma "Species identification of Mycoplasma "Species identification of Mycoplasma"
                                                                                                                               CTR BETA 2.
GALLUS (CHICKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              based on the uvrC genes by PCR."; MOL. CELL. PROBES 12:161-169(1998).
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BACTERIA; FIRMICUTES;
    SJOEBERG
                         TISSUE=EYE;
                                                SEQUENCE FROM N.A
                                                                                          NEOGNATHAE;
                                                                                                                 EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                            327 ILNLNDYYEKEHLV-IKNQLD :: :: | || : ||: |:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 VDESLRVFFEQFYE-DKILPDNLIVQEELLNFDLNLSSE-YK-FISPKIGTNKKVLD-LA 326
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22; Conser
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                                                                                                                 METAZOA;
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                                                                                          GALLIFORMES;
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                                                                                                               CHORDATA;
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    в.
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                                                                                        PHASIANIDAE; PHASIANINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                             346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 114; Db ...
nred. No. 1.52e-01;
nredes 27;
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LAST SEQ
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34; 1
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pred. No. 6.37e-02
    FORREST
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ANNOTATION UPDAT
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RESULT 14

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DE TRANSCRIPTION
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OG PLASMID UNDES
OC BACTERIA; PRO
OC ESCHERICHIA.
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RC STRAIN-RDEC-1
RX MEDLINE; 9020
RA WOLF M.K., BC
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RT ESCHERICHIA.
RN [2]
RL INFECT. IMMUN
RN [2]
RA CANTEY J.R.,
RT "Characterize
RT Genes necessa
RT adherence";
RL SUBMITTED (FI
DR PFAM: PFO016;
KW PLASMID.
FT CONFLICT
SQ SEQUENCE 2:
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Best Local S
Matches 1
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Best Local Similarity 25.0%;
Matches 24; Conservative
TLT 15
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069290;
01-AUG-1998
01-AUG-1998
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-RDEC-1; CANTEY J.R., MOSELEY S.L.; "Characterization of the Escherichia coli AF/R1 pilus operon: novel genes necessary for transcriptional regulation and pilus mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENT 114:39-47(1992).
EMBL; X62642; G63823; -.
THYROID HORMONE.
NON_TER 121 121
SEQUENCE 121 AA; 14088 MW
                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; AF050217; G3372510; -. FFAM: PF00165; HTH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WOLF M.K., BOEDEKER E.C.;
"Cloning of the genes for AF/Rl pili from rabbit enteroadherent Escherichia coli RDEC-1 and DNA sequence of the major structural subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-AN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
TRANSCRIPTIONAL ACTIVATOR AFRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLASMID UNDESIGNATED.
BACTERIA; PROTEOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 90202141.
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                                                                                                                                 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 HL 209
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                                                                                                                                                  61 TRAAI-LLR--FTNLKIVDISERLFYDSQQTFTREF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 TCSYPGN-V-FKSEYSDMDMALNQYNQPEYFTEEKPTFSQVQSPSYSQKKGYIPSYLDKD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 3.6%; Score 111; DB 13; Local Similarity 25.8%; Pred. No. 3.59e-01; nes 16; Conservative 19; Mismatches 22;
                                                                                                                                                                                             58 58 R -> S (IN REF. 1).
272 AA; 32359 MW; 559E9E09 CRC32;
(TREMBLREL. 07, CREATED)
(TREMBLREL. 07, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                PRELIMINARY;
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14088 MW;
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                                                                                                                                                                                                                                                           Score 111; DB 2; Length 272; Pred. No. 3.59e-01; 27; Mismatches 37; Indels
                                                                 PRT;
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STRAIN-NCTC 11168;
GRIFFITHS P.L., CONNERTON I.F.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAMPYLOBACTER. JEJUNI.
BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; CAMPYLOBACTER GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
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                                                                                                                                                                               219 YYYGFKDSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIA-ISYL
                                                  285 VKPDLKDLEKAISGFGGVCGRVEQ--VAKGVIVD-FAHTPDGIEKVLDTLKNK 334
                                                                                                                                                                                                                                                                              227 FTYGI-ENPALYQIKAYSLEEGISTIVTNKNQTF-HIDSPLLGLFNLYNLLVASACVNEL 284
278 EKLDVINIKEALETFGGVKRRFNETTIANQVIVDDYAHHPREISATIDTARKK 330
                                                                                                                                                                                                                                                                                                                                                    3.68;
Local Similarity 29.28;
nes 33; Conservation
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Pred. No. 3.59e-01;
                                                                                                                                                                                                                                                                                                                                                                                  26; Mismatches 48;
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Tabular output Run on: not generated. Sat Nov 27 08:52:25 1999; MasPar time 2239.67 Seconds 1371.578 Million cell updates/sec

Title: Description: Perfect Score: >US-09-103-287-2 (1-437) from US09103287.pep 5451

Z.A. Sequence: 1 ATGACNCAYTAYCAYTTYGT......TNGGNATGAARAAYGCNTTY 1311
TACTGNGTRATRGTRAARCA.....ANCCNTACTTYTTRCGNAAR

Scoring table: Gap TABLE bktranslate2

Nmatch STD Dbase 0; Query 0

Searched: 2883791 seqs, 1171580779 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database embl-est58

Database:

1:em\_est10 2:em\_est11 3:em\_est17 4:em\_est18 5:em\_est2 6:em\_est9 7:em\_gss1 genbank-est111 1:gb\_est12 12:gb\_est13 13:gb\_est1 9:gb\_est10 10:gb\_est11 11:gb\_est12 12:gb\_est13 13:gb\_est1 18:gb\_est15 15:gb\_est16 16:gb\_est17 17:gb\_est18 18:gb\_est19 19:gb\_est2 20:gb\_est20 21:gb\_est20 22:gb\_est20 22:gb\_est20 23:gb\_est20 23:gb\_est0 23:gb\_

Statistics: Mean 71.026; Variance 81.600; scale 0.870

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

	JOURNAL MEDLINE COMMENT	SOURCE ORGANISM REFERENCE AUTHORS TITLE	RESULT 1 LOCUS DEFINITION ACCESSION NID VERSION KEYWORDS
Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult 12-Day Embryo library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics The following repetitive elements were found in this cDNA sequence: 120-158, >GC_rich#Low_complexity	on Apr.14, 1993 this sequence version replaced gi:692983.	Norway rat.  Norway rat.  Rattus norvegicus  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  Eukheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  1 (bases 1 to 385)  Bonaldo,M.F., Lennon,G. and Soares,M.B.  Normalization and subtraction: two approaches to facilitate gene	AII13051 385 bp mRNA EST 11-FEB-1999 UI-R-E1-ff-e-02-0-UI.S1 UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1-ff-e-02-0-UI 3', mRNA sequence. AII13051. gg3513000 AII13051.1 GI:3513000

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primer:

M13 Forward

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REFERENCE
AUTHORS
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LOCUS
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AUTHORS
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ORGANISM
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Local Similarity 34.7%;
hes 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGGAAGTCCTGGCTGTCATTCAGGGCATCGGCGCCCCCTGGTGGCTTGAACACCTTGG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
Direct Submission Submitted (10-OCT-1997) Molecular Biology,
                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium.
Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                              GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment, genomic survey sequence AF029557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF029557 903 bp DNA Salmonella typhimurium strain LT2 clone
                                                           2 (bases 1 to 903) Wong, R.M.Y., Benson
                                                                                                                                                                     Wong, R.M.Y., Benson, N. and McClelland, M. End sequences of Salmonella typhimurium
                                                                                                                                                                                                                                                                 Salmonella
                                                                                                                                                                                                                                                                                         Eubacteria;
                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                            AF029557.1
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                                                                                                                                                sequences of Salmonella
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/clone="UI-R-E1-ff-e-02-0-UI"
/clone_lib="UI-R-E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacteria (Life Technologies) to generate the UI-R-E1 library. This procedure has been previously described
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/lab_host="DH10B (Life Technologies)"
113 c 101 g 99 t
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                                                                                                                                                                                                                                                                                            Proteobacteria;
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                                                              Benson, N. and McClelland, M.
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d. No. 1.25e-07;
Mismatches 50;
                                                                                                                                                                                                                                                                                         gamma subdivision;
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991-T3,
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1 (bases, 1 to 2275)

Tripodis; N. and Ragoussis, J.

Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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AF034173 Human mRNA (
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                                                                                                                                                                                                                                                                      Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
On Jan 19, 1998 this sequence
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                                                                                                                                                                                                                                             Guys Hospital
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                                                                                                                                                                                                Email: nikos@nki.nl
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ilarity 32.6%;
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/db_xxe"9="taxon:602"
/clone="991-T3, Li-Cor"
/clone="991-T3, Li-Cor"
219 c 265 g 217 t 24 oth
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/strain="LT2"
                                                                        /map="6p21.3"
/clone_lib="Human mRNA (Tripodis and Ragoussis)" 619 c 470 g 599 t 149 others
                                                    /clone="ntcon2 contig"
                                                                                                 /db_xref="taxon:9606"
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Pred. No. 2.77e-08;
53; Mismatches 185
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                                                                   NCCYTTRTCNGTDATYTGDATRTTYTGNGCRTADATRTCRTCNSWRTCYTTRAANCCR 663
                                                                                                                                      RTAYTGNGGNSWNARRAARTGRTCRTARAAYTCNCCRTCNACRTANACRTCRAANGCNGT 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tripodis, N. and Ragoussis, J. Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF034173 2275 bp mRNA EST 30-MAR-1
AF034173 Human mRNA (Tripodis and Ragoussis) Homo sapiens
clone ntcon2 contig, mRNA sequence.
AF034173
                                                                                                                                                                                                                                                                                                                                                                                                                                            Guys Hospital
7th floor, Gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
   FR0029201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Tripodis, Nikos
Division of Medical and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Primates;
1 (bases 1 to 2275)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF034173.1 GI:2707735
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Similarity 15.6%;
30; Conservative
                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jan 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                              floor, Guy's Tower, London
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  nikos@nki.nl
                                                                                                                                                                                                                                                                                      /clone_lib="Human mRNA (Tripodis and Ragoussis)"
619 c 470 g 599 t 149 others
                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                             /map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          /clone="ntcon2 contig"
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                                                                                                                                                                                                                         3.0%;
 576
dq
                                                                                                                                                                                                     Score 163; DB 20;
Pred. No. 7.59e-08;
68; Mismatches 40
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Pred. No. 1.67e-08;
86; Mismatches 74
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 DNA
                                                                                                                                                                                                       Mismatches 40; Indels
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 GSS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 AAAAAGCATCCACACATGGAAGTAGATTTGGATTTTCAACTAGAT-CCTGCTCACGTGCA 292
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                                                                                                                                                                                                                                                                                                                                                                                                                           AA110915 605 bp mRNA EST 04-FEB-1997 mm02c04.rl Stratagene mouse kidney (#937315) Mus musculus cDNA clone IMAGE:520326 5' similar to gb:J04953 Mouse gelsolin gene
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 605)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
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Elgar, G., Clark, M., Smith, S.,
Williams, G. and Brenner, S.
Direct Submission
                                                                            Unpublished On Apr 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-JUN-1998) MRC Centre, Hinxton, Cambridge,
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                                                                                                                   The WashU-HHMI Mouse EST Project
                                                                                                                                       Waterston, R.
                                                                                                                                                                                                                                                                                          Mus musculus
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Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
                                                                                                                                                                                                                                                                                                                                                         AA110915.1
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Similarity 43.0%;
                                                                          published (1996)
Apr 14, 1993 this sequence version
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/db_xref="taxon:3103"
/clone=lib="cosmid 038C04"
/clone="038C04aE2"
a 120 c 124 g 157 t
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4444 Forest Park Parkway, Box 8501,

St. Louis,

MO 63108

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REFERENCE
AUTHORS
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Local Similarity 40.2%;
                                                                                                                                       WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Apr 14, 1993 this sequence ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W29681 419 bp mRNA EST 11-SEP-1996 mc07e04.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:347838 5' similar to gb:J04953 Mouse gelsolin gene, complete
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    Location/Qualifiers
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 419)
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This clone is available royalty-free through LLNL; contact the {\tt IMAGE} Consortium (info@image.llnl.gov) for further information.
                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
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/dev_stage="4 weeks"
/lab_host="SOLR (kanamycin resistant)"
/lab_lost="SOLR (kanamycin resistant)"
/lab_lost="SOLR (kanamycin resistant)"
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/strain="C57/B16"
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                                                                                                                                                                                                                                                                           this sequence version replaced gi:785868
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                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 AGAGGTTCCTGGCGAGCTTATGCAGGAAGACCTGGCTACTGATGACGTCATGCTCCTGGA 158
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                                                                                                                               High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:219638
Seq primer: E
High quality
                                                                                                                                                                                                                                                                                     Primates: Catarrhin; Hominidae: Homo.

1 (Dases 1 to 429)

Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Furlong, J., Shaker, R., Schmidt, S., Traicoff, R. and Hood, L.E.

Construction of a Characterized Clone Resource for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ154023 429 bp
HS_2236_B1_B12_MR CIT
sapiens genomic clone
                                                                                                                                                                                                                                                          Unpublished (1998)
                                                                                                                                                                                                                                                                         Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                        GSS.
                                                                               Class: BAC ends
                                                                                              Sequence Tagged Connector
Plate: 2236 row: D colu
                                                                                                                              Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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34; Conserv
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                                            quality sequence stop: 429.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares mouse p3nMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
li2 c 122 g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ity sequence stop: 403 Location/Qualifiers
/note="Organ: sperm; Vector: pBeloBAC11;
                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:347838"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 152; DB 34;
Pred. No. 1.64e-05;
18; Mismatches 35
                                                                                              column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Approved Human Genomic Sperm Library Plate=2236 Col=23 Row=D, genomic surv
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                                                                                                                                                                              WA 98109, USA
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   BAC Clones
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 AATCATTTTGCAACTATTGGCTGAGATCACTCTGCAAAGCATGCAGTGTTTCTTCGTATC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 CAATTGATGAAGGGTTTAGGGAAATCTGCCAAGAACTTACCAT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.8%;
Local Similarity 33.0%;
hes 34; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence
                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyT not found Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier,L., Clark,M., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 436)
                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA063603.1 GI:1557570
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                                                                                                      E-Coli DH108"

/db_xref="taxon:9606"

/clone="plate=2236 Col=23 Row=D"

/clone_lib="CIT Approved Human Genomic Sperm Library
                                                                                           same fetus as the fetal lung library, Soares fetal lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                       /db_xref="GDB:1282671"
/clone="IMAGE:365967"
/clone_lib="Soares_fetal_heart_NbHH19W'
                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
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Pred. No. 6.32e-06;
26; Mismatches 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 DATDATYTGNCCNARRAARTCRTTRTANSWNACNACRTCNARYTTNARYTGRTGNGCNCK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 GAAGAGCTGACCATGGAGATGTTTGGGAAACAGCTCCATCAAGTTTGAGCTGGACATCGAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ve36b02.rl Soares mouse mammary IMAGE:820203 5' similar to gb:J0
                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 314 200 1017
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
This clone is available royalty-free through LLNL ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
On Apr.14, 1993 this sequence version replaced gi:716974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Eutheria; Rodentia;
1 (bases 1 to 455)
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AA423163
                                                                                                                                                                                                                                                                                                                                                            Seq primer: -28ml3 rev2 ET from High quality sequence stop: 165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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Similarity 34.7%;
41; Conservative
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                                                                                                                                                                        /dev_stage="19 weeks"
/lab_host="DH10B (amp
a 130 c 132 g
                                                                             adaptors (Pharmacia), digeste
the Not I and Eco RI sites of
RNA provided by Dr. Minoru Ko,
constructed and normalized by
/db_xref="taxon:10090"
/clone="IMAGE:820203"
/clone_lib="Soares mouse mammary gland NbMMG"
                                                             Bonaldo
                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                         double-stranded cDNA was ligated to Eco RI s (Pharmacia), digested with Not I and cloned into
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Pred. No. 6.32e-06;
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g 76 t 7 others
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Best Local Similarity 39.1%;
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ma82f05.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clon IMAGE:317217 5' similar to gb:X04412 GELSOLIN PRECURSOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 357
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
On May 8, 1995 this sequence version
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314 286 1810
                                                                                                            Dr. Minoru Ko (Wayne State University)."
/db_xref="taxon:10090"
/clone="IMAGE:317217"
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/dev_stage="4 weeks"
/lab_host="DH10B"
116 c 134 g 104 t
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
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Pred. No. 1.64e-05;
18; Mismatches 35
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                                                                779 AYGGNGAYCAYACNGTNYTNAAYGCNYTNGCNGTNATHGCNATHWSNTAYYTNGARAARY 838
                                                                                                 242 ATTGTGACCATACTTTATTTCATTTGCAATTTGCTGTATATAATACATAGGTTGAGAAAC 301
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                               302 TACATCTAACTCATTTGAGAGAAGCGTTTTAATTCTTT 339
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                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC, Hood I High Throughput Sequencing Center University of Washington
401 Queen Anne Avenue North, Seattle, WA Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2190 row: E column: 6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ304744 468 bp
HS_2190_A2_C03_T7 CIT
sapiens genomic clone
                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 468.
Location/Qualifiers
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                                                                                                                              h 2.8%;
Similarity 37.8%;
37; Conservative
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Shaker,R., Schmidt,S., Traicoff,R. and Hood,L.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 468)
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E-Coli DH10B"
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/clone="plate=2190 Col=6 Row=E"
/clone_lib="CIT Approved Human
                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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Pred. No. 1.02e-05;
20; Mismatches 41;
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Pred. No. 1.64e-05;
18; Mismatches 35
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Local Similarity 42.4%;
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                                                                                                                                                                                       RTTNGTCATDATNGCRTARTCNGGY 486
                                                                         AA097556 505 bp mRNA EST 15-FEB-1997 m002c08.rl Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:552398 5' similar to gb:J04953 Mouse gelsolin gene, complete
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1 (bases 1 to 482)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
91643240
AA097556.1 GI:1643240
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High quality sequence stop: 245.
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                                          AA097556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
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                                                          cds (MOUSE);, mRNA sequence.
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/lab_host="DH10B (ampicillin resistant)"
122 c 120 g 112 t 6 others
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/clone="IMAGE:295588"
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Marra, M.; Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuq Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schelleberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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On Sep 12, 1996 this sequence version replaced gi:1393053.
Mus musculus
Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                           AA839460 515 bp mRNA EST 27-FEB-1998 vw50cl2.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE:1247254 5' similar to gb:J04953 Mouse gelsolin gene, complete cds. (MOUSE); mRNA sequence.
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Similarity 39.1%;
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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house mouse.
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/lab_host="SOLR (kanamycin resistant)"
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Pred. No. 1.64e-05;
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Search completed: Sat Nov 27 09:30:05 1999 Job time: 2260 secs.
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Best Local Similarity 39.1%;
Matches 34; Conservative
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterstone D.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
WashIngton Park Parkway, Box 8501, St. Louis, MO 63108
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On Jan 19, 1998 this sequence version replaced gi:2151013.
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The WashU-HHMI Mouse EST Project
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/dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
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# ALIGNMENTS

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bacterial (especially S. aureus) infections. They are also useful against Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The MurC polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to identify modulators or specific receptors; in rational	the recombinant production of the polypeptide. Agonists of the Murc polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g.	Claim 1; Page 5; 39pp; English. The invention relates to a UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoded by the S. aureus MurC gene. Host cells containing an expression system comprising the MurC gene can be used for	N-PSDB; V80065.  N-PSDB; V80065.  New isolated MurC polypeptide from Staphylococcus aureus and related nucleic acid - useful in diagnosis, treatment and prevention of bacterial infections	07-JAN-1999. 07-JAN-1999. 26-JUN-1998; 305064. 03-JUL-1997; US-052720. (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. Burnham MKR, WALLIS NG; WPI; 99-062655/06.		URO100 standard. Drotpin. 215 ax

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                                                                                                                                                                                                                                                                                                                                                             New Isolated Murc polypeptide from Staphylococcus aureus and related promother acid - useful in diagnosis, treatment and prevention of promother acid - useful in diagnosis, treatment and prevention of promother acid - useful in diagnosis, treatment and prevention of promother acid - useful in fections a UDP-N-acetylmuramate:L-alanine ligase CC (Murc polypeptide) encoded by the S. aureus Murc gene. Host cells CC (Murc polypeptide) encoded by the S. aureus Murc gene can be used for the recombinant production of the polypeptide. Agonists or the Murc CC (CC polypeptide are used to treat conditions requiring increased activity or CC expression of the polypeptide. Antagonists, inhibitory nucleic acid or CC competitive polypeptide are useful for inhibiting the polypeptide e.g. CC bacterial (especially S. aureus) infections. They are also useful against CC The antibacterial agents are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The Murc polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising contained the polypeptide is also useful for antibodies; to identify modulators or specific receptors; in rational
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Best Local
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31-OCT-1996; US-029960.
(HUMA-) HUMAN GENOME SCI INC.
Choi GH, Hromockyj A, Johnson LS, Kunsch CA;
WPI; 98-27224/24.
N-PSDB; VZ-7381.
Nucleic acid encoding antigenic peptide(s) from Strept pneumoniae - or their epitope-containing fragments, us protective or therapeutic vaccines, and for diagnosis claim 11; Page 73; 118pp; English.
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Best Loo
Matches
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24-SEP-1996; US-027032.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus protein of unknown function.
Staphylococcus aureus protein; immune response induction; eye infection;
antibody production; T-cell immune response; gastrointestinal infection;
respiratory infection; inhibitor; bacterial infection; cardiac infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        especially useful Sequence 46 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respiratory tract and central nervous system Claim 11; Page 329; 390pp; English.
This sequence represents a Staphylococcus aureus protein of unknown function, and is encoded by a DNA sequence of the invention.
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Biosynthesis; recombinant; antibacterial; bacterial cell wall; uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to
                                           (ELIL ) LILLY & CO EL Hoskins JA, Peery RB, WPI; 99-008720/01.
                                                                                                                14-APR-1997; 843309.
18-JUN-1996; US-665435.
14-APR-1997; US-843309.
                                                                                                                                                                                                                              Streptococcus
                                                                                                                                                                                                                                                           drug design; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
  Streptococcus
                       N-PSDB; V33970.
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drug screening
Claim 2; Columns 21-22; 13pp; English.
The present sequence represents Streptococcus pneumoniae MurD protein
(uridine-diphosphate-N-acetylmuramy1-r-lany1-p-isoglutamate ligase).
The MurD protein is useful in a method for identifying compounds
that inhibit Streptococcus pneumoniae MurD activity. Compounds
that inhibit screptococcus pneumoniae MurD activity. Compounds
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This is the amino acid sequence of the Streptococcus pneumoniae murb biosynthesis protein. The murb gene encodes the enzyme uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligase. The nucleic acid can be used for the production of recombinant Murb protein and the implementation of large scale screens to identify new antibacterial compounds targeted at the stem peptide biosynthetic pathway involved in the synthesis of the bacterial cell wall. Structural analysis of the Murb protein will enable structure-based drug design to develop novel compounds for the treatment of antibiotic
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N-PSDB; T89154.
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18-JUN-1996; US-665435.
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Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are also useful for generating vaccines for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in pylori or for use in detecting the presence of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pMPX vectors to construct a series of shotgun subclone libraries. The purified DNA samples were then
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15-NOV-1996; U18542.
17-NOV-1995; US-561469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents an H. pylori cytoplasmic protein outer membrane or cell wall biosynthesis. This sequence
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33; Mismatches 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide(s) useful for vaccines to treat or infection, and to detect Helicobacter Claim 61; Page 335; 1481pp; English.
This sequence represents a H. pylori cytoplasmic outer membrane or cell wall biosynthesis.
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Cytoplasmic; vaccine; prevention; treatment;
identification; binding compound; bacterium;
bacteria; inhibitor; duodenal ulcer disease;
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N-PSDB; T67723.
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytoplasmic; o
Helicobacter p
WO9640893-Al.
19-DEC-1996.
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WPI; 97-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori nucleic acid sequences and polypeptide(s) - useful for vaccines to treat
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Vaccine; prevention; treatment; infection; location; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; cytoplasmic; outer membrane; cell wall; biosynthesis.
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W20606 standard;
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97-052306/05.
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gcncayconacngarathggnacnacnytnaarwsngcnmgna
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                                        standard;
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Similarity 38.0%;
63; Conservative
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US-487032.
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Mismatches 67;
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Sclaim 7; Page 22; 33pp; English.

The peptides W77376-W77390 can be modified by the method of the invention by substituting at least one amino acid of the peptide to provide a peptide having at least one amino acid which is modifiable by a reaction and replacing other amino acids in the peptide with amino acids which are not modifiable by the reaction. The methods can be used for the modification of biologically active peptides such as hormones, drugs, toxins and peptides which act on lipid bilayer membranes. The modified peptides can be used e.g. in the body of an animal or plant or parts in corder to affect the structure or integrity or permeability of a foreign body such as a microorganism, parasite or virus present in the body of the animal or plant or within the cells of the body of the animal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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18-MAR-1998; G00799.
18-MAR-1997; GB-005519.
(ANNA-) ANNAT TECHNOLOGY L'
Ajoula HS, Clarke DJ;
WPI; 98-521161/44.
                             Disclosure; Fig 7; 69pp; English.

The gene cluster nisABTCIPRK (see T29660 and T29661) of Lactococcus lactis includes the nisA gene coding for pre-nisin A (R95267, see also R95263) and the genes for nisin modification, secretion and immunity. nisB (R95268) and nisc (R95270) are believed to be involved in reactions that modify pre-nisin; nisT (R95269) is similar to a transport ATPase and is involved.
                                                                                                                                                                                                                                                 Making cell which expresses nisin but does gene by providing cell with variant nish modification, secretion and immunity Disclosure; Fig 7; 69pp; English.
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30-MAY-1996.
20-NOV-1995; G02699.
19-NOV-1994; GB-023404.
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Lactococcus lactis st
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R84924;
18-MAR-1996
                                                                                                                                                                                                                           The present peptide is a specific example of a cationic oligopeptide corresp. to the formula (b-1-1-b)n, where b is a hydrophobic amino act l is a hydrophilic amino acid and n is at least. In this case, when b is Leu, l is Lys and n = 10, the oligopeptide forms an alpha-helix which forms a stable complex with a nucleic acid. The complex is suitable for transferring nucleic acid, esp. in gene therapy.
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T 14
W20605 standard;
W20605;
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nucleic acid to cells in gene therapy.
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The protein may be used in a vaccine to prevent or treat

H. pylori infection or to identify H. pylori polypeptide binding

compounds, useful as potential H. pylori life cycle activators or

inhibitors. The genomic sequence of H. pylori ATCC 55679) was

determined from overlapping contigs generated by mechanically

shearing the bacterial DNA. The sequences were analysed for ORF of

at least 180 nucleotides, and the predicted coding regions defined

by computer evaluation. To identify likely H. pylori antigens for

vaccine development, the amino acid sequences predicted from

various ORF were analysed for significant homology to other known

or exported membrane proteins. Having identified and determined

the sequences of interest, particular regions can be isolated from

H. pylori by PCR amplification for recombinant polypeptide
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19-DEC-1996:
06-JUN-1996: U09122.
07-JUN-1995: US-487032.
01-APR-1996: US-630405.
                                                                                                                                                                                                                                                                                                     FIV PPR envelope protein sequer Feline immunodeficiency virus; T-lymphotropic lentivirus; FIV
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R51250 standard; peptide; R51250;
R51250; (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1032
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                             region
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Sequence
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                                               "Surface glycoprotein"
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                                                                                                                                                                                                                                                         feline immunodeficiency virus (FIV) envelope protein from different strains and serotypes. The consensus sequence basedon these, is given in R51247. The synthetic FIV peptides of the invention were derived principally from a combination of the sequences of the FIV UK 8 and Petaluma isolates, a composite sequence of which is given in R51246. Variations in the sequence may occur between different strains or serotypes, isolates of different geographical origin or even between different isolates from the same host.
                                                                                         1975
                                                                                                                                                                   1915
                                                                                                                                                                                                                                                                                                                                                                          Feline immunodeficiency virus antigenic polypeptide(s) and nucleic acid - used to prepare prods. for combating or diagnosis of feline immunodeficiency infection Disclosure; Figure 2; 68pp; English.

The sequences given in R51248-R51262 and R58584-85 represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                            (PITM ) PITMAN MOORE Francis MJ; WPI; 94-118168/14.
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20-SEP-1993; G01974.
21-SEP-1992; GB-019936.
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Similarity 33.7%;
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539..565
/note= "V5 region"
609..854
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~ "V4
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Pred.
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No. 7
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Collins.		********
Release 3 1A John F. Collins. Biocomputing Research Unit.		1. 移动的格式作品的格子的格式的格式的格式的格式的格式的表示表示表示的格式的表示的格式的表示的表示的表示的表示的表示的表现的表示的。
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Tabular output not generated. Run on: Wed Nov 24 02:02:02 1999; MasPar time 37.77 Seconds 1248.882 Million cell updates/sec

Title: >US-09-103-287-3 (1-660) from US09103287.seq 3300

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 ATTTAAAGATTCGGATGACA......GCGTTTTAATATGTTTATAA 660 TAAATTTCTAAGCCTACTGT.......CGCAAAATTATACAAATATT

Scoring table: TABLE bktranslate2 Gap 30

Nmatch STD : Dbase 0; Query 0 122461 seqs, 35738955 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 51.934; Variance 314.343; scale 0.165

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

5.4 4.2 4.2 4.2 4.2 4.2 1.3 2.3 2.3 2.3 2.3 2.3 2.3 2.3 2	% Result Query NO. Score Match Length DB ID 1 182 5.5 450 2 US-1 2 182 5.5 450 1 US-1
-08-934 Sequence 4, -08-934 Sequence 2, -08-687 Sequence 98, -08-649 Sequence 97, -08-649 Sequence 108-649 Sequence 108-649 Sequence 108-649 Sequence 108-649 Sequence 24, -08-649 Sequence 23, -07-999 Sequence 24, -08-426 Sequence 22, -08-401 Sequence 24, -08-40	Description
	Pred. No

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112	Sequence 2, Application US/08843309	ation US/08843	309			
1	Datont No 502/370					

GENERAL INFORMATION: APPLICANT: Skatrud, Paul
APPLICANT: Peery, Robert
APPLICANT: Hoskins, Johnn
APPLICANT: Hoskins, Johnn
APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: Biosynthetic Gene Mur D of Streptococcus pneumoniae
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana

COUNTRY:

ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/843,309
FILING DATE:
FILING DATE: CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D
REGISTRATION NUMBER: 39,

REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-334
TELEPAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2: x-9900

SEQUENCE CHARACTERISTICS:

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                                                                                                            TELEFAX: 317-276-3001
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2,
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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                             MOLECULE
                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                     TOPOLOGY:
                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-9900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/665,435A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                     LENGTH:
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                                                                          amino acid
                             TYPE:
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                                                                                             450 amino acids
PE: protein AA; 48579 MW; 1010380 CN;
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VENTION: Biosynthetic Gene MurD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peery,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peery, Robert
Hoskins, JoAnn
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Pred. No. 2.59e-01;
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45; Similarity

Conservative

47;

Indels

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Gaps

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Query Match
Best Local S
Matches 4
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Best Local Similarity
Matches 46; Conser
                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08934481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/0893448. Patent No. 5929045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 ACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTT 231
                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: ...267 amino acids
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,481
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wallis, Nichola G.
APPLICANT: Fueyo, Joanna L.
APPLICANT: Lonetto, Michael A.
TITLE OF INVENTION: NOVEL MUTD
NUMBER OF SEQUENCES: 6
                                                                                                             REFERENCE/DOCKET NUMBER: GN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
                                       TYPE: amino ac
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               STREET: 4000 Bell (CITY: Philadelphia
                                                                                               TELEX:
                                                                                                                                                                   FILING DATE:
                                                                                                       TELEFAX: 215-994-2222
                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                   267 AA; 29079 MW; 348410 CN;
                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ħ
Score 177; DB 2;
Pred. No. 4.83e-01;
18; Mismatches 47
                                                                                                                                         28,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 182; DB 1;
Pred. No. 2.59e-01;
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                Length 267;
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                                                                                      SEQUENCE
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                     820
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                                               SEQUE...
LENGTH: 4..
TYPE: amino actu
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: 146 AA; 47982 MW; 998066 CN;
5.4%; Score 177;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lonetto, Michael A. TITLE OF INVENTION: NOVEL MurD
                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
         ACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTT T N I K E A L E T F G G V K R R
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CATACAGTTTTAAAATGCATTAGCTGTAATTGCGGATTAGTTTAGAGAAAGCTAGATGTT H T V L N A L A V I A I S Y L E K L D V
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                                                                                                                                                               TELEPHONE: 215-994-22
TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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4000 Bell Atlantic Tower, 1717 Arch Stre
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                                                        Score 177; D
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                                                Mismatches
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                                                        DB 2;
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                                                                                     TELEFAX: (610)454-3808 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                       STRANDEDNESS:
TOPOLOGY: 11:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (610)454-3839
                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FR 9 FILING DATE: 08-FEB-1994
                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: PatentI
                                                                                                                   REFERENCE/DOCKET NUMBER: 38
                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                          STREET: 500 Arcola CITY: Collegeville
                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                     STATE:
                                                                     LENGTH:
                                                                                                    TELEPHONE:
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  Similarity 33; Conser
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                                                             amino acid
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  Conservative
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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                                               linear
                               1845 MW; 9
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        4.28;
27.78;
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                                9430 CN;
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Score 140; DB 2;
Pred. No. 4.01e+01
31; Mismatches 5
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ID US-08-649-991-98
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                                                      Query Match
Best Local S
Matches 2
                                                                                            SEQUENCE
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          168
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Natura, Remy
APPLICANT: Roques, Pierre
APPLICANT: Roques, Pierre
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS DERIVED FROM THE
TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES
TITLE OF INVENTION: MAPPLICATIONS AS REAGENTS FOR EVALUATION OF
TITLE OF INVENTION: MATERNOFOETAL TRANSMISSION OF HIV-1
NUMBER OF SEQUENCES: 130
                            269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 98, Application US/08649991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447
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                                                                                                                                                        TELEPHONE: 202-467-700
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                         MOLECULE TYPE: peptide
JENCE 132 AA; 14772 MW;
                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,991
FILING DATE: 17-MAY-1996
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acid
                                                                                                                                                                                                                     APPLICATION NUMBER: FR 9505914 FILING DATE: 18-MAY-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
AGAAGCTAGATGTTACAAATATTAAAGAAAGCATTAGAAACGTTTG
K L D V T N I K E A L E T F
                  K I D V K D T K E A L E K I ARAARATHGAYGTNAARGAYACNAARGARGCNYTNGARAARATHG
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                                                                                                             STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                            NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: OR
                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                             CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                       Similarity 23; Conser
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                                                                                                                              amino acid
                                                       Conservative
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                                                                                                                                                                 : 202-467-7000
202-467-7176
                                                                                                             linear
                                                              4.28;
                                                                                                                                        amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                               Score 137; DB 2;
Pred. No. 5.64e+01;
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                                                                                           82400 CN;
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                                                       Mismatches
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                                                      10; Indels
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                         US-08-649-991-97
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                                                                        Sequence 62,
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                                                                                                                                                                       Local Similarity
nes 23; Conser
                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: ~132 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FR 950
FILING DATE: 18-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,98
                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: OF TELECOMMUNICATION INFORMATION: TELEPHONE: 202-467-7000 TELEFAX: 202-467-7176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                            MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Narwa, Remy
APPLICANT: Roques, Pierre
APPLICANT: ROQUES, PIERRE
TITLE OF INVENTION: NUCLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                      TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1800 M S
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 17-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                             IE TYPE: peptide
132:AA; 14772 MW;
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llarity 51.18;
Conservative
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5919462
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                                                                                                                                                                                                                                            TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                          linear
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                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEIC ACID FRAGMENTS DERIVED FROM THE HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND APPLICATIONS AS REAGENTS FOR EVALUATION OF THE MATERNOFOETAL TRANSMISSION OF HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130
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                                                                                                                                                                    Score 137;
Pred. No. 5.
12; Mismatc
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5.64e+01;
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CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: FR 9505914
FILING DATE: 18-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
NAME: Adler, Reid G.
ODERSON
                                                                                                                                                                                                                                                                                                                              Sequence 108, Application Patent No. 5919462
                                                                                                                                                                                                                                                                                                                                                                                       269 ARAARATHGAYGTNAARGAYACNAARGARGCNYTNGARAARATHG
                                            Patent No. 5919462
GENERAL INFORMATION:
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Local Similarity 51.1%;
les 23; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Narwa, Remy
APPLICANT: Roques, Pierre
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: HIV-1 V
TITLE OF INVENTION: APPLICA
TITLE OF INVENTION: APPLICA
TITLE OF INVENTION: MATERNO
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: ORI
TELECOMMULICATION INFORMATION:
TELEPHONE: 202-467-7100
TELEFEAX: 202-467-7176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
JENCE 132 AA; 14772 MW; 82400 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
      APPLICANT:
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FILING DATE: 17-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 20036-5869
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                                                                                                                           108, Application US/08649991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 amino acids
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Roques, Pierre
                         Narwa, Remy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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12; M
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Pred. No. 5.64e+01;
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Best Local :
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                    ADDRESSEE:
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NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE_DOCKET NUMBER: ORES
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEPAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               Sequence 86, Application US/08649991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 86, Application US/08649991 Patent No. 5919462
                                                                                                                                                                                               GENERAL INFORMATION:
                                                                       APPLICANT: ROQUES, PIETRE
TITLE OF INVENTION: MUCLEIC ACID FRAGMENTS DERIVED FROM THE
TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES
TITLE OF INVENTION: APPLICATIONS AS REAGENTS FOR EVALUATION OF
TITLE OF INVENTION: MATERNOFOETAL TRANSMISSION OF HIV-1
                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
JENCE 132 AA; 14860 MW; 86327 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FR 9
FILING DATE: 18-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/00
FILING DATE: 17-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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Similarity 51.1%;
23; Conservative
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1800 M Street,
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  MORGAN, LEWIS
00 M Street, N
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                                                         130
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Pred. No. 5.64e+01;
12; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 109, Application US/08649991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269
                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Narwa, Remy
APPLICANT: Noques, Pierre
APPLICANT: Roques, Pierre
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS DERIVED FROM THE
TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND THEIR
TITLE OF INVENTION: APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF
TITLE OF INVENTION: MATERNOFOETAL TRANSMISSION OF HIV-1
                                                                                                                                                                                                                                                                                                                                              Sequence 109, Application US/0864999: Patent No. 5919462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-467-7176 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: ORES
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
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APPLICATION NUMBER: FR 9505914
FILING DATE: 18-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: 3412- 7213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                     COUNTRY: USA
ZIP: 20036-5869
                                                                                                                           CITY: Washington
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TOPOLOGY: 11
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/649,991 FILING DATE: 17-MAY-1996
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llarity 51.1%;
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                                                                                                                                             E: MORGAN, LEWIS & BOCKIUS LLP
1800 M Street, N.W.
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Pred. No. 5.64e+01;
12; Mismatches 1(
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Best Local
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Sequence 88, Application US/08649991
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                                                                                            ZIP: 20036-8869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER:, IBM PC compatible
OPERATING: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, \
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.2%;
Local Similarity 51.1%;
hes 23; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
             CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROQUES, PIETRE TITLE OF INVENTION: NUCLEI TITLE OF INVENTION: HIV-1 TITLE OF INVENTION: APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: OR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-407-7000
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 17-MAY-19
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                  STREET: 1800 M S. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                APPLICATION NUMBER: US/0:
FILING DATE: 17-MAY-1996
                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LE TYPE: peptide
135 AA; 15084 MW;
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Adler, NTMBER: 30,988
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                                                                                                                                                                                                                                                                      E: MORGAN, LEWIS & BOCKIUS LLP
1800 M Street, N.W.
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                                                                                                                                                                                                                       USA
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UMBER: FR 9505914
18-MAY-1995
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                                                                                                                                                                                                                                                                                                                                       NUCLEIC ACID FRAGMENTS DERIVED FROM THE HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES APPLICATIONS AS REAGENTS FOR EVALUATION OF MATERNOFOETAL TRANSMISSION OF HIV-1
                                                                                                                 Release #1.0, Version #1.30
                                                                                 US/08/649,991
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Pred. No. 5.64e+01;
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Best Local :
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US-07-999-280A-24
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Patent No.
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Local Similarity 51.18;
hes 23; Conservation
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/999,280A
FILING DATE: 28-DEC-1992
CLASSIFICATION: 435
                  ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip
REGISTRATION UTWBER: 31,395
REFERENCE/DOCKET NUMBER: 0681
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                 GENERAL
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TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 88:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                        APPLICANT: LADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTHA, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acid
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 24
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NAME: Adler, Reid G.
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                                                                                                                                                                                                      CITY:
STATE:
                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 94662-8097
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o. 5573930
                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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132 AA; 14758 MW; 86359 CN;
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: California
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                                                                                                                                                                                                                                                                                               COYNE, MAZIE YEE
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Pred. No. 6.32e+01;
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                                                                  Philip L.
                                                 0681.007
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Best Local Similarity 34.5%;
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXX
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                          INFORMATION FOR SEQ ID NO:
                                                                                                                               SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MCGATTIGLE JI., Phili
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 061
                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   CITY: Emveryville
STATE: California
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                                                                                                             FILING DATE: 21 CLASSIFICATION:
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                                            TELEFAX:
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NOBLE, JANELLE A.
MARTIN, GEORGE A.
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Pred. No. 7.91e+01;
25; Mismatches 32
                                                                                        Philip L.
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 552 AA; 60648 MW;

1595921 CN;

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Best Local S
Matches 3
APPLICATION NUMBER: US/07/999,280A
FILING DATE: 28-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCGATT191e JT., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 601-2718
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 552 AA; 60648 MW; 1595921 CN;
     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/07999280A
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Local Similarity 34.5%; Pred. No. 7.91e+01;
nes 30; Conservative 25; Mismatches 32; Indels
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APPLICANT:
APPLICANT:
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APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
TITLE THE TOTAL PRODUCT - R440, P.O. Box 8097
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YAAYAAYWSNTTYGCNAARTGYWSNWS 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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5573930
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NOBLE, JANELLE A.
MARTIN, GEORGE A.
KAWASAKI, ERNEST S.
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Matches 3
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CTGCAAATTCATTTAAAAAATGCTTGTG 378
C K F I * K C L
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YAAYAAYWSNTTYGCNAARTGYWSNWS
                                                       30;
                                                                                         1.18;
Similarity 34.58;
                                                                                  Conservative
              Score 134; DB 1;
Pred. No. 7.91e+01;
25; Mismatches 32
                      539
                                                                                                Length 552;
                                                                                   Indels
                                                                                  0;
                                                                                  Gaps
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                                                               512
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Search completed: Wed Nov 24 02:04:25 1999 Job time: 143 secs:

A. I. John F. Collins. Biocomputing Research Unit. (C) 1993-1998 University of Ednburgh. U. K. Distribution rights by Oxford Molecular Ltd A. I.	1 63 2 13 3 13 6 4 13 6 6 4 7 7 3 6 7 3 7 9 3 7 0 10 3 8 13 9 3 13	nd is	. "	Database: Database:	Post-processing	ched:	Scoring table	Title: Description: Perfect Score N.A. Sequence Comp:	MPsrch_nn i Run on: Tabular outp	Re.	
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## ALIGNMENTS

		CDS	gene		source	FEATURES		JOURNAL	TITLE	AUTHORS	REFERENCE	JOURNAL	TITLE	AUTHORS	REFERENCE		0101111011	SOURCE	KEYWORDS	VERSION	NID	ACCESSION	DEFINITION	RESULT 1 LOCUS
/protein_id="AAB87090.1"	/gene="murc" /function="cell wall biosynthesis" /note="Mirro: HTDP-N-acettlmuramate-alaning ligace"	/gene="mutC" 11314	11314	/organism="Staphylococcus aureus" /db_xref="taxon:1280"	11314	Location/Qualifiers	Hospital and Harvard Medical School, 181 Longwood Ave, Boston, MA 02115. USA	Submitted (11-NOV-1997) Channing Laboratory, Brigham and Women's	Direct Submission	Lowe, A.M. and Deresiewicz, R.L.	2 (bases 1 to 1314).	Unpublished	Cloning and sequencing of Staphylococcus aureus murC, a gene	Lowe, A.M. and Deresiewicz, R.L.	1 (bases 1 to 1314)	Bacillaceae: Staphylococcus.		Staphylococcus aureus.		AF034076.1 GI:2642658		AF034076		AF034076 1314 bp DNA BCT 26-NOV-1997

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KEYWORDS
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LEKLDYTNIKEALETFGGVKRRFNETTIANQVIYDDYAHHPREISATIETARKKYPHK
EVVANFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKIEG
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SVAVYGAHGXISTNIDFDHPDYFKDINDVFDAFQEMAHNVKKGIIAMGDDEHLRKIEADVPI
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/note="-
                                                   /note="open reading frame
/including the TGA stop)
                                                                                                                                                    /translation="MMSKDGINSKDFLIGTLIGGIIGATTALFLAPKSGKELRDDLGS
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1172. .1177
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/note="similar to plant water
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Best Local
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Local Similarity 61.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGTACGGCCACCAATGTATTAAACTCATTGGCGGTCATTGCGTTATGCCATTATGAAG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATATCCAAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATAAAAGTGACAATCGAGGCGGCAAGACAGAAGTATCCTGATCGGGAAATTGTCGCGG
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Kunst,F., Ogasawara,N., Moszer,I., Albertini,A.M., Alloni,G.,
Azevedo,V., Bertero,M.G., Bessieres,P., Bolotin,A., Borchert,S.,
Borriss,R., Boursier,L., Brans,A., Braun,M., Brignell,S.C.,
Bron,S., Brouillet,S., Bruschi,C.V., Caldwell,B., Capuano,V.,
Carter,N.M., Choi,S.K., Codani,J.J., Connerton,I.F., Cummings,N.J.,
Daniel,R.A., Denizot,F., Devine,K.M., Dusterhoft,A., Ehrlich,S.D.,
Emmerson,P.T., Entian,K.D., Errington,J., Fabret,C., Ferrari,E.D.,
Foulger,D., Fritz,C., Fujita,M., Fujita,Y., Fuma,S., Galizzi,A.,
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299119 AL009126
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Bacteria; Firmicutes;
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No. 1.11e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Regulation de l'Expression Genetique, 28 rue du Docteur Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E. Grandl, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwo Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \label{eq:Kunst,F.,Ogasawara,N.,Yoshikawa,H.} and \ Danchin,A. \\ \ Direct \ Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45 68 89 48
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TPILLSRKGLSPRKVVGTVDTSEFAIAVSATAGFLISLGWEDVNWLWVFSLMAGGIIA
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/protein_id="CAB14907.1"
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                                                                                                                                                                                                                                                                                                                                                                    complement(1020. .2270)
                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1020.
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/gene="ytnM"
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                                                                                                /db_xref="PID:g2635413"
                                                                                                                                                                                                                                                                                                                                                                                                       /gene="hipO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bacillus subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .215640
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                                                              'db_xref="GI:2635413"
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ech,J., Harwood,C.R.,
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gene

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DIDALPIEEKTGLPYASKHKGIMHACGHDFHTAALLGAAFLLKENQDSLKGKIRLLEQ
PAEEAGAGTKVIEDGQLDGIDAYGLHNKPDIAVGTVGKINGGSTWNVIPDG
KGAHAALPHNGEDPIIGASQLLVALQTIVSRNVNPLQSAILTVGKINGGSTWNVIPDT
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RDAAHKAKLQVIDPAPSTAGEDFAYYLEHIPGSFAFFGTDGDHDWHHPAFTIDETAII
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complement(4352. .4633)
/gene="ytn1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLWNSWEHDAFIHNKKTGQFFDQAKLHRLNHKGKYFQVEGPLNIGRSKQGEPVVFQAG
SSETGRQFAAKNADAIFTHSNSLEETKAFYADVKSRAADEGRDPSSVRIFPGISPIVA
DTEEEAEKKYREFAELIPIENAVTYLARFFDDYDLSVYPLDEPFPDIGDVGKNAFQST
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PfTISRQLMSLDHISGGRAGWNLVTSPQEGAARNHSKSNLPEHTERYEIAQEHLDVVR
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SYVEESEENILG"
                                                                                                                                                                                                                                                                                  complement(4648.
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/gene="ytnJ"
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SLTKQIKKDISCVAKRFELIGIMAPNKKESLLSHQELNLPDLCFYKKCNNLYGVNRGV
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                                                                                                                                                            /codon_start=1
                                                                                                                                                                                   'note="similar to hypothetical proteins"
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/db_xref="GI:2635414"
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//note="alternate gene name: ytnK"
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/translation="MIRLSILOQSLIGEGETAADTLOHTVKLAQMAEECGYHRFWVAE
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DLGVCKAPGGEVLSTDALQAEYKKPVRQFDEKLEELTHFVRDDFPDTHRYAALAPRPQ
VDRKPGIFLLGGSTESAISAAKLGISFVFAYFINGEEEVLKEARRAFDAHLPPGSEAE
FHLAPAVFAAHTKEEAEKHIVSRESIKVVLKDGRKVNVGSREQAEAYLENVTEPYDII
                                                                                                                                       complement(6425. .7132)
                                                                                                                                                                                       EQGTPEEVFRHTKKDRTRQFLRRVSPEYLFEPKEHIKEPVI"
complement(6425...7132)
                                                                                                                                                                                                                                             /translation="MIEIKNIHKQFGIHHVLKGINLTVRKGEVVTIIGPSGSGKTTFL
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LLFDEPTAALDPELVGEVLEVMLEIVKTGATMIVVTHEMEFARRVSDQVVFMDEGVIV
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/transl_table=11
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                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                               /db_xref="PID:g2635418"
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                                                                                                              /gene="ytmM"
                                                                                                                                                                      /gene="ytmM"
                                                                                                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:034900"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="histidine transport protein (ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQKTGIIAGTKEEVAEELTRLSGTYKINDFVIFTPIKNAVEKQLSYQLLSDAVLAAKR
                                                                                       function="unknown"
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                                                        amino acid ABC transporter (permease)"
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Note: remainder of annotations omitted.

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Ogasawara, N., Moriya, S., Mazza, P.G. and Yoshikawa,
Nucleotide sequence and organization of dnaB gene
genes on the Bacillus subtilis chromosome
Nucleic Acids Res. 14 (24), 9989-9999 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 153210 to 153762)
Connors,M.J., Mason,J.M. and Setlow,P.
Cloning and nucleotide sequencing of genes for three acid-soluble proteins from Bacillus subtilis spores
J. Bacteriol. 166 (2), 417-425 (1986)
CO-ordinate expression of the two threonyl-tRNA synthetase generallus subtilis: control by transcriptional antitermination involving a conserved regulatory segmence
                                                                                                                                                                                                                          7 (bases 133624 to 134990)
Henkin,T.M., Grundy,F.J., Nicholson,W.L. and Chambliss,G.H. Catabolite repression of alpha-amylase gene expression in Ba subtilis involves a trans-acting gene product homologous to Escherichia coli lacl and galk repressors
MOL. Microbiol. 5 (3), 575-584 (1991)
                                                                                                                                                                                                                                                                                                                                                     6 (bases 142232 to 144147)
Grundy, F.J. and Henkin, T.M.
Cloning and analysis of the Bacillus subtilis ribosomal protein S4
J. Bacteriol. 172 (11), 6372-6379 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seki,T., Yoshikawa,H., Takahashi,H. and Saito,H. Cloning and nucleotide sequence of phoP, the regulatory alkaline phosphatase and phosphodiesterase in Bacillus s. Bacteriol. 169 (7), 2913-2916 (1987)
                                                                                                                 Henkin, T.M., Glass, B.L. and Grundy, F.J.
Analysis of the Bacillus subtilis tryngene: conservation
regulatory sequence in multiple tRNA synthetase genes
J. Bacteriol. 174 (4), 1299-1306 (1992)
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Nucleotide sequence of the Bacillus subtilis pho
OCEACTE (1988)
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Putzer, H., Gendron, N. and G
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een, C.J., Stewart, G.C.,
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                                                                                        Yocum, R.R., Perkins, J.B., Howitt, C.L. and Perc
Cloning and characterization of the metE gene
S-adenosylmethionine synthetase from Bacillus
J. Bacteriol. 178 (15), 4604-4610 (1996)
                                                                                                                                                                                                                                                                                                                                                     18 (bases 129888 to 132207)
Varon, D., Brody, M.S. and Price, C.W.
Bacillus subtilis operon under the d
stress transcription factor sigma B
transcription factor sigma H
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Grundy, F.J., Waters, D.A., Allen, S.H. and Henkin, T.M.
Regulation of the Bacillus subtilis acetate kinase
J. Bacteriol. 175 (22), 7348-7355 (1993)
   21 (bases 100760 to 102298)
Kappes,R.M., Kempf,B. and Bremer,E.
Three transport systems for the osmoprotectant glycine
operate in Bacillus subtilis: characterization of OpuD
                                                                                                                                                                                                         Cloning, sequencing, and characterization biotin biosynthetic operon J. Bacteriol. 178 (14), 4122-4130 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 (bases 196487 to 200620)
Jin, S., De Jesus-Berrios, M. and Sonenshein, A.L.
A Bacillus subtilis malate dehydrogenase gene
J. Bacteriol. 178 (2), 560-563 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rowland, B., Hill, K., Miller, P., Drisco
Structural organization of a Bacillus
menaquinone biosynthetic enzymes
Gene 167 (1-2), 105-109 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis 168 and B. subtilis Marburg Microbiology 141 (Pt 9), 2219-2222 (1995) 96118703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kiel, J.A., Boels, J.M., Beldman, G. and Venema, G. Glycogen in Bacillus subtilis: molecular characterization operon encoding enzymes involved in glycogen biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grundy, F. J., Waters, D. A., Takova, T. Y. Identification of genes involved in ut acetoin in Bacillus subtilis

Microbiol. 10 (2), 259-271 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bolotin,A.,
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                                                                              96345628
                                                                                                                                                                                                                                                                 Pero, J
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Bolotin,A., Khazak,V., Stoy
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                                                                                                                                                     Perkins, J.B., Howitt, C.L. and Pero, J.
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Submitted (13-JUN-1997) Laboratoire de Genetique Microbienne,
Domaine de Vilvert, Jouy-en-Josas cedex 78352, France
Location/Qualifiers
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Similarity 61.8%;
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I66494.1
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Dorner, F., Schelflinger, F. and Falkner, F. Gunter
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Pred. No. 4.34e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 10772)
Gray,Y.H.M., Sved,J.A., Pr
Structure of the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 4546 to 4553)
Gray,Y.H., Tanaka,M.M. and Sved,J.A.
P-element-induced recombination in Drosophila melanogaster: hybrid
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2310.
               /codon_start=1
/product="cystcine proteinase-1"
/protein_id="AAB65749.1"
/db_xref="GI:2305221"
/db_xref="GI:2305221"
                                                                                                                                                                                                                                                         /gene="CP1"
372. .1000
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/db_xref="taxon:7227"
 translation="MRTAVLLPLLALLAVAQAVSFADVVMEEWHTFKLEHRKNYQDET/
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QLRAADESFKGVTEISPAHVTLDKSVDMRTKGAVTAKDQGHGSCGWAFSSTGALEGQ
HFRKSOYLVSLSEQNLVDCSTRYGNICCNGGLUMDNAFRYIKDNGGIDTEKSYYVEALD
DSCHFNKGTVGATDRGFTDIPQGDEKKMAEAVATVGPVSVAIDASHESFQFYSEGVYN
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TDGWTNYTPKILSYVGAKKHLOTDHPLSIIRQBIVNYEYGAYRNQRGBPLFSVVDQMN
PVVTVQQNFDNLLIPADHVSRQKSDCYYINQQHLLRAHTTAHQVELISGGLDNFLVVG
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6751. .7707
                                                                     GFLSQFSEKDLHNLPKYKPISHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
                                                                                                                    EVYRRDEIDSTHYPVFHQADAVRLYTKDKLFERNPGLELFEETWSGTLADPKLILPHP
SSWTKPNSPATRRAVKLMEHEMKHVLVGLTKDLFGPRIKYRWVDTYFPFTQPSWELEI
                                                 DMVEQISLVDKFKHPKTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFNVQ
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  158 others
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6.4%; Score 42; Pred. No. 70; Misma DB 21; 3.25e-08; Length 10772;

1691 AKRWWYWAWTTTMWKWMWTTWKWAMMKTYRTWWMWKMYWTSRTTTTSAMWMWYTWSTWTK 1750

Conservative

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53;

Indels

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ATTTTTAAATGAATTTGCAGAAAGTTTAAGTAAAGCAGATCGTGTATTCTTATGTGAAAT 444

1751 YWWAYAWMKMWUTRTWARMAWASWARWKWKTSAAAAYSAWRKMWKWWAYRAMKKTWMWAA 1810 TTT-TGGATCAATTAGAGAAAATACTGGCGCATTAACGATACAAGATTTAATTGATAAAA 503

1811 WKWRWKAAWWTWRWWYMTTTAAMRAAGCTTCTATT 1845

TTGAAGGTGCATCGTTAATTAATGAAGATTCTATT 538

Drosophila melanogaster Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachyce Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds. AF012089 Gray, Y.H., AF012089.1 AF012089 fruit fly. (bases 4546 to 4553) Tanaka, M.M. and Sved, J.A. GI:2305220 10772 bp Brachycera; 05-AUG-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-JUN-1997) School of Biological Sciences, University of Sydney, Biology Al2, Sydney University, NSW 2006, Australia Location/Qualifiers
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Gray,Y.H.M., Sved,J.A.,
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6751.
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2310. .2426
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eerfklkifnenkkliakhogrfaegkysfklavnkyabllheefrqlmngfnytlhk
qlraadesfkgvffispahvtlpksvdmrtkgavtavkDoghcheesgystsalegq
hfrksgvlvslseqnlydcstkkgnngcngglmdnafkyikDnggidteksypveald
bcchenkgtvgatdroftdipqdekknaeavatvgpvsvaidashesfqfysegvyn
PVVTVQQNFDNLLIPADHVSRQKSDCYYINQQHLLRAHTTAHQVELISGGLDNFLVVG
EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFERNPGLELFEETWSGTLADPKLILPHP
SSWTKPNSPATRRAVKLMEHEMKHVLVGLTKDLFGPRIKYRWVDTYFPFTQPSWELEI
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TDGWTNVTPKILSYVGANKHLQTDHPLSIIRQRIVNYFYGAYRNQRGNPLFSVYDQMN
                                                                                                        /product="phenylalanyl tRNA synthetase"
/protein_id="AAB65750.1"
/db_xref="pli-92305222"
/db_xref="GI:2305222"
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product="phenylalany1 tRNA synthetase"
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/note="potential orf"
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/gene="CP1"
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/protein_id="AAB65749.1/
/db_xref="PID:g2305221"
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/gene="CP1"
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∕gene="CP1"
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/db_xref="taxon:7227"
join(872. .1000,2310. .2426,6476. .
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'gene="CP1"
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                                                               401 CAPATTCATTTAAAAATGCTTGTGTTCTAGAGAAAGTGTGTGGTTGAAATACTGCAACAA 342
                                                                                 706 YARRKMYGTGAAWASATAYSTGAGTTBWRYTSWKMBKYKKTGMMHHCAWKYGKGTCGCCY 765
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                             766 CWCHTTTATGBGTATMGTGTTWWWSTG 792
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Brusgaard, K., Shukri, N.M., Malchenko, S., Koroleva, I.
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OFLSQFSEKDLHNLPKYKPISHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
DMVEQISLVDKFKHPKTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFNVQ
IX."
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98: .119
                                                                                                                                                                                                                                                                                                                                        /organism="Mustela vison"
/db_xref="taxon:9667"
/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyme disease spirochete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 15079)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 15079)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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FFFELMSTYLLATION="FFFELM"
LLATION="MLLNTYFFFELM"
LLATION="MLLNTYFFFELM"
LLATION="MLLNTYFFELM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene=
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                                                                                                                  VLNVALKVLNPFSCEMFFIGLLSAIMSTVDSNLLLITSVLIKSIFIYKEDLKEDVKIG
RIIMISNIFFILIILIFSLFPPNFLFFINIFAFGALEVSFFPIIVFGLYLNFVSKIAA
FASMELGLIFYLSILFFGLNIWFFHPVFPSFFVSIFTFLVVNFFCKKNSKVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identity: 33.64;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein; identified by Glimmer;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transi_table=11
/transi_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Borrelia burgdorferi"
/db_xref="taxon:139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note-"similar to PID:606198 GB:U00096 PID:1789656 percent identity: 33.64; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="BB0814"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "FPSIIFFWFVFLF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="BB0813"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MRNGILYAILLYVEMFVLWECFAYFIDTSTTIFNIPLWFFLSGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ′codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coding region BB0813"
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RLNGLKSHFSCRVCKGDKIYLYKSLAQNLNLTTDKCFKSNIDFQYIRKRIIYEDSDLL
VLDKQKGILVHGGKNSLDFLVNSYLLSQNLRSLSFKPSAVHRLDRNTSGIIIFAKNIN
TARKLSEAFSGGSIIKKYFAILLGEVKSPVVYKNHLFRNKRLRKTFVLEDKNFVNAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:1045895 percent identity: sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MMSMNFQNFSSDFFLKKILSKVKDFAISIKHKFVRVKVYALVGS
AGTGKSFRSHLVADKYSIPLIIDDGVLIKNMKIIAGSSAKFEDNVFKAVVRSVFEDDA
HCREMLEVLAKEEFNKILILIGTSLKMIDKIISKILLPNVFKIIYITDVSTRQEIEKAR
ISROMGEHVVPAAAFEITSIRRNLLLMSIKVFFKSGWFFARKKNYIRSVVRPHFYEEG
VLSISKRAVRQIIEHCVSEYDRNYIYYDLKIKKDGNNYLFKLFLNIPLGNNLLNNTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVNPILSCKRATLVEIVIETGFTHQIRSQCSFNNHPLINDKKYCNKFKKSDYFLHAFI
/translation="MKSMTGFFYLEKIIGNYMFSVNLKSYNGKFLEFKFRLPEIFSGY
DLDIRNLISKYISRGNVFLNVGYKELVPSVNFTINPNYIEAISRLRDSLAHTNLNIKN
ELSLGDFLSLKGALIIDEDSEHQEEIYGLFKGVLEEALLHYNNGRSFEGENTKSDIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EENGVIYMDDYAHHPREIKNTLFGIKNFYKNKRIILDFMPHTFTRTKEFFADFVEVLS
AADILILHNIYLSNRENFNPDELSVKLFLNIKKINKNTYFFKDVKDSINFIKSLLISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGILIINSDDNNLLKIKRQINRKDISIFSYGSGDLSDFOISNIAVRSEYFCFSFLGLL
NVELKTVLFHNVLNFSAALLALNLFLESNGKSIFDFEEAIKRIAKNYSGIKRRVEVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKVDFDDLNNIFFVGIKGSGACSLACFLNSKGYCVEGVDVSDKF
/TDETLSNNKISYYNNIYEFGIKQLDRSFDLLYYSSAYNKDGLOVLLEAKELNIPILS
YPEALGELSRKYYSJGIAGSHGKTTTTAFLGYLFNKLGLNPRVIVGSSYKDFKDNSAI
AGISNIFIVETCEYKKHFLNFSPNMLILTNVDYEHVDFFKNYEALEEAFLQYINNLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKFNGTFFKKNEFCSKPSLDF"
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/protein_id="AAC67167.1
/db_xref="PID:g2688762"
                                                                                                                        /product="conserved hypothetical protein"
/protein_id="AAC67165.1"
/db_xref="PID:92688760"
                                                                                                                                                                                                                                                                                                                       /note="similar to GB:L10328 SP:P23839 GB:X14235 PID:290494 PID:42721 percent identity: 29.96; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLFITMGAGNNFILHDFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="PID:g2688761"
/db_xref="GI:2688761"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="UDP-N-acetylmuramate--alanine ligase (murC)"
/protein_id="AAC67166.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:L42023 SP:P45066 PID:1006469
PID:1221261 PID:1205384 percent identity: 28.70;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="B. burgdorferi predicted coding region BB0816"
/protein_id="AAC67175.1"
/db_xref="pID:92688770"
/db_xref="GI:2688770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="BB0815"
/note="similar to GB:U02214 GB:L43967 SP:P47451
                                                                                                                                                                                                                                                                                            similarity;
                                                                                                                                                                                                                                                                                                                                                                                          /gene="BB0818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="BB0817"
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3518. .4924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GI:2688762"
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                                                                                             'db_xref="GI:2688760"
                                                                                                                                                                                                                         transl_table=11
                                                                                                                                                                                                                                                           'codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene≖
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB0818"
                                                                                                                                                                                                                                                                                            putative"
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                                                                                                                                                                                                                                                                                      Matches
                                                                                                        4664
                                                                                                                                                                              4604
                                                                                                                                                                                                                                    4544 GACGATTATGCTCATCCTAGGGAAATTAAAAATACTCTTTTTTGGTATTAAAAATTTT 4603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                             326
446
                                                                                                                                                                                                                 266
                                                                                                                                                                                                                                                                                                     Match 4.7%;
Local Similarity 57.7%;
 TTTGGATCAATTAGAGAAAAT
                                 TATCTTTCAAATAGGGAAAAT 4744
                                                                                                    TTTTTTGCCGATTTTGTTGAAGTTCTAAGTGCTGCCGATATATTAATTTTGCACAATATA 4723
                                                                                                                                         TATCCACATAAAGAAGTTGTTGCAGTATTTCAACCACACTTTCTCTAGAACACAAGCA
                                                                                                                                                                            TATAAGAATAAACGTATAATTTTGGATTTTATGCCTCATACCTTTACAAGAACAAAAGAA 4663
                                                                                                                                                                                                              TTTTTAAATGAATTTGCAGAAAGTTTAAGTAAAGCAGATCGTGTATTCTTATGTGAAATT 445
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MKEDRVVFIFGPTAVGKSNILFHFPKNKAEIINVDSIQVYKBFN
IASSKPSKNLMKHIKHHLVDFLDPEKDYTIGIFYEQALKIVKEIRQKKKIPIFVGGTA
FYFKHLKDGFPSTPLVTSKIRIYVNNLLELKGKSYLLKELKNVDPIRFNMLNKNDIYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product "2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA)"
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/db_xref-"GI:2688758"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
/product="B. burgdorferi predicted
/protein_id="AAC67174.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein; identified by Glimmer;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKIALSGKSGCGNTTVSGMIAKHYGLEFINYTFHDIAREHNIPF
SEFYEKEIIGRNDYYWDKYLDNRLSVLSRKNNTVLASRLAIWISKSADLKIYLYAKME
VRAERIMTREGGMYSDVLSSTFIRDENDKKRYLAIYNIDIDDYFSETDLVIDVTNINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identity: 38.76; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="BB0819"
5798. .6340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEKIKEQIRNVE"
5798. .6340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GP:216567 percent identity: identified by sequence similarity; putative" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                          IKRSLEVYYQTGIPISQFQKKQSSEFKNIVIIGLKRSFEDLKTRISIRINEMLNSGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="cytidylate kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KILGQAFNDVLTGKFRYSIEGR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7483
466
                                                                                                                                                                                                                                                                                                     Score 31; DB 18;
Pred. No. 2.01e-02;
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                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SP:Q58071 PID:1591369 percent by sequence similarity;
                                                                                                                                                                                                                                                                                      85;
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Hypothetical indicates similarity Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 15862)
Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,
Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M., Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V. The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative indicates no similarity to known proteins Hypothetical indicates similarity to a protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aquifex aeolicus
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AE000736 AE000657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aquifex aeolicus.
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939. .1469
                                                                                                                                              /transl_table=11
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/codon\_start=1

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                                     complement(5649.../note="aq_1355"
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MLERNIIEIAPLAFMRGRTLNDAFIILDEAQNATRDQMKMFLTRIGFGSKAVITGDVT
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KLNFEEEVKKENFSASLVLGSITLGVSVVLYGAISGEEMGSLIFDLFSTYLFVVSQV
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2753. .
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2753. .4234
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LSTKLYCELFSKGRFLEVAGERFTPPSALKVVTFVELKEGLFLWFLERVRAQGGGGGG
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                      (5649. .6479)
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                                                                     318
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Note: remainder of annotations omitted.
                                                                                                                                                   10322 GTTCTTGAGTACCTGTGGGGTTGAAAAACTACGAGAAGATTTTTGTCCGGGTACATATCC 10381
                                                      10382 CGGAGTGAGTTTATTACGGCCTTTATCTCCGTAGGGTGGTGTCCGTAATCGTC 10434
CGTGCTGTGTCAATTGTAGCACTAATTTCTCTTGGATGGTGTGCATAATCATC
                                                                                                                  GTTCTAGAGAAAGTGTGTGGTTGAAATACTGCAACAACTTCTTTATGTGGATATTTCTTT 319
                                                                                                                                                                                                                               4.7%;
Similarity 63.7%;
72; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="cydB"
8464 .9564
/gene="cydB"
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6505. .6939
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                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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/protein_id="AACO7329:1"
/db_xref="pID:q2983770"
/db_xref="GI:2983770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8464
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IPKLLSILAYHDDAKVYGIKDLVQTFQKIAKGEEVGEDELPELMLDPRQFAGROSLY
ITEEEIIPFYNIPFWSLRGMWFLGFFSAFITSLGFIFYVGDDIEDGRWLLKLFFYSIPL
PIVANILGWIVAEVGRQPWVVYYILKTKDAASPLPAGQILTSIILFSSIYFIVFLIFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MDAVLLARIQFALTAMYHFLFVPITIGLSLLLAIIWTKWAREED
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AIFAFFLESVFGTGVLLFGRDRVSPKFYAFSTWAVAIGTINLSALWILVANSWOOTEKGF
YLEGGKAYLASFFDAVVNYSTPYRFVHMFLAGVITGAIFVAGISAYYILKRKHLDVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /prodein_id="AAC07356.1"
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LYBSQVKDILGVIGLGEKYGDEKFVGLLMWEHYKHSHPLVSSEVAVLKGDKLEKISF
LYBSQVKDILGVIGLGEKYGDEKFTEELMRGLFELKERFEKGEI"
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GGASHFAKCIRVLKENIEDIKVEVLIEDFRGNKKALEVVLKKEEVYLNHNVETVPRLY
PSVRTGANYKRSLNILKWSKEIDKSVYTKSALLIGFGERKEEVIKVMEDLRSVDCDFL
VLGQYYQPSLKHHPVVKYYSEEEFKEFEEIGYEMGFKFVVSKPNARSSYKAFESLLST
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/protein_id="AACO7325.1"
/protein_id="AACO7325.1"
/db_xref="pID:92983766"
/db_xref="GI:2983766"
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/protein_id="AAC07328.1"
/db_xref="pi:92983769"
/db_xref="GI:2983769"
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/gene="cydA"
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                                                                                                                                                                                                                                  Score 31; DB 18; Pred. No. 2.01e-02; 0; Mismatches 41
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                                                                    Query Match 4.7%;
Best Local Similarity 13.1%;
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1451 ARRRGKKKYMWKSMRRARRGSAGKKKKKYYYYYYYYYYYYYYYCMGRAMMAAAWYYKRRS 1510
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Address all correspondence to: Mark Adams The Institute for Genomic Research 9712

Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Mp 20850, USA e-mail address: humgen@tigr.org. The orientation of the sequence is from SP6 end to T7 end. Genes were identified by a combination of five methods including: XGRAII (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/-chris/GENSCANW.html)searches of the complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/html).

Genes without pepetide homolyy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1998) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J., Mason,T.M., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C. Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10
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Homo sapiens Chromosome
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Adams, M.D. and Loftus, B.J.
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1 (bases 1 to 216021)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens"
                                                                                                                                                                                                                                    /note="16316, CHLC.GCT15C04, Chr.
/db_xref="dbSTS:G09935"
199463. .199572
                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens"
                                                                                                                                                            /note="9824, WI-3555, Chr. 16,
/db_xref="dbSTS:G04338"
51778 c 49172 g 53987.t
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/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                 /note="16084, CHLC.GCT10B02, /db_xref="dbSTS:G09703"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="7608, STS1-cSRL-24g1-uA/cSRL-24g1-uZ, Chr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="7766, STS1-cSRL-27g3-uA/cSRL-27g3-uZ, Chr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   map="#16q21-22"
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26. .73943
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                                            Score 31; DB 31;
Pred. No. 2.01e-02;
55; Mismatches 38
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BAC clone CIT987SK-A-952F10, compl
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Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A.,
Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A.,
Kirkness,B.F., Kerlavage,A.R., Bult,C.J., Tomb,J., Dougherty,B.A.,
Merrick,J.M., McKenney,K., Sutton,G.G., FitzHugh,W., Fields,C.A.,
Gocayne,J.D., Scott,J.D., Shirley,R., Liu,L.I., Glodek,A.,
Gocayne,J.D., Scott,J.D., Shirley,R., Liu,L.I., Spidgek,A.,
Kelley,J.M., Weidman,J.F., Phillips,C.A., Spriggs,T., Hedblom,E.,
Cotton,M.D., Utterback,T., Hanna,M.C., Nguyen,D.T., Saudek,D.M.,
Brandon,R.C., Fine,L.D., Fritchman,J.L., Fuhrmann,J.L.,
Geoghagen,N.S., Gnehm,C.L., McDonald,L.A., Small,K.V., Fraser,C.M.,
Smith,H.O., and Venter,J.C.
Smith,H.O. and Venter,J.C.
                                                                                                                                                                                         Medical Center Dr. Rockville, MD 20850, USA
The whole genome was shifted by 588 nucleotides for a new start
                                                                                                                                                                                                                                                                                             White,O., Clayton,R.A., Kerlavage,A.R., Fleischmann,R.D. Peterson,J., Hickey,E., Dodson,R. and Gwinn,M.
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-SEF-1997) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
The H. influenzae sequence has been updated by R. Fleischmann. New database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. We gratefully acknowledge the work of Tatusov et. al. We have incorporated their annotation into the /notes fields of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medical Center Dr, Rockville, MD 20850, USA
4 (bases 1 to 12085)
White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White, O., Clayton
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tatusov,R.L., Mushegian,A.R., Bork,P., Brown,N.P., Hayes,W.S., Borodovsky,M., Rudd,K.E. and Koonin,E.V. Metabolism and evolution of Haemophilus influenzae deduced from a whole-genome comparison with Escherichia coli
                                                                                                                                                                                                                                               Submitted (28-MAY-1998) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                             corresponding H. influenzae genes (bases 1 to 12085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-JUL-1995) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 269
95350630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae Rd Eubacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus
                                                                                                                                                                                                                                                                           Direct Submission
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99. .1526
                                                                                                                                              1996 this sequence Location/Qualifiers
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                                                                                                                                                                        version replaced gi:1221895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:145725 percent similarity; putativ
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2518. .3282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GB:D10483 SP:P07862 GB:K02668 pID:145724
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1598. .2518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3301.
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gene CDS gene

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gene
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LEKIDLSNAQGILVNITAGMDLVFEEFNIIGETIGSFASEEATVVVGTSLVPEMSDEI
RVTIVATGLGEIAGNEPIQVVRQGLSTQNIEGEGRVNIVPELHRRESVEVSRTASEEY
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5966. .6883
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ITGGGAQIEDLKECASNVFHCQVRIASPLNITGLTDYVNRPQYSTVVGLLQYNYSNSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to SP:002286 GB:M74134 GB:X60420 PID:148468 PID:43344 percent identity: 55.32; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MIKQRTLKQSIKVTGVGLHSGEKVTLTLRPAMPMTGVVYYRTDL
NPAVAFPADPNSVMLCTALINEQGVRISTVEHLMALAGLGIDNIIIEVDAPEID
IMDGSASPFIYLLLDAGIEBQNAAKKEIRIKQYVRVBDGDKWALEFKPYMGFRLDFTID
FDHPAIGKDVRNYEMNFSAQAFVHQISRARTFGFMKDIEYLQSQGLVLGGSLDNAIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deacetylase (lpxC)"
/protein_id="AAC22799.1"
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/db_xref="GI:1574700"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="cell division protein (ftsZ)"
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/db_xref="PID:91574699"
/db_xref="GI:1574699"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:D10483 SP:P06138 GB:X02821 PID:216509
PID:40863 percent identity: 67.53; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity; putative"
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/gene="HI1145"
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7010. .8167
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Note: remainder of annotations omitted

gene

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δõ
                                                            Query Match
Best Local
                                                   Matches
                        1125
263
GTAGATGATTATGCACCATCCAAGAGAAATTAGTGCTACAATTGACACAGCACGAAAG 322
                        GTTGATGATTATGGTCATCCAACAGAAGTAGGCGTAACCATTAAAGCGGCGCGAGAA 1184
                                                            Similarity
                                                            4.5%;
                                                            Score 30;
Pred. No.
                                                 Mismatches
                                            DB 18; Le.. 6.23e-02; -hes 57;
                                                                        Length 12085;
                                                Indels
                                                0,
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTGGGGAGATAAACGTATTGTAATGATTTTCCAACCGCATCGTTATTCTCGCACTCGT 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-MAY-1998) Microbiology, Plum Island Animal Disease Center, U.S. Dept. Agriculture, Agricultural Research Service, P Box 848, Greenport, NY 11944-0848, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Afonso, C.L., Tulma
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Melanoplus sanguinipes entomopoxvirus.
Melanoplus sanguinipes entomopoxvirus
Viruses; dsDNA viruses, no RNA stage; Poxviridae;
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AF063866
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onso,C.L., Tulman,E.R., Lu,Z., Oma,E., Kutish,G.F.
e genome of Melanoplus sanguinipes entomopoxvirus
yirol. 73 (1), 533-552 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Melanoplus sanguinipes/isolate="Tucson"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .236120
                                                                                                                /gene="MSV004"
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                                                                                                                                                                                                                                                                                                             /gene="MSV002"
                                                                                                                                                                                                                                                                                                                                                    /gene="MSV002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="MSV001"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="ORF MSV001 62 amino acid repeat gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_type=inverted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="left inverted terminal repeat"
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                                    amino acid repeat gene family
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SW:P28854"
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NCNECKIIDFKFLESLINLEILDISYNKNSNIYKCKLSSLLKNLNCNECKIIDFKFLE
SLINLEILDVSYNKNSNIYECTLPISLIELKCISCKIIDFKFLESLINLEILDVSSNE
                                                                                                                                                                                                                                                                                                              SLIELYCSKCNIKNFNFLQPLINLQKLDISVNDFYSFNILNHFNYPPFIN"
                                                                                                                                                                                                                                                                                                                                                                                                 YSNISDCKLPVSLIKLNCEFCYIYDFKFLETLNNIKILNISYNKNSNISDCKKLPVSL
IKLNCGYCYIYDFKFLEPLINLQKLNISSNSYSNISKCKLPISLIKFKSEYCDITNFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(9825. .11327)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFEFLLPDTSNILILINGSKNLKSIISQSLQ"
complement(9825. .11327)
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/gene="MSV005"
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/gene="MSV003"
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CNKCNKINFVHDGVCGECYANKIVCNGDNTKSTCYIIIINDQKVIEEGVVESSKDIFI
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                                                                                                                                                                                             /gene="MSV007"
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/gene="MSV003"
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/translation="MFESLFSDMCNILRLINDSKNVKFLILQEIHFNSINDISNVHSY
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/db_xref="PID:94049909"
/db_xref="E11:4049909"
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/db_xref="GI:4049908"
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db_xref="PID:g4049648"
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                                                           Query Match 4.5%;
Best Local Similarity 63.5%;
Matches 94; Conservative
20567 ATACTGTACTTATTTCACAAAATTTATG-TATATCATTAATATCTAAATATTGTATTATA 20625
                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                           annotations omitted.
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ICVRCDIKDFNFLERLFRLQMLDISYNYIKSNISKCKLPISLLELYCKRCTNNNYFFL
NDLPPRLEILDISCNNKININIRLSKKLIKLNCSNNNISDIKFLEHLSNLEILNISY
NKISYIYYKLPNNLIELNCKNNIKNFKFIERLHNLKKKLNISKOKLPYSLRVLKSTDRY
IINLNIKACDITDFSFLEPLNNLEKLNITEENYDNETNLSKCKLPVSLRVLKSTDRY
CNYLFLERLINLEILYINDFFDFSILIRSLPJSLKEINLSSCCYIDDIKFLEPLINL
KKLNISDNRNLKITECKLPISLIELDCSSCDITDFKFLEPLINLKKLNISDSRNLKII
KKLNISDNRNLKITECKLPISLIELDCSSCDITDFKFLEPLINLKKLNISDSRNLKII
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YYKNYYKPYRHYBAFA
KKFICYRCDITDFKFLEDLINLEVLDISYNIKSNISHYKLSKOLKEFICECKOHITDFF
FLKKLNLKYLDISENKISHISKCKLPKTIKKFICDRCDITDFTFLEELINLEILDIS
KKKLYCNOCFIKNNFLIKKLINLTILINISFKHKITDKFLENLTNLEILDISENKKNI
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SLKKLYCNOCFIKNNFLIKKLINLTILINISFKHKITDKFLENLTNLEILDISENKUS
ISKCKLSKTIKKFICSRCAITDFKFLEHLINLEILDVSYNYEANISEFKLSISLKELN
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15855. .16247
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DSNISICKLPLSLIELNCMYCYISDFKFLEPLKSLKILNICKNGSSNIIYCNLSPTLE
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/gene="MSV010"
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/gene="MSV010"
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ITDFKFLENLYNLEKLFIINNKKSNISDCKLPISIIEFCCNKCEITDFKFLEDLYNLK
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/db_xref="PID:g4049897"
/db_xref="GI:4049897"
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protein, similar to Amsacta moorei entomopoxvirus Q3
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/db_xref="PID:g4049898"
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protein, similar to Amsacta moorei entomopoxvirus Q3
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14293. .15810
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/translation="MNNLTYYKEKLKKLNNDLNKIHKLAARNKLYRKYNSILNIPLHE
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                                                                                                                                                                                                                                                   /product="ORF MSV012 hypothetical protein"
/protein_id="AAC97611.1"
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                                                        Score 30; DB 37; Pred. No. 6.23e-02 0; Mismatches 5:
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Matches 25; Concount
     TITLE
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                                                                                                                                                                                                                                                                                      AF012886 6757 bp DNA BCT 21-JAN-1991 Buchnera aphidicola UDP-N-acetylmuramate: L-alanine ligase (murC157), D-alanine: D-alanine ligase (ddlB), cell division protein (ftsA), cell septation protein (ftsZ), and pfs genes, complete cds.
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1 (bases 1 to 215)

1 (bases 1 to 215)

Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.

Plant inhibitors of fungal polygalacturonases and their use control fungal disease
control fungal disease
Patent: US 5569830-A 29-OCT-1996;
Baumann,L. and Baumann,P.
Direct Submission
Submitted (07-JUL-1997) Microbiology, University
                                                                                Characterization of ftsz, the cell division aphidicola (endosymbiont of aphids) and detacter. Microbiol. 36 (2), 85-89 (1998)
                                                                                                                                                         Eubacteria; Proteobacteria; gamma subdivision; Buchnera
1 (bases 1 to 6757)
                                                                                                                                                                                        Buchnera aphidicola.
Buchnera aphidicola
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                                                                                                      sion gene of Buchnera
detection of the pro
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     of California,
                                                                                                                                                                                                                                                                                                                                                              21-JAN-1998
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKKKIAVLLGGILSERKISIKSGYAILQSLLRSGFNAYAIDTRD FPIMQLKKQGFDSAYIALHGTGGEDGSIQGILEYLNIPYTGSGIMSSAISLDKWRTKL LWKSLSLRVLPDIYLQKKDISKYTYSYILKKILKKFVVYIKPNNAGSSIGITIVHHP DLLIDSINLAENYSNNIIIEKFLKGTEYTVSILNKKVLPPIKIITKNNFYDYSSKYIE SSTEYICPSGLNYQKEEELKKIVEIAWNSLGCKGCGRIDAILDNKDKFWLLEINTIPG
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HLNGNDIILIQGAGDIDTIINKIFILKNKKVII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPSYGIAILCTDNKAILNILPKIKCKVITYGFNKSAEFRITSYKOSDFISNFTLIRKK
QLNNLEIILNLPGEHNALNATAAIAFATYQKIPDEKIYQSLKNFKGTSRRFEYVGKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mninkikknnffkekkilkihligiagsgmsgialilfnlgyki
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                                                                                                                                                                                                                                                                                                                                                                                                ITYIDGSIQDSQVIPYAGNIVTKDISYAFSTSYSDSEKIKIKYGSAIKLSPGTSKNID
LSSKYGNFQKNLQQDTVIEVIDSRYNELLHLINNRILYVQKKLYKEGRKYQLTGGIVL
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AKLGFSKYFIAEADESDGSFLCLNPTTAIITNIEPDHIDNYNGEFKLLKKTFLDFLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="UDP-N-acetylmuramate: L-alanine ligase"
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                                                                                                                                                                                                                             1147. .5301
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of the aphid Schizaphis graminum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /specific_host="Schizaphis
/db_xref="taxon:9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95616-8665, USA
ocation/Qualifiers
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7.1"
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BASE COUNT
ORIGIN
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1171 TAAATGATTATGGACATCCTACTGAATTATCTGAAACTATTAAAACAATACGAAAAA 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
384 CATTITTAAATGAATTTGCAGAAAGTTTAAGTAAAGCAGATCGTGTATT 432
                                                                                                                                                                                            324
                                                                                                                                                                                                                                                                                                                                                                               264 TAGATGATTATGCACCACCATCCAAGAGAAATTAGTGCTACAATTGACACAGCACGAAAGA 323
                                                                                              ATCTATATTTCGATTTTATTAAAATTTTATCTCAAGTAGACTCTTTATT 1339
                                                                                                                                                                                       AATATCCACATAAAGAAGTTGTTGCAGTATTTCAACCACACACTTTCTCTAGAACACAAG 383
                                                                                                                                                                                                                                                                                 GCTGGCCTAAAAAAATTTAATAATGATATTTCAACCTCATCGATATACAAGAACCCGAA 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
99; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2787
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ilarity 58.6%;
Conservative
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750 c 957 g
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IKNQESSAIGYDMESTAIGOVCHNFKIPFIIIKSISDLSDNNATSHEEKNIPIASLKS
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5576...
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ITIPNDKLLKYLSRGISLLDAFGAANNVLKGAVGIAELITRGLMNVDFADVRTVMV
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TVGNTIRSFASDNATVVIGTSLDPDMNDTLRVTVVATGIGMEKYSDVNQTKNKSSKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,...c- similar to E. coli product encoded by GenBank
Accession Number AE000125"
/codon e**-* '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5576.
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Accession Number AE000125; ORF235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMDYRYQYLNISPTAIDKKNVKNEIKETDNKKRKEPEYLDIPAFLSKRSD"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="pfs"
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Pred. No. 1:
0; Mismatcl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18;
1.90e-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6757;
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Search completed: Sat Nov Job time: 1241 secs. 27 12:12:34 1999

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MPsrch\_ntp n.a. - n.a. Smith-Waterman search, using a protein database which has been backtranslated into n.a. using IUPAC symbols

Tabular output not generated. Wed Nov 24 02:01:39 1999; MasPar time 1.52 Seconds  $1010.802\ \mbox{Million}$  cell updates/sec

Run on:

>US-09-103-287-3 (1-660) from US09103287.seq 3300

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 ATTTAAAGATTCGGATGACA......GCGTTTTAATATGTTTATAA 660 TAAATTTCTAAGCCTACTGT.......CGCAAAATTATACAAATATT

Scoring table: TABLE bktranslate2

Gap 30

Dbase 0; Query 0 1479 segs, 1162203 bases x 2

Nmatch

STD :

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

HIV-AA8 1:ALL

Statistics: Mean 73.374; Variance 209.617; scale 0.350

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

1 3 3 4 4 4 4 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
137 137 137 137 135 136 126 127 127 127 127 127 127 121 121 122 118 118	Score
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HIVM2S1, GAG HIVPH136, GAG POLYPRO HIVCAMI, GAG POLYPRO HIVUL69, GAG POLYPRO HIVB200, GAG POLYPRO HIVB257, GAG POLYPRO HIVB257, GAG POLYPRO HIVUL557, GAG POLYPRO HIVUL557, GAG POLYPRO HIVUL557, GAG POLYPRO HIVUL0, GAG POLYPRO HIVUL0, GAG POLYPRO HIVLHV310, GAG POLYPRO HIVLHV310, GAG POLYPRO HIVLEST, GAG POLYPRO HIVLEST, GAG POLYPRO HIVL6S1, GAG HIVC4S1, GAG HIVC4S1, GAG HIVVAS1, GAG POLYPRO HIVLSS1, GAG HIVC4S1, GAG	Description
2.42e-01 2.42e-01 2.42e-01 2.42e-01 3.43e-01 1.33e-00 1.56e+00 1.56e+00 1.33e+00 1.33e+00 1.33e+00 3.46e+00 3.46e+00 3.46e+00 3.46e+00 5.49e+00 5.49e+00 5.49e+00 5.49e+00	Pred. No.

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SIVSMMPBJ, ENV POLYPR	HIVU08790, ENV POLYPR	HIVU08789, ENV POLYPR	HIVU08769, ENV POLYPR	HIVMAL, GAG POLYPROTE	HIVZ2Z6, GAG POLYPROT	HIVELI, GAG POLYPROTE	HIVNY5CG, GAG POLYPRO	GAG		HIVJRFL, GAG POLYPROT	HIVUG280, GAG POLYPRO	HIVVI203, GAG POLYPRO	HIVK112, GAG POLYPROT	-	AG PO		HIVVI415, GAG POLYPRO	HIVCI4, GAG POLYPROTE	HIVVI32, GAG POLYPROT	HIVCI59, GAG POLYPROT	HIVHAN, GAG POLYPROTE	ç	HIVPH153, GAG POLYPRO	, GAG	HIVSE365, GAG POLYPRO	
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# ALIGNMENTS

Query Match  4.2%; Score 137; DB 1; Length 103;  Best Local Similarity 51.1%; Pred. No. 2.42e-01;  Matches 23; Conservative 12; Mismatches 10; Indels 0; Gaps  Db k i d v k d t k e a l e k i  Dt 80 arraarathgaygtnaargayacnaargargcnytngaraarathg 124	RESULT 2  ID GAGSE10S1 PRELIMINARY; PRT; 103 AA  AC L21375  DT 09-SEP-1993  DE HIVF10S1, GAG  PET PEPT <1 >103 GAG (AA AT >1 103)  CC -i-5':N 3':N  CC TRANSLATED USING PHASE 1  SQ SEQUENCE 103 AA; 11552 MW;	Query Match  4.2%; Score 137; DB 1; Length 91;  Best Local Similarity 51.1%; Pred. No. 2.42e-01;  Matches 23; Conservative 12; Mismatches 10; Indels 0; Gaps  Db k i d v k d t k e a 1 e k i  Dt 80 araarathgaygtnaargayacnaargargcnytngaraarathg 124   :  ;  ;   ;   ;   ;  ;  ;  ;  ;  ;  ;	RESULT 1 ID GAG\$M2S1 PRELIMINARY; PRT; 91 AA AC L21492 DT 09-SEP-1993 DE HIVM2S1, GAG FT PEPT < 1 >91 GAG (PREMATURE TERMINATION) CC TRANSLATED USING PHASE 1 SO SEQUENCE 91 AA; 10138 MW;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Nov 27 12:35:51 1999; MasPar time 5.14 Seconds 381.563 Million cell updates/sec

Tabular output not generated.

Title:

Description:
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Comp: >US-09-103-287-3 (1-660) from US09103287.seq 660 1 ATTTAAAGATTCGGATGACA......GCGTTTTAATATGTTTATAA 660
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Scoring table: TABLE default Gap 6

Nmatch STD: Dbase 0; Query 0

Searched: 1052 seqs, 1486975 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

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Statistics:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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### SUMMARIES

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# ALIGNMENTS

CDS	FEATURES source		TITLE JOURNAL STANDARD COMMENT	REFERENCE	SOURCE	ACCESSION KEYWORDS	RESULT 1 LOCUS DEFINITION
/organism="Human immunodeficiency virus type 1" /isolate="Djibouti" /cell_type="lymphocyte" /proviral /sequenced_mol="DNA" /tissue_type="blood" /oin(87302,2619>2707) /note="tat protein, exon 2 (first expressed exon)" /translation="MEPVDPLEPWNHPGSQFKTACTKCYCKKCSYHCLVCFQTKGL GISYGRKRRQRRASAPSSEDHQNLISKQ" /note="tat protein, exon 3 (AA at 2620)" /translation="plsRTQGDPTGFEESKKKVESKTKADPLD"	tion/Qualifiers	Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory Rockville, Maryland. Twenty-one full length gp100 coding sequences from eight African countries (Djibouti, Gabon, Kenya, Senegal, Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with thirty-two previously published full-length gp160 env sequences. Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274, VI191, and VI525 have corresponding gag sequences published by Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993 compendium. This sequence clusters with C subtype env sequences. See also accession numbers L22939-L22957 and L23064.	3. and Burke,D. Lycoprotein c to publication	Viridae; ss-RNA enveloped viruses; Positive strand RNA virus; Retroviridae; Lentivirinae.  1 (bases 1 to 3340) Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,		proviral DNA encoding env, tat, vpU, rev, and nef genes. L23065 env gene; envelope glycoprotein; nef gene; rev gene; tat gene;	

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                                                                                              These sequences were kindly provided prior to publication by Dr. Joost Louwagie of the Henry M. Jackson Foundation Research Laborator; Rockville, Maryland. Twenty-one full length gp160 coding sequences from eight African countries (Dj1bouti, Gabon, Kenya, Senegal, Somalla, Uganda, Zaire, and Zambia) were sequenced and analyzed with thirty-two previously published full-length gp160 env sequences. Sequences DJ258, DJ259, K124, SE355, SM145, UG256, UG258, UG274,
   Sequences DJ258, DJ259, K124, SEJDD, DJ259, VIII91, and VII925 have corresponding gag sequences published by ronwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional et. al. in AIDS 7, 769-780 (1993) and in the 1993 compensional etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Retroviridae; Lentivirinae.
l (bases 1 to 3340)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             env gene; envelope glycoprotein; nef gene; rev gene; tat gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226
                                                                                                                                                                                                                                                                                                                                                               full automatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vpu gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1191 a 568 c 791 g 790 t
bp upstream from the beginning of rev cds start
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DKGRSTRLVSGFLALAWDDLRSLFLFSYHRLRDLILIVARVVELLGQRGWETLKYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENLTNNAKIIIVQLNQSVEINCTRPNNNTRQSIRIGPGQTFYATGDIIGDIRQAHCN
ISROKWEETLQQVKGKLKEHFNKTIKFAPSGGDIEITHSTNCGGEFFYCRTSALF
LDSTTAAPINNSSTDAHTILQCHIKQIINMOGEVGRAMYAPPIGGIIACKSNITGLL
LTRDGGTNSTDETFRPGGGDMRDNWRSELYKYKVVEIKPLGLAPTKAKRRVVEREKR
ARLAAVFLGFLGAAGSTWGAASITLTVQARQLLSGIYQQQSULKAIEVHQHHLQLM
VWGIKQLQTRULAIERKLKDQLLLGIWGCGSKLICTTAVPNNSSWSNKSQEELWDNL
TWMQMDREINNYTETIYRLLEVSQTQQEDNEKDLLALDKWQNLWSWFDITKWLWYIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITTELRDKKQKKYALFYKLDIVPLGNGNEEYRLINCNTSSITQACPKVSFEPIPIHY
CAPAGYAILKCRDTKFNGTGPCKNVSTVQCTHGIKPVVSTQLLLNGSTAEEDIIIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mrvmgiQmnCQQwwiggiLgfwMLLmCngmgnLwvtvyYgvpvwQeanPTLFCASDaKaYETEVHNVWATHACVPTDPSPQELVMENVTENFNMWKNGMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALTTSNTPANNADCAWLETQEEEEEVGFPVRPQVPLRPMTYKGAFDLSFFLKEKGG
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motte="rev protein, exon 2 (first expressed exon)"
/translation="MAGRSGDSDEALLQAVRIIKILYQS"
/notte="rev protein, exon 3 (AA at 2621)"
/translation="SPYPEPKGTRQAQRNERERERERGRQFIHSISERILSTCLGRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="nef protein"
/translation="MGNKWSKGWPAVRERIRKTKPAAERVAAAAEGVGAASQDLDKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLVQYWGLELKKSAVSLLDTTAIAVAEGTDRIIEIIQRIWRAFCNIPRRIRQGFEAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDRLIERIRERAEDSGNESDGDTDELSTMVDRGNLRLLDAVDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3036..>3340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"vpu protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 3; I
Pred. No. 2.69e-01;
0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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   See also
                                                                                                                                                                                                                                                                                      Laboratory
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REFERENCE
AUTHORS
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LOCUS
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Best Local
                                                                                                                                         ORGANISM
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1642 tacatcagccttgtttaatgattcaattacaaatgcacccattaataa 1689
                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type
Human immunodeficiency virus type
Viridae; ss_RNA enveloped viruses;
Retroviridae; Lentivirinae.
  Zhu, T., Mo, H., Wang, N., Nam, D.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.0%;
Similarity 70.8%;
34; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     accession numbers L22939-L22957 NCBI gi: 437346
                             (bases 1 to 303)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119\tilde{i} a 568 c 791 g 790 t bp'upstream from the beginning of rev
                                                                                                                                                                                                                                                   s1 303 bp ss-RNA immunodeficiency virus
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AAAVFLGFLGAAGSTMGAASITLTVQARQLLSGIVQQSUNLLKA LEVHQHMLQLT
VWGIKQLQTRVLAIERYLKDQOLLGIWGCSGKLICTTAVPWNSSWSMKSQEELWDM
TWMQMDREINNYTETIYRLLEVSQTQQEQNEKDLLALDKWQNLWSWFDITKWLWYIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALTTSNTPANNADCAWLETQEEEEEEVGFPVRPQVPLRPMTYKGAFDLSFFLKEKGG
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DKGRSTRLVSGFLALAWDDLRSLFLFSYHRLRDLILIVARVVELLGQRGWETLKYLG
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ENLTNNAKIIIVQLNQSVEINCTRPNNNTRQSIRIGPGQTFYATGDIIGDIRQAHCN
ISRQKWKETLQQVKGKLKEHFNKTIKFAPSSGGDIEITTHSFNCGGEFFYCNTSALF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="nef protein"
/translation="MGNKWSKGWPAVRERIRKTKPAAERVAAAAEGVGAASQDLDKY
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DQMHQDIISLWDEGLKPCVKLTPLCVTLNCSNKVTATGNGSVTYNSTEKDMRNCSFN
ITTELRDKKQKKYALFYKLDIVPLGNGNEEYRLLNCNTSSITQACPKVSFEPIPIHY
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/translation="MIDLLAKVDYRLAVAAFIIAFIIAIVVWTIAYIEYRKLLRQRK
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/note="rev protein, exon 3 (AA at 2621)"
/translation="SPYPEPKGTRQAQRNRRRRWRARQRQIHSISERILSTCLGRPA
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/translation="PLSRTQGDPTGPEESKKKVESKTKADPLD"
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/translation="MEPVDPNLEPWNHPGSQPKTACTKCYCKKCSYHCLVCFQTKGL
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|oin(87..>302,2619..>2707)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Human immunodeficiency virus type
/isolate="Djibouti"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 3; L
Pred. No. 2.69e-01;
0; Mismatches 14
                                                                                                                                                                                                                                                         type
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Cao, Y.,
                                                                                        Positive
                                                                                                                                          (HIV-1),
                                                                                                                                                                                                                                                            clone 2,
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                                                                                                                                                                                                                                                                                       VRL
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  Koup, R.A. and Ho, D.D.
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                                                                                  strand
                                                                                                                                             clone
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ADC sample M, partial
                                                                                                                                                                                                                                                                                                                                                                                                         572
                                                                                     RNA virus;
                                                                                                                                             2, ADC sample M.
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FEATURES
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AUTHORS
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STANDARD
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STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.9%;
Best Local Similarity 77.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
     COUNT
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                                                                                                                                                                                                                                                                                  full staff_review

This sample has been taken from patient F, one of the seven
patients (A,M,L,F,C,V,R), in the study(1). All patients had acute,
self-limited symptomatic illness with measurable viremia followed
by seroconversion. Patient F was infected by patient M via sexual
transmission. The authors report that the sequences in this study
are found to be uniformly macrophage-tropic and nonsyncytium-
inducing. The sequence for sample F clone 10, along with other
patient F clones 1-9, 11, and 12, is shown in alignment following t
printed text entry. These gag sequences cluster with HIV-1 B subty
sequences. See also L21224-L21591 and L24161, L24162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sample has been taken from patient M, one of the seven patients (A,M,L,F,C,V,R), in the study(1). All patients had acute, self-limited symptomatic illness with measurable viremia followed by seroconversion. Patient M was a chronically infected male who subsequently transmitted the virus to patient F. The authors report that the sequences in this study are found to be uniformly macrophage-tropic and non-syncytium-inducing. The sequence for sample M clone 2, along with other patient M clones 1, 3-9, 11, and 12, is shown in alignment following the printed text entry. These gag sequences cluster with HIV-1 B subtype sequences. See also L212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125
190 bp d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (HIV-1), clone 10, ADC sample Human immunodeficiency virus type 1 Viridae; ss-RNA enveloped viruses; Positive Strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gag cds, p17
L21375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhu T., Mo.H., Wang,N., Nam,D.S., Cao,Y., Koup,R.A. and Ho,D.D. Genotypic and phenotypic characterization of HIV-1 in patients with primary infection science 261, 1179-1181 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               full staff_review This sample has be
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Science 261, 1179-1181 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIVF10S1
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     128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OS1 309 bp ss-RNA VRL 09-SEP-1993
immunodeficiency virus type 1, clone 10, ADC sample F, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                               /translation="LQPSLQTGSEELRSLYNTIAVLYCVHQKIDVKDTKEALEKIEEE
QNKSKKKAQQATAAADTANSSQVSQNYPIVQNIQGQMVHQPISPRTLNAWVKVVEEKA
/sequenced_mol="RNA"
64 c 62 g
                                                                              <1..>309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sequenced_mol="RNA"
61 c 62 g
                                                                                                                                                                                                        /product="myristylated gag protein p17"
/gene="gag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="myristylated
/gene="gag"
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                                                   /organism="Human immunodeficiency virus type 1"
                                                                                                                                                                             codon_start=1
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Pred. No. 1.15e+00
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IV-1 B subtype
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RESULT 6
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DEFINITION
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SOURCE
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STANDARD
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Best Local Similarity 77.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                          TITLE
                                                                AUTHORS
                                                                                                                                                                                                                                     168
                                                                                                                                                                                                                                                            269 agaggatagatgtaaaagacaccaaagaagctttaga 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 aagatagatgtaaaagaccccaaagaagctttaga 116
                                                                                                                                                                                                                                     AGAAGCTAGATGTTACAAATATTAAAGAAGCATTAGA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCTAGATGTTACAAATATTAAAGAAGCATTAGA 204
                                                                                                     SIVMNDGB1
Simian immunoo
M27470 X15781
                                                                                                                                                                                                                                                                                                                                                                                                         gag
Tsujimoto,H., Hasegawa,A., Maki,N., Fukasawa,M., Miura,T., Speidel,S., Cooper,R.W., Moriyama,E.N., Gojobbri,T. and Hayami,M. Sequence of a novel simian immunodeficiency virus from a wild-caught African mandrill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. The VI415 gag sequence clusters with HIV-1 A subtype sequences. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Louwagie, J.J., McCutchan, F., Brennan, T., Peeters, M., Brennan, T., Sanders-Buell, E., Eddy, G., van der Groen, G., Fransen, K., Gershy-Damet, M., Deleys, R. and Burke, D. Phylogenetic analysis of gag genes from seventy international HIV-1 isolates provides evidence for multiple genotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1 (HIV-1), Rwandan isolate VI415.
Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIVVI415 1459 bp ss-RNA
Human immunodeficiency virus
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                                                                                                                                                                                                                                                                                                                                         2.9%;
Similarity 75.7%;
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                                                                                 (bases 1 to 9215)
                                                                                                                                                                                                                                                                                                                                                                                                                               542
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                                                                                                                           3B1 9215 bp ss-RNA immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MGARASVLSGGKLDAWEKIRLPPGGRKKYRMKHLVWASRELDRF ALNGGLLETABGCQOILEQLQPALKTGTEEIKSILVMYATIXCYHQRIDVKDTKEALD KIEEIKMKKOKTQOAAGTONSSUNGSUNFIYVONOGOMIHQAISPETLUAWYKYLE EKAFSPEVIPMFSALSEGATPQDLNMKLNIVGGHQAAMOMLKDTINEEAAEWDRLHPV HAGPIPPGDYDRFGSIJAGTTSTTDEDIAMWTGHPNPVGDIYKRWIILGLAKIVRM YSPTSILDVKOGFKEPFRDYVDRFFKILRAEDATQEVKGMMTETLLVQUNANPDCKTIRALAGTGATLEEMMTACGGVGGGHKARVLAEAMSQVOHTNIMMQRGNEKGGNRIKCFN CGKEGHLARNCRAPRKKGCWKCGKEGHOMKDCTEROANFLGKIWSSSKGRPGNFPQSR
                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="blood" 278 c 366 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTAPPAEIVGMGGEISPPKQEQREQAPPLVSLKSX"
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/gene="gag"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sequenced_mol="DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Human immunodeficiency virus type 1"
/isolate="VI415"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _type="lymphocyte"
                                                                                                                                                                                                                                                                                                                     Score 19;
Pred. No.
0; Misma
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Pred. No. 1.15e+00
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                                                                                                                                                                                                                                                                                                                                                                                                                               273
                                                                                                                           UNA mandrill;
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                AUTHORS
TITLE
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STANDARD
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Best Local Similarity 90.9%;
Matches 20; Conservative
                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                485 tttggataaatttgagaaaata
                                                                                                                         HIVLAI 9229 bp ss-RNA VRL 01-MAR-1989 Human immunodeficiency virus type 1, isolate LAI, complete genome (original LAV-1; formerly HIVBRU).

K02013 M64186-190 M64194-198 M64203-223 acquired immune deficiency syndrome; complete genome; env gene; gag gene; long terminal repeat; pol gene; polyprotein; provirus; reverse transcriptase; trans-activator. Human immunodeficiency virus type 1 (HIV-1), isolate LAI proviral DNA clone lambda-J19 (Infectious clone available; formerly HIVBRU).
1 (bases 1 to 9229)
Wain-Hobson,S., Sonigo,P., Danos,O., Cole,S. and Alizon,M.
Nucleotide sequence of the AIDS Virus, LAV
Cell 40, 9-17 (1985)
                                                                                           Human immunodeficiency virus type 1
Viridae; ss-RNA enveloped viruses; Positive strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The mandrill virus is distinct from all other primate immuno-deficiency viruses, thus it can be regarded as a type 4 virus. There is neither a vpx nor a vpU coding sequence. The splice sites and coding regions for tat and rev are tentative.
                                                                             Retroviridae; Lentivirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      full staff_review
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9191..9196
/note="poly-A signal"
1478 c 2196 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="rev protein, 8170..8814
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/codon_start=5661
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/codon_start=450
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/note="rev protein"
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join(5471..5730,7950..8037)
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/codon_start=5227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="vif"
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Pred. No. 4.46e+00
0; Mismatches
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All LAV BRU and IIID viral samples are now believed to have been derived from this source, LAI [3]; viruses from the person BRU are now designated HIVJB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             full staff_review 2 (bases 1712 to 1749; correction of [1] in gag-pol cds) Alizon, M., Wain-Hobson, S., Montagnier, L. and Sonigo, P. Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolates from African patients cell 46, 63-74 (1986) full staff_review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (gag, tat-rev, env V1 and env V3 regions of LAI samples)
Wain-Bobson,S., Vartanian,J.-P., Henry,M., Chenciner,N., Cheynier,R.
Delassus,S., Pedroza Martins,L., Sala,M., Nugeyre,M.-T., Guetard,D.,
Barre-Sinoussi,F. and Montagnier,L.
Lav revisited: origins of the early viral HIV-1 isolates from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The original LAV, sometimes called LAV-1 to distinguish it from
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                                                 /note="5627..7
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(1712.1749)..(1712.1749)
/location=Cell 40, 9-17
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182..199
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/note="rev protein"
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/note="tat protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note-"gag polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="tat, rev, nef subgenomic mRNA intron 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="primer (Lys-tRNA) binding site"
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                                                               cds intron 2"
                      rev, nef subgenomic mRNA intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 9229)
Wain-Hobson,S., Sonigo,P., Danos,O., Cole,S.
Nucleotide sequence of the AIDS Virus, LAV
Cell 40, 9-17 (1985)
                                                                                                                                                                                                                                                                                                                                                                                       Alizon, M., Wain-Hobson, S., Montagnier, L. and Sonigo, P. Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolates from African patients Cell 46, 63-74 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome (original LAV-1)
K02013
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                                                                                                                                                                                                                                                                          clone having for its sequence for the L20
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1874
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5803..8388
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8679..>9229
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7972..8246
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clone is available
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Pred. No. 4.46e+00;
0; Mismatches 7
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5' i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kindly submitted prior to publication and in a computer readable form by Phillip Johnson, Georgetown University, Rockville MD (301 496-2976). The 155 isolate is from a monkey imported from Kenya. Location/Qualifiers join(6051..6268,8492..8633)
/note="tat protein"
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Simian immunodeficiency virus from African
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full staff_review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simian
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Similarity 78.1%;
25; Conservation
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/note="rev
8724..9416
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931..2493
                           /note="tat
8492..8700
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727..744
                                                      8492..8633
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/codon_start=2199
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="rev protein"
/codon_start=6208
                                                                   /note="env polyprotein"
/codon_start=6275
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/codon_start=5741
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/codon_start=931
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'codon_start=5260
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STANDARD
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Best Local
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Restriction of HIV-1 production in human astrocy
associated with a cellular block in REV function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1 (HIV-1), isolate TH475A.
Human immunodeficiency virus type 1
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIVTH475A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <HIVTH475A> clusters with subtype B viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neumann, M.W.F., Kleinschmidt, A., Felber, B.K., Froese, B., Erfle, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retroviridae;
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larity 78.1%;
Conservative
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9675..9680
/note="poly-A signal"
a 1905 c 2450 g 2:
                                                                GYELHPDKWTVQPIVLPEKDSWTVNDIQKLVGKLNWASQIYPGIKVRQLCKLLRGTK
ALTEVIPLTEEAELELAENREILKEPVHGVYYDPSKDLIAEIQKQGQGQWTYQIYQE
PFKNLKTGKYARWRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETW
                                                                                                                              VFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGDAYF
SVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLPQGWKGSPAIFQSSMTKILEPFRK
QNPDIVIYQYMDDLYVGSDLEIGQHRTKIEELRQHLLRWGFTTPDKKHQKEPPFLWM
                                                                                                                                                                                                                 /translation="FFREDLAFLQGKAREFSSEQTRANSPTRRELQVWGRDNNSPSE
AGADRQGTVSFNFPQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKP
KMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFPI
                                                                                                                                                                                                                                                                                                                                           QRKIVKCFNCGKEGHTARNCRAPRKKGCWKCGKEGHQMKDČTEROANFLGKIWPSYK
GRPGNFLQSRPEPTAPPEESFRSGVETTTPPQKQEPIDKELYPLTSLRSLFGNDPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAVNPGLLATSKGCRQILGQLQPSLQTGSEERRSLYNTVATLYCVHQRIEIKDTKEA
LDKIEEEQNKSKKKAQQAAADTGHSSQVSQNYPIVQNIQGQMVHQAISPRTLNAWVK
VVEEKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAEWDR
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9578..9794
                                            WTEYWQATWIPEWEFVNTPPLVKLWYQLEKEPIVGAETFYVDGAANRETKLGKAGYV
                                                                                                                                                                                             SPIETVPVKLKPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTP
                                                                                                                                                                                                                                                                                                          <2123..>5128
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DCKTTLKALGPAATLEEMMTACQGVGGPGHKARVLAEAMSQVTNSATIMMQRGNFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                    VHPVHAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKRWIILGLN
                                                                                                                                                                                                                                                                                 /note="pol polyprotein (AA at 1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="gag polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"MGARASVLSGGELDRWEKIRLRPGGKKKYKLKHIVWASRELER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain≖"IIIb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Human i
/isolate="TH4-7-5"
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9070..9794
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Pred. No. 4.46e+00
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    433
  CTTATGTGAAATTTTTGGATCAATTAGAGAAA 464
                                                                                                        2.7%;
Similarity 78.1%;
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2 bp downstream from
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463..>560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSSNTAANNAACAMLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGL
IHSQRRQDILDLWIYHTQGYFPDMQNYTPGPGIRYPLTFGWCYKLVPVEPEKLEEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRPEGIEEEGGERDRDRSIRLVNGSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVEL
LGRRGWEALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQGAYRAIR
                                                                                                                                                                                                 /note="R repeat 5' copy"
1782 c 2389 g 2188 t
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                                                                                                                                                                                                                                                                                                                                                                                          /note="5' LTR (AA at
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KAKRRVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQARQLLSGIVQQQNNLL
RAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSGKLICTTAVPWNAS
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NSTQLFNSTWSNSTLSTEGSNNTEGSDTITLPCRIKQIINWWQEVGKAMYAPPISGQ
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nmr.rebaensgnesegersarvemgvemghhapwnlddl "
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/translation="NepPyNEGTROARRNRRRWRERGHSISERILSTYLGRSA
/translation="NepPyNEGTROARRNRRRWRERGHSISERILSTYLGRSA
/translation="NepPyNEGTROARRNRRRWRERGHISISERILSTYLGRSA
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YESPHPRISSEVHIPLGDARLVITTYWGLHTGERDWHLGQGVSIEWRKRRYSTQVDP
ELADQLIHLYYFDCFSDSAIRKALLGHIVSPRCEYQAGHNKVGSLQYLALAALITPK
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GKVILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKTIHTDNGSNETSATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MSGKWSKSSVIGWPAVRERMRRAEPAADGVGAVSRDLEKHGAI"/
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/translation="PTSQSRGDPTGPKE"
join(6007..>6082,8416..>8689)
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/translation="MEQAPEDQGPQREPHNEWTLELLEELKNEAVRHFPRI"
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NFKRKGGIGGYSAGERIVDIIATDIQTKELQKQITKIQNFRVYYRDSRDPLWKGPAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="nef protein"
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/translation="MEPVDPRLEPWKHPGSQPKTACTTCYCKKCCFHCQVCFMTKAL
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Pred. No. 4.46e+00;
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This sample is part of a set of sequences generated through the WHO Global Programme on AIDS. The virus was derived from an asymptomatic individual, from Rwanda, whose route of infection is thought to be due to heterosexual contact. The blood sample was taken in 1992. This env sequence clusters with HIV-1 A subtype sequences. The full name of this sequence is HIV192RW016WHO.01_GlgCR; it was presented in alignments in an abbreviated form in the April 94 Human Retroviruses and AIDS compendium update as A2RW016W.01_GlgCR.
                                                                                                                                                                                                                      HIVU08638 276 bp ss-RNA VRL Human immunodeficiency virus type 1, sample Rwanda, C2V3 of env cds.
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                                                                                                                                           WHO Global Programme on AIDS.
                                                                                                                                                            Human immunodeficiency virus type 1 (HIV-1), sample 016 clone from Rwanda; derived from a primary isolate.

1 (bases 1 to 276)
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Pred. No. 4.46e+00;
0; Mismatches 15
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Local Similarity 84.0%;
mes 21; Conservative
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                                                                                          NIAID/NIH DAIDS Variation Program.

This sample is part of a set of sequences generated through the NIAID/NIH DAIDS HIV variation program. The virus was derived from an asymptomatic individual, from Baltimore, U.S., whose route of infection is thought to be due to parenteral IVDU contact. The blood sample was taken in 1992. This env sequence clusters with HIV-1 B subtype sequences. The full name of this sequence is HIV92US712DAIBA.01d1isED; it was presented in alignments in an abbreviated form in the April 94 Human Retro. AIDS compendium update as BAUS712D.01dilgED.
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    835
                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1 (HIV-1), isolate 712, Baltimore, U.S.; cultured on PBMCs.
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1 (bases 1 to 276)
WHO Global Programme on AIDS.
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Similarity 84.0%;
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45 c 48 g 64 t
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43 c 55 g 77
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                                                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                     Orloff.G.M., Kalish,M.L., Chiphangwi,J., Potts,K.E., Ou,C.,
Schochetman,G., Dallabetta,G., Saah,A.I. and Miotti,P.G.
V3 loops of HIV-1 specimens from pregnant women in Malawi uniformly
lack a potential N-linked glycosylation site
AIDS Res. Hum. Retroviruses 9, 705-706, 1993
RD full staff_review
Partial HIV-1 envelope sequences obtained from PCR amplified
PBMC-cell DNA of infected pregnant women enrolled in a study
of risk factors for HIV-1 in Blantyre, Malawi. An alignment of
the sequences in this set (accession numbers L15721-L15735),
follows the printed text entry. All of the sequences in this
study belong to the env subtype C.

Study belong to the env subtype C.
                                                                                                                                                                                                                                                             /sequenced_mol="DNA"

146 a 53 c 59 g 76 t

826 bp downstream from the beginning of env cds
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Human immunodeficiency virus type 1, sample M12199 from Malawi,
partial env cds, V3 region.
                                                                                                                                                                                                                                                                                                                             /organism-"Human immunodeficiency virus type 1"
/isolate-"Malawi patient 12199"
/proviral
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1..334
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CRGEFFYCNX"
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/codon_start=1
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/product="envelope glycoprotein"
/gene="env"
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### ALIGNMENTS

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polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
Claim 1; Page 1287-1288; 3271pp; English.
This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
                                                                                                                                                                                     EP-786519-A2.
30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
BARASH SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus contig SEQ ID #392.

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                Rosen CA;
WPI; 97-374922/35.
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V74703;
16-MAR-1999 (first entry)
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Key Locat
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/*tag= a
/note= These bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence
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So Sequence 2424 BP; 839 A; 302 C; 462 G; 759 T;
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V80065;
17-MAR-1999 (fir:
Partial nucleotide sequence of the MurC gene. MurC gene; UDP-N-acetylmuramate: L-alanine ligas; bacterial; infection; H. pylori; cancer; ulcer; immunogen; drug; genetic immunisation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing an expression system comprising the Murc gene can be used for the recombinant production of the polypeptide. Agonists or the Murc polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. the dictorial (especially s. aureus) infections. They are also useful against the Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The Murc polypeptide is also useful for antibodies; to identify monogen for vaccines. The Murc gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant Murc gene; for chromosomal mapping; to determine bacterial serotype; and for genetic sequence (Murc ORR) of the Murc gene.

Sequence (Murc ORR) of the Murc gene.

233 A; 83 C; 120 G; 224 T;
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07-CAN-1999
26-JUN-1998; 305064
03-JUL-1997; US-052720
(SMIK) SMITHKLINE BEECHAM C
(SMIK) SMITHKLINE BEECHAM P
BUICHAM MKR, WAILLS NG;
WPIL 99-062655/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Pages 4-5; 39pp; English.
The invention relates to a UDP-N-acetylmuramate:L-alanine (MurC polypeptide) encoded by the S. aureus MurC gene. Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
Key Location/Qualifiers
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agatogtgtattcttatgtgaaattttttggctcaattagagaaaaattctggcgcattaac
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larity 98.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    aureus UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide). Host C cell containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC copypeptide are used to treat conditions requiring increased activity or c expression of the polypeptide. Antagonists, inhibitory nucleic acid or CC competitive polypeptide are useful for inhibiting the polypeptide e.g. CC bacterial (especially S. aureus) infections. They are also useful against CC Helicobacter pylori infections and related cancers, ulcers and gastritis. CC The antibacterial agents are useful to treat in dwelling devices for cinfection prevention or generally as wound treatments to prevent adhesion CC of bacteria to matrix proteins. The MurC polypeptide is also useful for CC diagnosing or prognosing a (susceptibility to) disease, for raising CC antibodies; to identify modulators or specific receptors; in rational CC useful in antisense/ribozyme therapeutics; to detect mutant MurC gene; constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constraint of the constr
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MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide;
bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine;
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03-JUL-1997; US-052720
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07-JAN-1999.
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17-MAR-1999
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present sequence represents a MurC gene encoding
ttttgatgtgtatgtggatggtgagttttatgatcacttcctgtctccacaatatggtga
                                                                                                   attacaaaatgcatatttagataaattaggcatgaaaaatgcgttttaatatgtttataa
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          New nucleic acid sequences from Staphylococcus aureus WCHU29 - useful in vaccines and for treatment of bacterial infections of e.g. respiratory tract and central nervous system Claim 1; Rage 146; 390pp; English.

This sequence encodes a Staphylococcus aureus protein of unknown function, and represents a DNA Sequence of the invention. The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to
                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; cardiac infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus. EP-841394-A2.
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                                                                                                                                                                                                                                                                                                    24-SEP-1997; 307485.
24-SEP-1996; US-027032.
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24-SEP-1997;
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30-OCT-1998
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 produce antibody and/or
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Antagonists of the
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Best Local
                 Enterococcus faecalis genome con
Enterococcus faecalis; contig; de
vaccine; attenuation; computer re
Enterococcus faecalis.
WO9850555-A2.
12-NOV-1998; U08985.
14-NOV-1997; US-046009.
16-MAY-1997; US-044031.
16-MAY-1997; US-044031.
                                                                                                               X13717 standard; DNA; 677
X13717;
19-MAR-1999 (first entry)
Enterococcus faecalis gend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection.

Sequence 619 BP: 208 A; 117 C; 79 G; 215 T;
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 SC, Dillon PJ, Kunsch
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l Similarity 98.8%;
599; Conservative
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Pred. No. 0.00e+00;
r; ematches 6;
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g; detection; Enteroccer readable medium; ds
 CA;
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                                                                                                 Streptococcus pneumoniae SP0070 nucleotide. Streptococcus pneumoniae; antigen; vaccine; detection; pneumonia; otitis media; meningit streptococcus pneumoniae.
                                                                    Key
                                                                                                                                                                         V27381 standard; DNA; 1267
V27381; ... (first entry)
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A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome
 WO9818930-A2
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New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
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Similarity 62.4%;
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                  no.
                                    "SP0070"
              stop codon
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Pred. No. 1.41e-45;
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                given"
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The present sequence encodes a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid applification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered.
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Best Local 9
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07-MAY-1998.
30-OCT-1997; U19588.
31-OCT-1996; US-029960.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Dougherty BA,
KUNSCh CA, ROSEN CA;
WPI; 98-272225/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose. Sequence 1267 BP; 365 A; 269 C; 261 G; 372 T;
                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae genome fragment SEQ ID NO:61. Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; as computer readable medium; vaccine; pharmaceutical composition; Streptococcus pneumoniae.
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Nucleic acid encoding
pneumoniae - or their
                                                                                         Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays,
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30-OCT-1997; U19422.
31-OCT-1996; US-0299
                                                                pharmaceutical compositions and vaccines
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Choi GH, Hromockyj A, Johnson LS, Kunsch
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171; Conser
Page 524-530; 1409pp; English
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Pred. No. 5.16e-35;
0; Mismatches 79;
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(SMIK) SMITHKLINE BEECHAM CORP. (SMIK) SMITHKLINE BEECHAM PLC. Black MT, Hodgson JE, Knowles DJ(Reid RH, Zarfos PN; WPI; 98-322654/28.
                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae polypeptide coding region. Polypeptide; ORF; open reading frame; infection; bacterial; streptococcal; bacteremia; diagnosis; prophylaxis; ds.
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V43027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical
                                                                                            WO9823631-A1.
04-JUN-1998.
04-JUN-1997; U21976.
27-NOV-1996; US-031879
                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                Streptococcus
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l Similarity 68.4%;
171; Conservat'
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                                                                                                                                                                                      /note= "polypeptide"
complement (731..868)
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Pred. No. 5.16e-35;
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Best Local
                                                                                                                                                                                                                         Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (O51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis

Claim 1; Page 151-152; 18Lpp; English.

The sequence is that of a Streptococcal polypeptide coding region. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection.

It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrosphnal fluid.

Sequence 1825 BP; 550 A; 385 C; 366 G; 524 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 93-378844/48. New oligo:nucleotide probes specific for Mycobacteria detection and amplification of Mycobacteria nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BECT ) BECTON DICKINSON Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide probe MK14-
Oligonucleotide; DNA probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                 samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651
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     228
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                                                        11
                                                                                                                                               Local Similarity
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                                                     ssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhyhvyvsvctcaagcctc 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gagccataaatttgcgctagataaacagcatctgcttggtttaaagcatgggcaaagtcg 998
CGACGTTTAACACCACCAAACGTTTCTAATGCTTCTTTAATATTTTGTAACATCTAGCTTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCAAACGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tccaacagggcaatggttcttgtaaaggtatgcggtggaaagaactgctacaatttcctt 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCCAAAAATTTCACATAAGAATACACGATCTGCTTTACTTAAACTTTCTGCAAATTCA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAATCATCTACAATAACTTGATTTGCAATTGTAGTTTCATTGAAACGACGTTTAACACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spears PA;
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11.7%;
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                                                                                                                                            Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 80; DB 47; Le
Pred. No. 1.94e-28;
0; Mismatches 82;
                                                                                                                    Mismatches
                                                                                                                                            DB 9; I
1.37e-06;
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                                                                                                                                                                         Length
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Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all consible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which see also P80575.

See also P80575.

See also P80575.

21 A; 47 C; 17 G; 11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bami WPI; 88-279927/40.
Introducing random point mutations into by prepn of single stranded template, ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Introducing random point mutations into nucleic acods by prepn of single stranded template, annealing a prime misincorporation, completion of molecules and screening
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Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
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                                                                                                                                                                                                                                                                                                                                                                                            primer_bind
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Lehtovaara P, Knowles J,
WPI; 88-279927/40.
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03-APR-1987;
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187..204
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9.0%;
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Pred. No. 4.14e-06
48; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 14; 23pp; English.
Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
EP-571911-A.
01-DEC-1993.
24-MAY-1993;
26-MAY-1992;
                                            070466 standard; DNA; 114 BP.
070466;
070466;
05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR-9 petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding dome
effector domain; concateneated heterofunctional protein; linker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and them expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shank DD, Spears WPI; 93-378844/48.
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Random point mutations were introduced into the
direct; rapid; detection; screening; treatment;
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New oligo:nucleotide probes detection and amplification
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                                                                                                                                                                                                                                                                             169 GAAGCTAGATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCG 228
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                                                                                                                                                                                                                                                                                                         12 svhsyyvvhvvshhhsvhhvvhhvhvhvvhhvvhhvhyhvyvsvctcaagcctcg 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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ide probe MK14-A
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Pred.
57; M
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40; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PT Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure; Page 35, 255pp; English.
CC Synthetic Affinity Reagents) peptides. This generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generate formula can also be
CC represented as follows: X(NNB)1(TGC)(NNB)10(TGC)2(NNB)4Z(NNB)8(TGC)(NNB)
CC +9Y. X and Y are flanking restriction sites (X is not the same as Y)
CC that are not specific peptides generated by these generic sequences
CC 070466-68. Other specific peptides generated by these generic sequences
CC are shown in R65151-54. TSARs are concatenated heterofunctional proteins
CC domain with affinity for a ligand and a second effector peptide portion
CC that is chemically or biologically active. They may further comprise a
CC linker peptide between the 2 domains. The oligonucleotides are also
CC designed so that the expressed peptide contains 2 or 4 cysteine residues
CC positioned in, or flanking, the unpredicted or variant residues. These
CC residues confer some degree of conformational rigidity to the peptides.
CC vivo to deliver a chemically or biologically active moiety, eg. metal
CC on the cell. They can also replace the function of macromolecules, eg.
CC monoclonal or polylonal antibodies and therefore circunvent the need for
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Best Local S
Matches
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(UYNC-) UNIV NORTH CA
Fowlkes DM, Kay BK;
WPI; 94-279739/34.
                     25-JUN-1998.
12-DEC-1997;
21-MAY-1997;
16-DEC-1996;
(UYMC-) UNIV
                                                                                                                                                                                                                                                            Mammalian DNA replication origin consensus sequence, uniorsconsensus. DNA replication origin; human; mammal; alphaconsensus; uniorsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation
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                                                                                                                                                                                                                                      gene therapy;
                                                                                                                                                                                                                                                                                                                                                                06-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                         V44650 standard;
V44650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 4 C; 4 G; 4 T;
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Pred. No.
30; Misma
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Best Local :
                                                                                                  This sequence represents a human or mammalian DNA replication origin consensus sequences of the invention, designated uniorsconsensus. Administration of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication in vivo or in vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of
                                                                                                                                                                                                                                                                                                                                                                                         W09827200-A2.
25-JUN-1998.
12-DEC-1997; CA0972.
21-MAY-1997; US-047322.
16-DEC-1996; US-033374.
16-DEC-1996; US-033374.
Cossons NH, Nielsen TO, Price GB, Zannis-Hadjopoulos M; WPI; 98-362770/31.
                                                                                                                                                                                                                                                                                                    inhibiting DNA replication, for controlling replication, maintaining circular plasmids artificial chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V44650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           semi-conservative replication in proliferating mammalian cells, or inserted into mammalian or human artificial chromosome vectors for gene therapy. Particularly, they are used to create shuttle vector constructs for defining the essential mammalian elements required for maintenance of chromosomal function. The consensus sequence can be combined with cloned human telomeres and large centromeric blocks for assembly of human artificial chromosomes and maintained as bacterial plasmids, circular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Administration of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication in vivo or in vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of
               semi-conservative replication in proliferating mammalian cells, or inserted into mammalian or human artificial chromosome vectors for gene therapy. Particularly, they are used to create shuttle vector constructs therapy the essential mammalian elements required for maintenance of the constructs are the constructs.
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Mammalian DNA replication origin consensus sequence, uniorsconsensus.
DNA replication origin; human; mammal; alphaconsensus; uniorsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation;
                                                                                                                                                                                                                                                                                                                                                                     Human or mammalian origin of replication consensus sequences -
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                                                                                                                                                                                                                                                                                Claim 1; Page 42; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V44650 standard; DNA; 91 BP
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18; Conser
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558 TCAAATTGTTCTAATACATTAATAGAA
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51; }
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Search completed: Sat Nov 27 12:35:34 1999 Job time: 168 secs.

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Sat Nov 27 12:36:19 1999; MasPar time 50.78 Seconds 1124.053 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence: Title: >US-09-103-287-3 (1-660) from US09103287.seq 660

Comp: 1 ATTTAAAGATTCGGATGACA......GCGTTTTAATATGTTTATAA 660 TAAATTTCTAAGCCTACTGT.......CGCAAAATTATACAAATATT

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 165359 seqs, 43243793 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-issued 1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1

Statistics: Mean 7.989; Variance 4.833; scale 1.653

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

### SUMMARIES

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US-08-118- US-08-909- US-07-867-	US-08-238- US-08-280- US-08-388-	5555			PCT-US95-0 US-08-242- PCT-US95-0 US-08-545- PCT-US91-0
Sequence 1, App Sequence 1, App Sequence 2, App	0 0 0 0 0 122, , ,	e 94, e 99, e 99,	1934	• • • • • • • • • • • • • • • • • • •	sequence 2, App Sequence 5, App Sequence 5, App Sequence 1, App
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## ALIGNMENTS

8888888888888888888888888888888888888 Sequence 14, Application US/08232463 Sequence 14, Application US/08232463 Patent No. 5670367 JT 1 US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP. XXXXXX TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS: GENERAL INFORMATION: FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A
BEGITETTE NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELECHONE: (703)336-9300 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463 COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: STREET: 1800 Ding CITY: Alexandria STATE: TELEFAX: FILING DATE:
APPLICATION NUMBER: ADDRESSEE: ٧A È: Foley & Lardner 1800 Diagonal Road, Suite 500 (703)683-4109 US/07/935,313 30472/114 IMMU

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Matches
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-238-163-5 STANDARD; DNA; UNC;
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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
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APPLICANT:
APPLICANT:
APPLICANT:
                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE
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               FILING DATE: (CLASSIFICATION:
                                                                                                                                                ZIP:
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TOPOLOGY: lir
                                             APPLICATION NUMBER:
                                                                                                                                                           COUNTRY:
                                                                                                                                                                                        CITY: San Francisco
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Steuart Street Tower, One Market Plaza
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LABAVITCH, John M.
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STOTZ, Henrik
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                                             US/08/238,163
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Pred. No. 5.22e-:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /standard_name= "Deduced amino acid OTHER INFORMATION: sequence of PGIP from bean." SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5541077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 4.48;
Local Similarity 15.28;
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ,IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                         FILING DATE: 14-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          APPLICANT: BURNIE Mr., James P.
APPLICANT: MATTHEWS Ms., Ruth C.
TITLE OF INVENTION: FUNGAL STRESS PROTEINS
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 543-9600
                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                      APPLICATION NUMBER: FILING DATE: 16-NOV APPLICATION NUMBER:
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                                                                                                                 CLASSIFICATION:
                                                                                                                                FILING DATE:
                                                                                                                                             APPLICATION NUMBER:
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TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER:
 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                 20005-3918
                                                                                                                                                                                                                                                                                        Washington
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1100 New York Avenue,
                                                                                                                                                                                                                                                               USA
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                                                                      16-NOV-
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Pred. No. 2.70e-04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-672-514-2 STANDARD; DNA; UNC; 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                     TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
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Local Similarity 43.6%;
nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                             FILING DATE: 14-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION UNMER: 16773
REFERENCE/POCUM
                                                                                                                                                                                                                                               CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman, Darby & Cushman
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BURNIE Mr., James P.
APPLICANT: MATTHEWS Ms., Ruth C.
TITLE OF INVENTION: FUNGAL STRESS PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
  MOLECULE TYPE:
                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 16-NOV-APPLICATION NUMBER: APPLICATION NUMBER:
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TELEFAX: 6714627 C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 28-JUN-1996
                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                    STRANDEDNESS:
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         TOPOLOGY:
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RAL INFORMATION:
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                                  nucleic acid
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        linear
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DNA (genomic)
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Pred. No. 3.46e-02;
15; Mismatches 7
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FRAGMENT TYPE:
ORIGINAL SOURCE:
SEQUENCE 108 BP; 20 #
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Sequence 2, Application US/08878106
Patent No. 5817466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-878-106-2 STANDARD; DNA; UNC;
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592 ATCACCTGCACCCATAAATAAAACAACAGCATTATCAAAATTGTTCTAATACATTAAT 536
                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                        MOLECULE TYPE: G
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 GATCATAAAACTCACCATCCACATACACATCAACAGCAG
                            39 RTCNTWYGCHACHACHACHRTDACYGSWCCWCCWRGWRGHACYGAYWCHGTDMT 95
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Local Similarity 43.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SUCCESSION OF STREET OF SMITHKLINE Beecham Corporation ADDRESSEE: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/3
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hoyer, Lois
APPLICANT: Livi, George
APPLICANT: Shatzman, Allan
TITLE OF INVENTION: CONSERVED YEAST NUCLEIC ACID SEQUENCES
                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5019
                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P50278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                       TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                      NAME:
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                                                                            Similarity
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                                                                                                                                                                                                                                                       nucleic acid
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                                                            3.6%;
larity 31.6%;
Conservative
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                                                                                                                           A; 23 C;
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                                                                                                                                                                                                            DNA
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Pred. No.
15; Misma
                                                                    Score 24; DB 3; Li
Pred. No. 1.11e-01;
                                                            Pred.
22; N
                                                                                                                           12 G; 10 T; 43 OTHER
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                                                             Mismatches
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Matches
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                                        Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A Patent No. 5795961
                                                                                       XXXXXX
                                                                                                US-08-388-672A-22 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                  SEQUENCE 108 BP; 20 A; 23 C; 12 G; 10 T; 43 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JT 6
US-08-357-962-2 STANDARD; DNA; UNC; 108
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Sequence 2, Application US/08357962
Patent No. 5668263
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                                 GENERAL INFORMATION:
                                                                                                                                             592 ATCACCTGCACCCATAAATAAAACAACAGCATTATCAAATTGTTCTAATACATTAAT
                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                        Local Similarity 31.6%;
nes 18; Conservative
                                                                                                                                                                  39 RTCNTWYGCHACHACHACHRTDACYGSWCCWCCWRGWRGHACYGAYWCHGTDMT
APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5019
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APPLICANT: Hoyer, Lois
APPLICANT: Livi, George
APPLICANT: Shatzman, Allan
APPLICANT: Shatzman, Allan
APPLICANT: CONSERVED YEAST NUCLEIC ACID SEQUENCES
                                                                                                                                                                                                                                               FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                   HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 108 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jervis, Herbert H
REGISTRATION NUMBER: 31,171
REGISTRATION NUMBER: P50278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 16-DEC-1994
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Wallace, T. Paul
Harris, William J
Carr, Frank J.
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22; M
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Pred. No. 1.11e-01
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Best Local :
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SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.
                                                                                                                                                                                                                                                  PCT-US95-11934-98 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                838 TSSNSRSSYTAADTAVYYCVRGRSYDSDGGDYWGGTTVTVSSHUVKDM 885
                                                                                                                                                                                                                                                                                                                                                                         778 TKKGURHUVHVSGGVRSTSTCTASDYTTSYWGWVRGRGWGDYGGGYTNYNGKRGRVTMAD 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  174 TAGATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTA 221
                                                                                                                                                                                                                                                                                                                                                 115 TGGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATT-TAGAGAAGC 173
                                  ZIP: 10036
COMPUTER READABLE FORM:
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APPLICATION NUMBER: US/08/388,67
                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
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NAME: Hanson, No. 579596
REGISTRATION NUMBER: 30,
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Old, Lloyd J.
APPLICANT: Welt, Sydney
APPLICANT: Kitamura, Kunio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Antibodies
                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: Z12 LT TELEPHONE: Z12-838-3884
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                       MEDIUM TYPE: Floppy disk
                                                            COUNTRY:
                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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Similarity 18.5%;
20; Conservative
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RY: USA
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                                                                                                                                                                         Cytogen Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                               Antigen Binding Peptides (Abtides) From Peptide Libraries
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Pred. No. 1.11e-01;
47; Mismatches 40
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MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP; 6 A; 6 C; 4 G; 5 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                                                         Sequence 97, Application PC/TUS9511934 Sequence 97, Application PC/TUS9511934 GENERAL INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 TGTGGAGACAGGAAGTGATCATAAAACTCACCATCCACATACACATCAACAGCAGTACCT 52
                      TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 TTATCCGTA 43
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Local Similarity 10.1%;
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                          APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
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                                             TELEFAX: (
                                                                                                                         APPLICATION NUMBER: FILING DATE: 20-SEI CLASSIFICATION:
                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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                                                                                                                                                                                                                                                                              1155 Avenue of the Americas
                                             (212) 790-9090
(212) 869-9741/8864
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(212) 869-9741/8864
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Pred. No. 3.53e-C
19; Mismatches
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Best Local Similarity
Matches 14; Conser
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INFORMATION FOR SEQ ID No.
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
TYPE: nucleic single
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Sequence 1, Application US/08273846
Patent No. 5641863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 61 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-273-846-1 STANDARD; DNA; UNC; 290
                                                                                            SEQUENCE
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 480
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                                                                                        TOPOLOGY: li
MOLECULE TYPE:
EQUENCE 290 BP; 1
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                       53 DURERFDESCCRFPROC*FXPCALLEDFROMCRFRFORM*FXPCALLEDFROMCRFCONV 112
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Local Similarity 13.2%;
es 10; Conservet
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SCHREIBER, AL APPLICANT: PARK, JONG-GU
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
GTTAATGCGCCAGTATTTCTCTAATTGATCCAAAA-ATTTCACATAAGAATACACGATC
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WILSON, MARY J.
WILSON, MARY J.
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llarity 12.6%;
Conservative
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1100 NORTH GLEBE ROAD
                                                                                                                                                                                     (703) 816-4100
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                                                                                        : DNA (genomic)
17 A; 34 C; 8 G
                                                                                                                                                                                                  (703) 816-4000
                                                                                                                                                                                                                                                                                 12-JUL-1994
                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
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                                             Score 23; DB 1; 1
Pred. No. 3.53e-01;
28; Mismatches 68
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Pred. No. 3.53e-01;
19; Mismatches 47
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                                              68;
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                                              Indels
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Query Match
Best Local
                                                                       Sequence 100, Application PC/TUS9511934 Sequence 100, Application PC/TUS9511934 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       1164 AAGGATKWGWKARWRWYGCWAYGYARKTGTACTYGAAGYGATYSATTYYCATTTKGTT 1223
                                                                                                                                                                                                                                    1224 RATYKMTTSATYMAAWRWRWWAAWW 1248
                                                                                                                                   XXXXXX
                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cDNA
SEQUENCE 1288 BP; 203 A; 368 C; 349 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08440856A Sequence 9, Application US/08440856A Patent No. 5750873 GENERAL INFORMATION:
                                                                                                                                              PCT-US95-11934-100 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XXXXXX
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                                                                                                                                                                                                        441 AAATTTTTGGATCAATTAGAGAAAA 465
                                                                                                                                                                                                                                                               381 AAGCATTTTTAAATGAATTTGCAGAAAGTTTAAGTAAAGCAGATCGTGTATTCTTATGTG 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 TGCTTTACTTAAACTTTCTGCAAATTCATTTAAAAATGCTTGTGTTCTAGA 371
                                                                                                                                                                                                                                                                                                                                    Match 3.5%;
Local Similarity 31.8%;
                            APPLICANT: Cytogen Corporation TITLE OF INVENTION: Antigen Bit TITLE OF INVENTION: Peptide Lil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND
TITLE OF INVENTION: PLANTS WITH S
   CORRESPONDENCE ADDRESS:
                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 15-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,217
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                              Antigen Binding Peptides (Abtides) From Peptide Libraries
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27; Mismatches
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Pred. No. 3.
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3.53e-01;
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Best Local Similarity
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Sequence 100, Application PC/TUS9511934
GENERAL INFORMATION:
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SEQUENCE 74 BP; .6 A; 6 C; 1 G; 1 T; 60 OTHER
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      300 CTACAA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NNVNNA 66
                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT
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               CLASSIFICATION
                            FILING DATE:
                                          APPLICATION NUMBER:
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(212) 869-9741/8864
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INFORMATION:
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                                        PCT/US95/11934
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Pred. No.
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Sequence 99, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      XXXXXX
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SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 AGACAGGAAGTGATCATAAAACTCACCATCCACATACACATCAACAGCAGTACCTTTATC 47
                                                                            TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
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Local Similarity 6.2%;
nes 4; Conservative
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                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding P.
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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 MOLECULE TYPE:
UENCE 75 BP; 1
                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                 REGISTRATION NUMBER: 18, REFERENCE/DOCKET NUMBER:
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                       TOPOLOGY:
                               STRANDEDNESS:
                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/11934 FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                  CITY: New York
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STREET: 1155 Avenue of the Americas
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Sequence 98, Application PC/TUS9511934
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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TELEFAX: 66141 PENNIE
TELEFAX: 66141 PENNIE
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TYPE: nucleic acid
STRANDEDNESS: single
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_ntp n.a. - n.a. Smith-Waterman search, using a protein database which has been backtranslated into n.a. using IUPAC symbols

Run on: Wed Nov 24 02:04:43 1999; MasPar time 108.96 Seconds 1456.244 Million cell updates/sec

Tabular output not generated

Perfect Score: Description: Title: (1-660) from US09103287.seq >US-09-103-287-3

N.A. Sequence: 1 ATTTAAAGATTCGGATGACA......GCGTTTTAATATGTTTATAA 660 TAAATTTCTAAGCCTACTGT......CGCAAAATTATACAAATATT

Scoring table: TABLE bktranslate2

Gap 30

Nmatch STD: Dbase 0; Query 0 122810 seqs, 120205779 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

1:pirl 2:pir2 3:pir3 4:pir4

Database:

Statistics: Mean 73.220; Variance 175.053; scale 0.418

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ubiquinolcytochrome	Arr-dependent protein	coII intron protein 2	hypothetical protein	mRNA maturase bI2 - y	GTP-binding regulator	ribosomal protein var		hypothetical protein	cell division control	hypothetical protein	G-box-binding factor	hypothetical 58.0K pr	asparagine-rich prote	ribosomal protein VAR	thymidine kinase (tdk	ubiquinolcytochrome	conserved hypothetica	hemoglobin beta C(NA)	hypothetical protein	conserved hypothetica	_	NADH dehydrogenase (u	DNA-directed RNA poly	Charles and the contract of
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## ALIGNMENTS

RESULT ENTRY TITLE

#authors	REFERENCE	ACCESSIONS		DATE	ORGANISM		TITLE	ENTRY
<pre>Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;</pre>	A69580	C69662; S71002	17-Mar-1999	05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change	#formal_name Bacillus subtilis	Bacillus subtilis	<pre>UDP-N-acetylmuramatealanine ligase (EC 6.3.2.8) murc -</pre>	C69662 #type complete

Kunst, F.: Ogasawara, N.: Moszer, I.: Albertini, A.M.:
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Borlss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Chol, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.;
Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Anueel, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T.M.; Portetelle, D.; Porvolik, S.; Prescott,
Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Roche, B.; Rose, M.; Sadaie, Y.; Satto, T.; Scanlon, E.;
Schowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soddo,
B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
Takemaru, K.; Takeuchi, M.; Tanakoshi, A.; Tanaka, T.;
Vandenbol, M.; Vannier, F.; Vassarotti, A.; Varai, A.;
Vanders, P.; Wedler, E.; Wedler, H.; Weitzenegger, T.;
Winters, P.; Wipat, A.; Yasamoto, H.; Yamane, K.; Yasumoto,
K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.;

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##cross-references EMBL:L31845; NID:g556013; PID:g556014
##experimental_source strain 168, substrain Marburg
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The complete genome sequence Bacillus subtilis.
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UDP-N-acetylmuramate-alanine ligase -
#formal_name Aquifex aeolicus
08-May-1998 #sequence
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#length 454  #molecular-weight 50893  #checksum 2346
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J.M.; Olson, G.J.; Swan
Nature (1998) 392:353-358
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A.L.; Graham, D.E.; Ove
M.; Aujay, M.; Huber,
Lson, G.J.; Swanson, R.
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##residues_ 1-491 ##label YUR
##rross-references EMBL:D10483; NID:g216434; PID:d1001828; PID:g216505
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##residues 1-491 ##label BLAT
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, Fujita, N.; Isono, K.; Mizobuchi, K.; Nakata, A. submitted to the EMBL Data Library, December 1992
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Nucleic Acids Res. (1990) 18:4014
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                                     ##residues 1-475 ##label TIGR
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TIGR:HI1139
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                                                                                                ##molecule_type DNA
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Similarity 43.0%;
one
                                                                                                                                                                                                                  Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Doughertty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.; Science (1995) 269:496-512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  one of the ligases responsible for the synthesis of UPD\text{-}N\text{-}acetylmuramyl} pentapeptide, an intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)
Haemophilus influenzae (strain Rd KW20)
#formal_name Haemophilus influenzae
18-aug-1995 #sequence_revision 18-aug-1995 #text_change
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Pred. No. 2.82e-20;
responsible
                                                          GB:L42023;
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                              ##molecule_type DNA
##residues 1-468 ##label KLE
##cross-references GB:AE001180; GB:AE000783;
#TIGR:BB0817
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                       #length
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K.; Roberts, K.; Hatch, B.;
Nature (1997) 390:580-586
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ATP; cell division; cell wall; ligase; P-loop;
biosynthesis
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                                                                                                                                                                                                                                                    aser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Ton J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.;
                                                                                                                                                                                                                                                                                                                                                           spirochete
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No. 6.96e-19;
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Smith, H.O.; Venter, :
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##residues 1-505 ##label KAN
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GGATGACATTTATGCTCAAATATTTCAAATTACGGATAAAGGTACTGCTGCTGTTGATGTGTA
                         RGCNGAYTAYCARGCNMGNCARATHAARMGNCARGCNCAYGGNAAYGARGTNGARGTNTG
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F G S I R E N
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UDP-N-acetylmuramoylalanine--D-glutamate ligase
""mechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                       DNA Res. (1996) 3:109-136
Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

Res. MUID:97061201
                                                                                                       #length
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                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                   aneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sujura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo,
S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
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Library, June 1996
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##residues
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##residues 1-803 ##label ARN
##coss-references GB:AE001348; GB:AE001273; NID:g3329216; PID:g3329224
##avnarimental_source serotype D, strain UW-3/Cx
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                                                                                                                                                                                                                    murC/ddlA
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probable muramate-Ala ligase and D-Ala-D-Ala ligase
Chlamydia trachomatis (serotype D, strain UW3/Cx)
#formal_name Chlamydia trachomatis
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##cross-references GB:AE001213; GB:AE000520;
##experimental_source strain Nichols
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Similarity 37.4%;
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Science (1998) 281:375-388
Complete genome sequence o
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#formal_name Treponema
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24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change
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                                                                                          Score 252; DB 2;
Pred. No. 6.15e-13;
36; Mismatches 91
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Best Local
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#title
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##cross-references GB:AJZ35271; G
PID:g3860809
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                                                                                                                                                                                                                                                                                                                                                   ##experimental_source strain
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Similarity 42.9%;
87; Conservation
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#length 495
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#formal_name Rickettsia prowazekii
21-Nov-1998 #sequence_revision 21-
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                                                                                                                                                                                                                                                                        Score 213; DB 2;
Pred. No. 5.51e-08;
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#title
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S Y L · E K L D V T N I K E A L E T F G G
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Similarity 39.2%;
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Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
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                                                                     A64520
                                                                                                           #formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 0
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Döig, P.C.; Smith, D.R.; Noonan, B.; Gulld, B.C.;
B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.;
Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson,
Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.;
G.F.; Trust, T.J.
Nature (1999) 397:176-180
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A71800
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udp-n-acetylmuramate--alanine ligase
(strain J99)
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12-Feb-1999 #sequence_revision 12-Feb-1999
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Pred. No. 3.48e-06;
34; Mismatches 65
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                                                                                                            #text_change
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or, D.E.;
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Best Local Similarity 50.8%;
Matches 32; Conservative
Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal Nature (1997) 388:539-547
#title The complete genome sequence of the gastric pathogen
#cross-references MUID:97394467
#accession G64597
                                                                                                                                                                                                                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                              #journal
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                                                                                                                                              ##residues 1-494 ##label COL
##cross-references GB:Z95388; GB:AL123456;
PID:g2104326
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##residues 1-44
                                                                                                                          ##experimental_source
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Similarity
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Nature (1998) 393:537-544

Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
                                                         murC
#length 494
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17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
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54.5%;
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Pred. No. 4.06e-04;
14; Mismatches 17;
Score 172; DB 2;
Pred. No. 3.09e-03;
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                 Length 494;
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RESULT ENTRY

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                                                                                                #authors #journal
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                                                 #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #submission submitted to the Atlas, January 1969
#contents annotation; revision to residue 103
#ENT This type of beta C chain is found in nonanemic Barbary sheep,
whereas the other type of beta C chain is found in anemic Ba
                                                                                  #title
                                                                                                                                                                                                                                     #submission
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##residues 1-141 ##label HUI
                                                                                                                                                                                  ##residues
                                                                                                                                                               ##residues 1-398 ##label FOUI
##cross-references EMBL:AJ011856;
##cross-references
               ##residues
                             ##molecule_type DNA
                                                                                                                                                                                               ##molecule_type DNA
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                                                                                                                                                                                                                  Foury, F.; Roganti, T.; I submitted to the Protein S78670
                                                                                                                                                                                                                                                                                                                 protein Q0140
#formal_name mitochondrion Saccharomyces cerevisiae
18-Apr-1984 #sequence_revision 29-Jan-1999 #text_change
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                                                                                                                                                                                                                                                                     S78670; S78671; A02751
S78634
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blood; chromoprotein; erythrocyte; h
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Studies of haemoglobin types
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hemoglobin beta C(NA) chain - aoudad
#formal_name Ammotragus lervia #comm
                                                                                The complete sequence of the
                                                                                              Foury, F.; Roganti, T.; Lecre FEBS Lett. (1998) 440:325-331
                                                                                                                                                                                                                                                                                                                                                                     ribosomal protein var1, mitochondrial -
cerevisiae) mitochondrion (SGC2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 10-Jul-1998
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source strain FY1679, isogenio
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#status predicted
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predicted\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #domain globin homology #label GLB\
#binding_site oxygen (His) (distal axial ligand) #status
              1-398 ##label FOU2
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EMBL: AJ011856
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n Sequence Database, Decen
                                                                                                              Lecrenier, N.; Purnelle,
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                        #authors Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, Monfort, A.; Orsat, B.; Spielmann, A.; Stutz, #journal Nucleic Acids Res. (1993) 21:3537-3544 #title Complete sequence of Euglena gracilis chloropla #cross-references MUID:93347989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              grossman, L.I.

#journal Cell (1982) 30:617-626

#title Location and structure of the va

mitochondrial DNA: nucleotide

#cross-references MUID:83050946
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       ##residues
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DNA
1-516 ##label HAL
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##cross-references EMBL:AJ011856; MIPS:Q0140
##experimental_source strain FY1679, isogeni
                   ##residues 1-398 ##label FOU2 ##cross-references EMBL:AJ011856
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                                       ##molecule_type
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FEBS Lett. (1998) 440:325-331
The complete sequence of the :
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##mote the reading frame was confirmed by determination of the
##note amino acid composition
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Grossman, L.I.

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Grossman, L.I.

Grossman, L.I.

Shumard, D.S.; Butow, R.A.;

#title

Location and structure of the var1 gene on yeast

mitochondrial DNA: nucleotide sequence of the 40:0 allele.

#cross-references MUID:83050946
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502 TITATCAATTAAATC 488
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_ntp n.a. - n.a. Smith-Waterman search, using a protein database which has been backtranslated into n.a. using IUPAC symbols

Run on: Wed Nov 24 02:21:30 1999; MasPar time 75.56 Seconds 1481.508 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
N.A. Sequence: >US-09-103-287-3 (1-660) from US09103287.seq 3300

1 ATTTAAAGATTCGGATGACA......GCGTTTTAATATGTTTATAA 660 TAAATTTCTAAGCCTACTGT.......CGCAAAATTATACAAATATT

Scoring table: TABLE bktranslate2

Gap 30

Nmatch

STD :

Dbase 0; Query 0

Searched: 77977 seqs, 84804879 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 74.399; Variance 152.487; scale 0.488

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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Query Match 77.8%; Score 2568; DB 1; Best Local Similarity 59.4%; Pred. No. 0.00e+00; Matches 383; Conservative 159; Mismatches 103;

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## ALIGNMENTS

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EMBL; AF034076; G2642659; PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE; ATP-BINDING. NP_BIND 109 114 ATP (POTENTIAL). SEQUENCE 437 AA; 49176 MW; 64D68582 CRC32;	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  DERESIEWICZ R.L.;  LOWE A.M., DERESIEWICZ R.L.;  LOWE A.M., DERESIEWICZ R.L.;  SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.  SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.  -I FUNCTION: CELL WALL FORMATION (BY SIMILARITY).  -I CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE =  ADP + ORTHOPHOSEHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.  -I PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.  -I SUBCELULIAR LOCATION: CYTOPLASMIC (PROBABLE).  -I SIMILARITY: BELONGS TO THE MURCDEF FAMILY.	ACETIMUKANOXL-L-ALANINE SYNTHETASE). MURC. STAPHYLOCOCCUS AUREUS. BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; STAPHYLOCOCCUS.	031211; 15-JUL-1998 (REL. 36, CREATED) 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) UDP-N-ACETYLAURAMATEALANINE LIGASE (EC 6.3.2.8) (UDP-N-	ILT 1 MURC_STAAU STANDARD; PRT; 437 AA.

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CATALTYIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.

SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).

SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
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Best Local
RILEY M., COLLADO-VIDES J. GREGOR J., DAVIS N.W., KIR MAU B., SHAO Y.;
                                                                SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (REL. 16, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UP
15-JUL-1998 (REL. 36, LAST ANNOTATION
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (
ACETYLMURANOYL-L-ALANINE SYNTHETASE).
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BACTERIA; PI
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                                                                                                                                                                                                                                                                                                               "Nucleotide sequence involving murG ar
region of Escherichia coli.";
NUCLEIC ACIDS RES. 18:4014-4014(1990)
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'Systematic sequencing'
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RES. 20:3305-3308(1992).
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GOEDEN M.A., ROSE I
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Query Match
Best Local S
Matches 8
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EMBL; X55034; G40859; -.
EMBL; D40483; G216505; -.
EMBL; AE000118; G1786279; -.
EMBL; U67892; G2177094; -.
1223
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poly-gamma-glutamate ligases: identification of a ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 95324553
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CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

PATHWAY: PEPTILOGLYCAN BIOSYNTHESIS.

SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).

SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                 V D D Y G H H P T E V D A T I K A A R A TOGINGAYGAYTAYGGNCAYCAYCCNACNGARGTNGAYGCNACNATHAARGCNGCNMGNG 1102
                                                               AAGCATTTTTAAATGAATTTGCAGAAAGTTTAAGTAAAGCAGATCGTGTATTCTTATGTG A F L N E F A E S L S K A D R V F L C E
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ENE; EG10619; MURC
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ARGINI
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15-JUL-1998 (REL. 36, LAST ANNOTATION UPD
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15-JUL-1998 (REL. 36, LAST ANNOTATION
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CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALI
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE
PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.

SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
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or send an email to license@isb-sib.ch).
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MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.
FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
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CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

PATHWAY: PEPPTIDOGLYCAN BIOSYNTHESIS.

SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).

SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
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SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
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CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-AL
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Pred. No. 4.23e-22;
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SEQUENCE 5
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15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE
15-JUL-1998 (REL. 36, LAST ANNOTATION UPD)
UDP-N-ACETYLMURAWATE--ALANINE LIGASE (EC
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-!- FUNCTION: CELL WALL FORMA
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CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

PATHWAY: PEEFTIDOGLYCAN BIOSYNTHESIS.

SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
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AGAAGCATT
                                                                                         Q A I A S F N G A K R R F E C K G Y C N NCARGCNATHGCNWSNTTYAAYGGNGCNAARMGNMGNTTYGARTGYAARGGNTAYTGYAA
                                                                                                                                                                                            AAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTAGATGTTACAAATATTAA
N A L A V I A I S Y L E K L D V T N I K
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V D G E F Y D H F L S P Q Y G D H T V L
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D D I Y A Q I F Q I T D K G T A V D V Y
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Similarity 36.9%;
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PCC6803. II. Sequential
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051926;
15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UP
15-DEC-1998 (REL. 37, LAST ANNOTATION
UDP-N-ACETYLMURAMPTE-ALANINE LIGASE
ACETYLMURANOYL-L-ALANINE SYNTHETASE).
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"Characterization of ftsZ, taphidicola (endosymbiont of
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                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: CELL WALL FORMATION (BY SIMILARITY). CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL
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CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALA
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

PATHMAY: PEPTIDOGLYCAN BIOSYNTHESIS.

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15-JUL-1998 (REL. 36, LAST ANOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANOTATION UPDAT
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.
                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; HP0623; -.
PEPTIDOGLYCAN SYNTHESIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
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SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
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CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
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                                                                                                                                                                                                                                                               Similarity 32; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an email to license@isb-sib.ch).
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97394467.
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50793 MW;
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Pred. No. 2.28e-05;
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(See http://www.isb-sib.
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006225;
15-JUL-1998
15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                                              MITOCHONDRION.
EUKARYOTA; EUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQ
01-NOV-1997 (REL. 35, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1048
                                                                                                                                      MEDLINE; 83050946.
HUDSPETH M.E.S., AINLEY W.M., SH
"Location and structure of the v
nucleotide sequence of the 40.0
CELL 30:617-626(1982).
                                                                                                                                                                                                                                                                                                                                                                                                   VAR1
                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BADCOCK K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: CELL WALL FORWATION (BY SIMILARITY).
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
       This
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SUBSELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                     FUNCTION: ESSENTIAL FOR MITOCHONDRIAL PROTEIN SYNTHESIS REQUIRED FOR THE MATURATION OF SMALL RIBOSOMAL SUBUNITS SUBCELLULAR LOCATION: MITOCHONDRIAL.
                                               SIMILARITY: BELONGS
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Pred. No. 2.:
10; Mismatcl
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  through a collaboration
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P47486;
01-0CT-1996 (REL. 3
01-0CT-1996 (REL. 3
01-NOV-1997 (REL. 3
                                                                                                                                                                                                                                                                                   STRAIN-ATCC 33530 / G-37;

MEDLINE; 96026346.

FRASER C. M., GOCAYNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,

FLEISCHMANN R.D., BULT C.J., KERLAVAGE A.R., SUTTON G., KELLEY J

FRITCHMAN J.L., WEIDMAN J.F., SNALL K.V., SANDUSKY M., FUHRVANN

NGUYEN D.T., UTTERBACK T.R., SANDUEK D.M., PHILLIPS C.A., MERRICK

TOMB J.-F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUCIER T.S.,

PETERSON S.N., SMITH H.O., HUTCHISON C.A. III, VENTER J.C.;

"The minimal gene complement of Mycoplasma genitalium.";
PETERSON S.N., SCHRAMM N., HU P.-C., BOTT K.F., HUTCHISON C.A. III;
"A random sequencing approach for placing markers on the physical me
of Mycoplasma genitalium.";
NUCLEIC ACIDS RES. 19:6027-6031(1991).
-1- FUNCTION: HAS BOTH ATPASE AND HELICASE ACTIVITIES. UNWINDS DNA
DUPLEXES WITH 3' TO 5' POLARITY WITH RESPECT TO THE BOUND STRAND
AND INITIATES UNWINDING MOST EFFECTIVELY WHEN A SINGLE-STRANDED
REGION IS PRESENT. INVOLVED IN THE POSTINCISION EVENTS OF
NUCLEOTIDE EXCISION REPAIR AND METHYL-DIRECTED MISMATCH REPAIR
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EMBL; J01525; G343949;
PIR; A02751; R3BYM1.
SGD; L0002455; VAR1.
                                                                                                                                                                    SEQUENCE OF 277-345 FROM N. STRAIN-ATCC 33530 / G-37; MEDLINE; 92051396. PETERSON S.N., SCHRAMM N.,
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the European Bioinformatics Institute. There are no resi
use by non-profit institutions as long as its content
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(REL. 34, LAST SEQUENCE UPDATE)
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paterial infections

Scalaim 1: Page 5: 39pp; English.

The invention relates to a UDP-N-acetylmuramate:L-alanine ligase

(Murc polypeptide) encoded by the S. aureus Murc gene. Host cells

containing an expression system comprising the Murc gene can be used for

the recombinant production of the polypeptide. Agonists or the Murc

polypeptide are used to treat conditions requiring increased activity or

expression of the polypeptide. Antagonists, inhibitory nucleic acid or

competitive polypeptide are useful for inhibiting the polypeptide e.g.

competitive polypeptide are useful for inhibiting the polypeptide e.g.

bacterial (especially S. aureus) infections. They are also useful against

Helicobacter pylori infections and related cancers, ulcers and gastritis.

The antibacterial agents are useful to treat in-dwelling devices for

infection prevention or generally as wound treatments to prevent adhesion

of bacteria to matrix proteins. The Murc polypeptide is also useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus.
Ep-889123-A.
O7-JAN-1999.
O7-JAN-1999; 305064.
O3-JUL-1997; US-052720.
(SMIK ) SMITHKLINE BEECHAM C.
(SMIK ) SMITHKLINE BEECHAM P.
Burnham MKR, Wallis NG;
WPI; 99-062655/06.
N-PSDB; V80065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W89199;
17-MAR-1999
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Partial sequence of the MurC polypeptide.
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infection; H. pylori; cancer; ulcer; gastritis; vaccine;
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Pred. No. 5.87e-251;
0; Mismatches 0;
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HDLGHEVQGSDIENYVFTEVALRNKGIKILPFGANNIKEDMVVIQGNAFASSHE-EIVRA

Query Match Best Local S Matches 20

Similarity

47.2%; larity 48.6%; Conservative

Score Pred. 94; M

re 1473; DB 33; d. No. 1.03e-110; Mismatches 114;

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PT Nucleic acid encoding antigenic peptide(s) from Streptococcus proneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis Claim 11; Page 73; 118pp; English.

CC The present sequence represents a protein from Streptococcus pneumoniae. The present sequence encoding the Streptococcus pneumoniae protein CC and be useful in vaccines for inducing protective antibodies against CC streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, oitiis media or meningitis. Probes based on the nucleic acid CC are used to detect Streptococcus infection (by usual hybridisation or CC amplification methods), also for isolating Streptococcus genes or their CC allelic variants. The protein can be used similarly to detect specific CC antibodies in standard immunoassays, especially for diagnosing or CC detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, CC g. by injection, orally or through the skin, typically at 0.01-1000 CC (especially 10-300) mu g/ml per dose.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosing or prognosing a (susceptibility to) disease, for antibodies; to identify modulators or specific receptors; drug design and as an immunogen for vaccines. The MurC get
                                                                                                                                                                                                                                                                                                                                                   Choi GH, Hromockyj
WPI; 98-272224/24.
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No. 9.35e-114;
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1670 1670 1670 432 806 187

W20049 W41314 R94616 W20733

DNA polymerase. Full length heat-resi

envelo

thermostable DNA

.06e+01

Statistics: Mean	Database: a-gen 8:p 8:p 14: 19: 24: 24: 34: 39:	Post-processing: Minimum Listing	Searched: 170751	Scoring table: PAM :	Title: >US-( Description: (1-4: Perfect Score: 3121 Sequence: 1 MT	ular output not ge	Run on: Wed I	MPsrch_pp protein -	Release 3.1a Copyright (c	
34.980; Variance 176.086; scale 0.199	-geneseq35 1: part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part20 31:part31 32:part37 38:part33 34:part34 35:part35 36:part36 37:part37 38:part38 39:part39	num Match 0% Ing first 45 summaries	31 seqs, 21266608 residues	150 11	>US-09-103-287-2 (1-437) from US09103287.pep 3121 1 MTHYHFVGIKGSGMSSLAQIGDIQKLQNAYLDKLGMKNAF 437	533.81	Nov 24 00:38:50 1999; MasPar time 17.41 Seconds	protein database search, using Smith-Waterman algorithm	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	

H. pylori cytoplasmic Amino acid sequence H. pylori cytoplasmic H. pylori ORF 05ae302 H. pylori transmembra H. pylori transmembra

H. pylori cytoplasmic H. pylori cytoplasmic

H. pylori protein. N-acetylmannosamine d Plasmodium var-7.

RP-III residual pylori protein. pylori cell

3060 4000 622 112 112 283 293 426 5100 5100 1019 1312 1312 1312 1312 1312 1312 1426 677

R27481 R12878 R12878 W222475 W220505 W220505 W20505 
H. pylori surface or Helicobacter pylori f Pyrococcus sp DNA pol

2. 90e+01 2. 54e+01 2. 94e+01 3. 39e+01 3. 91e+01 5. 91e+01 5. 91e+01 7. 96e+01 8. 91e+01 91e

Pyrococcus sp. DNA DNA polymerase of Pyrococcus sp.

g

Deep Vent DNA polymer
H. pylori cytoplasmic
Canine herpesvirus gD
Canine herpes virus p
Canine herpesvirus gl

Streptococcus TYP1 protein. Human CD36 antigen.

occus pneumon protein clon

ALIGNMENTS

PT New isolated MurC polypeptide from Staphylococcus aureus and related PT nucleic acid - useful in diagnosis, treatment and prevention of PT bacterial infections
Claim 1; Page 4; 39pp; English.

CC The present sequence represents a UDP-N-acetylmuramate:L-alanine ligase CC (MurC polypeptide) encoded by the S. aureus MurC gene. Host cells containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC CC polypeptide are used to treat conditions requiring increased activity or CC polypeptide are useful for inhibiting the polypeptide or competitive polypeptide are useful for inhibiting the polypeptide acid or CC competitive polypeptide are useful for inhibiting the polypeptide e.g. CC bacterial (especially S. aureus) infections. They are also useful against CC Helicobacter pylori infections and related cancers, ulcers and gastritis. CC Helicobacter pylori infections are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion CC diagnosing or prognosing a (susceptibility to) disease, for raising CC diagnosing or prognosing a (susceptibility to) disease, for raising continuously design and as an immunogen for vaccines. The MurC gene sequences are CC useful in antisense/ribozyme therapeutics; to detect mutant MurC gene; for the continuously design and as an immunogen for vaccines. The MurC gene sequences are continuously design and as an immunogen for vaccines. The MurC gene sequences are continuously design and as an immunogen for vaccines. The MurC gene sequences are continuously design and as an immunogen for vaccines. The MurC gene sequences are continuously design and sequences are continuously design and sequences are continuously design and sequences are continuously design and sequences are continuously design and sequences are continuously design and sequences are continuously design and sequences are continuously design and sequences are continuously design and sequences are 07-JAN-1999.
26-JUN-1998; 305064.
03-JUL-1997; US-052720.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
BURDHAM MKR, Wallis NG;
WPD; 99-062655/06. MurC gene; bacterial; JT 1 W87771 standard; Protein; 4 W87771; 17-MAR-1999 (first entry) Staphylococcus aureus. EP-889123-A2. UDP-N-acetylmuramate:L-alanine ligase (Murc polypeptide). Murc gene; UDP-N-acetylmuramate:L-alanine ligase; Murc polypeptide; bacterial: infection; H. pylori; cancer; ulcer; gastritis; vaccine; immunogen; drug; genetic immunisation. N-PSDB; V99650 for chromosomal mapping; Ö 437 determine bacterial serotype; and B for genetic

Result

Score

Query Match

Length

ВВ

IJ

Description

Pred. ö

UDP-N-acetylmuramate:

Staphylococcus aureus Streptococcus pneumon Partial sequence of t

pylori cytoplasmic

SUMMARIES

3121 1509 1473 405 273 239 143 1143 1143 1143 1143 118 118 118

100.0 448.3 113.2 113.7 7.7 7.7 7.7 4.6 4.6 4.4 4.4 4.4 3.5 3.5

437 422 455 450 286 286 286 286 286 150 1670 1670

Streptococcus pneumon S. pneumoniae MurD pr Streptococcus pneumon H. pylori cytoplasmic
H. pylori cytoplasmic

5.87e-251 9.35e-114 1.03e-110 6.99e-22 1.71e-09 6.71e-09 6.71e-09 6.65e-02 6.65e-02 1.72e-01 3.09+00 9.12e+00 1.06e+01

W87771
W89199
W55120
W20606
W77686
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W24585
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W01107 R97048 R85599

Murf protein.

P. falciparum
Helicobacter producted polymerase
DNA polymerase
DNA polymerase

polypept 2.

polymerase, contg polymerase from s

falciparum liver

Pred. No. is the nu score greater than and is derived by a

is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

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BASE COUNT
ORIGIN
                                                                              Ouery Match 1.9%; Score 25; DB 10; Length 307; Best Local Similarity 76.6%; Pred. No. 6.31e-04; Matches 36; Conservative 0; Mismatches 11; Indels
110 a
                                                                                                                                                                                                                                  subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

/db_xref="taxon:9606"
/clone="IMAGE:1011307"
/clone_lib="NCI_CGAP_Pr3"
/sex="Male"
                                                                                                                                                                          /dev_stage="45 years old"
/lab_host="DH10B"
49 c 51 g 97 t
                                                                              0;
                                                                            Gaps
                                                                              0;
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Search completed: Sat Nov 27 11:43:28 1999 Job time: 2324 secs.

ç В

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FEATURES
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Best Local Similarity 76.6%;
Matches 36; Conservative
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1 (bases 1 to 296)

ORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Washu-Merck EST Project

Unpublished (1995).

On Nov 29. 1000 1000
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                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA041443 296 bp mRNA
zf09g05.rl Soares_fetal_heart_NbHH19W
IMAGE:376472 5', mRNA sequence.
                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                          Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA041443.1 GI:1517668
                                                                                             primer: -28M13 rev2 from Amersham
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                                                              quality sequence stop: 259.
Location/Qualifiers
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modified polylinker; Site_1: Not I; Site_2: Eco RI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              constructed by Bento Soares and M. Fatima Bonaldo." /db_xref="GDB:5945547"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="germinal center B cell"
/lab_host="DH10B"
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Pred. No. 6.31e-04;
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TITLE
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Best Local Similarity
Matches 42; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 CTGTGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCCTGCATTACATGTGTTTAT 173
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                                                                                                                                                                                                                                                                                               cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: WCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 th
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nc47f10.r1
                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                     Insert Length: 388 Std Error:
Seq primer: -28m13 rev1 ET from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 307)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                    M.D., Michael Emmert-Buck, M.D.,
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                                     5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI
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/note "Vector: pAMPIO; site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
adaptors, 5 cycles of PCR applied to the c\bar{D}NA with an adaptor-specific primer, and the resulting PCR product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B (ampicillin resistant)"
74 c 68 g 87 t 1 other
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nc47f10.s1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1394273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D. Michael Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 388
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36; Conser
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larity 76.6%;
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Conservative
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                                                                                                                                                                                                                                                                                                                               histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Homo sapiens"
/note-"Vector: pAMP10; with oligo(dT)17 on 50 ng of
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
                                                                                                                                                                                                                                                                                                                             directionally cloned.
                                                                                                                                                                                                                                                    /clone="IMAGE:1011307"
/clone_lib="NCI_CGAP_Pr3"
                                                                                                                                                                                                                                                                                                                       David Krizman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                              'dev_stage="45 years old"
'lab_host="DH10B"
                                                                                                                                                                                                                                       /sex="Male"
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Primates; Catarrhini; Hominidae; Homo.
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NCI_CGAP_Pr3
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Homo sapiens cDNA clone IMAGE:1011307, mRNA
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Best Local Similarity 63.3%;
Matches 31; Conservative
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Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.
Fujiwara et al. (1995)
Unpublished (1995)
Unpublished (1995)
Un May 9, 1995 this sequence version replaced gi:803040.
                                                                                                                      Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version
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High quality sequence stop: 145
Location/Qualifiers
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                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 292)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                         AA419477 292 bp mRNA EST 16-OCT-1997 zu99a03.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746092 3',
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Otsuka Pharmaceutical Co., Ltd
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Otsuka GEN Research
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1 (bases 1 to 287)
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1 56 c 32 g 80 t 8 others
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/db_xref="taxon:9606"
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6; Mismatches 1
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g1636707
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On Jan 24, 1995 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA090223 238 bp mRt cchp0673.seq.F Human fetal cDNA 5', mRNA sequence.
                                                                                                                                                                                              FORWARD: 5' GCCAAGCTCGAAATTAACCCCTCACTAAAGGG 3' BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG Seg primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
                                                                                                                                                                                                                                                                                                                  Banting Institute, 100 College St., Tel: 4169788758
                                                                                                                                                                                                                                                                                                                                                        Department of Laboratory Medicine and Pathobiology University of Toronto
                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: M13 Reverse Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                             Email: liewcc@utcc.utoronto.ca
                                                                                                                                                                                                                                                                                                 Fax: 4169785650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNAs from fetal heart (1996)
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1 (bases 1 to 238)
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are available from Research
                /note-"Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhOI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhOI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhOI, for directional cloning into predigested lambda ZAP Express."
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                                                                                                                                                                            Location/Qualifiers
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/clone="2338N10"
/clone_lib="CIT-HSP"
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/note-"Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                       /organism="Homo sapiens"
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107 c 96 g
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Pred. No. 4.24e-06;
0; Mismatches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                   version replaced gi:634334.
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                                                                                                                                                                                                                                                                                                                                    Toronto, Ontario, M5G1L5
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Query Match
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RESULT LOCUS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, F. DNA Sequencing by: Washington University Genome Sequencing Conne distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1394311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
AA229467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 256
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: W. Marston Linehan, M.D., M.D., Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA229467 277 bp mRNA EST 21-AUG-1997 nc45f02.rl NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1011099, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria; Primates; Catarrhini;
1 (bases 1 to 277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
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                                                                                                                                                                                       adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by
                                                                                                                                                                                                                                                                      cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an
                                                                                                                                                                                                                                                                                                 /note-"Vector: pAMP10; Site_1: Not1: Site_2: Eco strand cDNA was primed with oligo(dT)17 on 50 ng DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant cancer cells. Double-stranded cDNA was ligated
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/lab_host="E. coli XL1-Blue"
1 60 c 48 g 69 t
                                                                                                                                                                       David Krizman
                                    /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                   /sex="Male"
                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:1011099"
                                                                                                     clone_lib="NCI_CGAP_Pr3"
                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"/
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6.31e-04;
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Best Local Similarity 13.5%;
Matches 26; Conservative
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                                                                                                                                                                                                                                            769 GAGTTTATGATCACTTCCTGTCTCCACAATATGGTGACCATA-CAGTTTTAAATGCATT 827
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                                                                                                                                   RKRGAGTTTTGG 1667
                                                                                                                                                                                                                                                                                                                                                       WRYKRWKRRKGRRKRMTGMYKRMYRAMMAMCAMMACWWYYWKMRGMKKCWKYRK-YKKY 1537
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                                                                                               AGAAACGTTTGG 899
                                                                                                                                                                        AGCTGTAATTGCGATTAGTTATTTAGAGAAGCTAGATGTTACAAATATTAAAGAAGCATT 887
                                                                                                                                                                                                      C-YGMTKRYYRYSWTGWTKWTTWWYMWSMTRWTMTTYTTWWTWRTTKTWWWWWWWTTCWTM 1655
                                                                                                                                                                                                                                                                                 T-STYYKSWSRWYWYTTYTYWYCWCCTSMKSASCAMMRWMGYMGSRSSRSYWGYWGSMSG 1596
                                                                                                                                                                                                                                                                                                                     TATGCTCAAAATATTCAAATTACGGATAAAGGTACTGCTTTTGATGTGTATGTGGATGGT 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKYKKYTSTYYKSWSRWYWYTTYTYWYCWCCTSMK-SASCAMMRWMGYMGSRSSRSYWGY 1590
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1 (bases 1 to 2275)

Tripodis, N. and Ragoussis, J.

Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF034173 2275 bp mRNA EST AF034173 Human mRNA (Tripodis and Ragoussis) Homo clone ntcon2 contig, mRNA sequence.

AF034173
     B50349 439
CIT-HSP-351C15.TV
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7th floor, Gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
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On Jan 19, 1998 this sequence version replaced gi:2045115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Human mRNA (Tripodis and Ragoussis)" 619 c 470 g 599 t 149 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="ntcon2 contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
DNA cor CIT-HSP Homo sapiens genomic
                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 20;
Pred. No. 4.23e-17;
98; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9RT, UK
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2275;
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     clone 351C15,
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B50349.1
                                                        Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 694)

Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Ung-Jin Kim
Callech Genome Research Lab
California Institute of Technology
Division of Biology, MS 147-75, Pasadena, CA 91125, USA
Tel: 626 796 7066
Fax: 626:395 4901
                                                                                                                                                                                                                             genomic survey sequence. AQ056084
                                                                                                                                                                                                                                                         AQ056084 694 bp DNA
CIT-HSP-2338N10.TR CIT-HSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ung@ash.tree.caltech.edu
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Other_GSSs: CIT-HSP-351C15.TP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 439)
Kim,U.-J., Adams,M.D. and Simon,M.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence. B50349
                 Unpublished (1997)
                                            Use of a random BAC
Other_GSSs:
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Similarity 72.6%;
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/note="Yector: pBeloBAC11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Sperm"
115 c 75 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="CIT-HSP"
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/clone="351C15"
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CIT-HSP-2338N10.TF
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                                             End
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Pred. No. 3.14e-07;
                                            Sequence Database for Sequence-Ready Map
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Homo sapiens genomic clone 2338N10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTCCACAATATGGTGACCATA-CAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTA 848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTAGAGAAGCTAGATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAA 908
                                                                                                                                                                       Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seg primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                          Department of Cytogenetics
National Inst. of Agri. Sci.
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                               Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
On Jan 14, 1998 this sequence version replaced gi:1797455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA754458 247 bp mRNA EST 20-JAN-1998
97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Eun M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 247)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
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Similarity 12.4%;
26; Conservative
/organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhOI; Directional cDNA library inserted into lambda ZAPI
vector at 5'end with EcoRI and 3' end with XhO I site."
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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                                                                                                                                                Location/Qualifiers
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Pred. No. 2.47e-32;
99; Mismatches 82
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Best Local Similarity 14.7%;
Matches 33; Conservative
                                 1472 AAAAAMWRYKRWKRRKGRRKRMTGMYKRMYRAMMAMCAMMACWWYYWKMRGMKKCWKY 1531
                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1029 AACTTCTTTATGTGGATATTTCTTTCGTGCTGTGTCAATTGTAGCACTAATTTCTCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1146 TCTAATTGAGCCAAAAATTTCACATAAGAATACACGATCT-GCTTTACATAAACTT-TCT 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1088 GCAAATTCATTTAAAAATG-CTTGTGTTCTAGAGAAAGTGTGTGGAAATACTGCAAC 1030
851
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AAATAACTAATCGCAATTACAGCTAATGCATTTAAAACTGTATGGTC-ACCATATTGTGG 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGTGTGCATAATCATCTACAATAACTTGATTTGCAATTGTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2275)
Tripodis, N. and Ragoussis, J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF034173 2275 bp mrNA
AF034173 Human mRNA (Tripodis and
clone ntcon2 contig, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g2707735
AF034173.1
                                                                                                                                                                                                                                                                                                                                                           Guys Hospital
                                                                                                                                                                                                                                                                                                                                                                                Division of Medical and
                                                                                                                                                                                                                                                                                                                                                                                                                                     On Jan 19, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF034173
                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            numan
                                                                                                                                                                                                                                                                                                                      floor, Guy's Tower, London il: nikos@nki.nl.
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 104;
                                                                                                                                                                                                                                                                                                                                                                                                  Tripodis, Nikos
                                                                                                                                                               /clone_lib="Human mRNA (Tripodis and Ragoussis)" 619 c 470 g 599 t 149 others
                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coll SOLR"
16 c 21 g 34 t 169 otl
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/map="6"
                                                                                                                                                                                                        /clone="ntcon2 contig"
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                                                                                         2.9%;
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Pred. No. 6.86e-31;
Wismatches 84;
                                                                      Score 39; DB 20;
Pred. No. 4.24e-21;
92; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                Molecular Genetics
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                                                                                                           Length 2275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HMWHBBMYBBTGCMTCTMWCWBHYNTKCTASGWHTSTNYDVKS-STNTWGVTBSYDKSMH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATTCATTTAAAAATGCTTGTGTTCTAG-AGAAAGTGTGTGGTTGAAATACTGCAACAA 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTAATTGAGCCAAAAATTTCACATAAGAATACACGATCTGCTTTACATAAACTTTCTGC 1087
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                                                                                                                                                                                                                                                                  Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
On Jan 14, 1998 this sequence version replaced gi:1797457.
                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 252)

Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sc
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence.
                                                    Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of
University, Yongin, Korea. 449-728
Seq primer: M13 Reverse Primer.
                                                                                                                                   Department of Cytogenetics National Inst. of Agri. Sci. Suwon, Kyunggido, Korea Tel: 82 331 290 0307 Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa
                                                                                                                                                                                                                              Contact: Eun M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                         Poaceae;
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larity 15.6%;
Conservative
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
xhoI; Directional cDNA library inserted into lambda ZAPI
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 otl
                                  Location/Qualifiers
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/organism="Oryza sativa"
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Pred. No. 8.55e-63;
126; Mismatches 79
                                                                                                                                                                                           and
                                                                      of Biological Science, Myongji
28 bhnahm@bioserver.myongji.ac.kr
                                                                                                                                                                                           Tech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79; Indels
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                                                                                                                                                                                                                                                                                                                                               Kang, K.Y.,
                                                                                                                                                                                                                                                                                                                                                               Moon, E.P.,
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TITLE

FEATURES

/organism="Oryza sativa"

Ср g Ср

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 MYBBTGCMTCTMWCWBHYNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBB 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 4.0%;
Local Similarity 12.4%;
les 30; Conservative
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Nahm,B.H., Kim,J.K., (
Kim,W.T., Kim,W.Y., Ya
Lee,M.C. and Eun,M.Y.
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                                                                                                                                                                                                                                                                                                                        Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                    Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.
Seq primer: M13 Reverse Primer.
                                                                                                                       Suwon, Kyunggido, Kon
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                           Department of Cytogenetics
National Inst. of Agri. Sci.
                                                                                                                                                                                                                                                                                              On Jan 14, 1998 this sequence
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                                                                                                   Email: myeun@sun20.asti.re.kr
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 oth
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                               Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
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Pred. No. 1.11e-42;
Pred. No. 1.11e-42;
                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                              version replaced
                                                 bhnahm@bioserver.myongji.ac.kr
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lambda ZAPII
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# ALIGNMENTS

FEATURES Source	AUTHORS TITLE JOURNAL COMMENT	VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 1 LOCUS DEFINITION ACCESSION
Contact: Eun M.Y.  Department of Cytogenetics National Inst. of Agri. Sci. and Tech, RDA  Suwon, "Kyunggido, Korea  Tel: 82 331 290 0301  Fax: 82 331 290 0307  Email: myeun@sun20.asti.re.kr Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr Seq primer: M13 Reverse Primer. Location/Qualifiers  1252 /organism="Oryza sativa"	Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, B.H., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.  Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)  On Jan 14, 1998 this sequence version replaced gi:1797457.	AA754459.1 GI:2801165 AA754459.1 GI:2801165 EST. Oryza sativa. Oryza sativa Cryza sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza. 1 (bases 1 to 252)	AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence. AA754459

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RESULT 15
ID 081057;
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UTTERBACK T., WATTHEY L.,
GARLAND S., FUJII C., COT
SMITH H.O., VENTER J.C.;
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KINETOCHORE
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NATURE 390:580-586(1997).
EMBL; AE000791; G2689915;
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SUBMITTED (DEC-1989) TO EMBL
EMBL; X17483; G9843; -.
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     ARABIDOPSIS
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391 AA;
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(TREMBLREL.
(TREMBLREL.
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larity 37.3%;
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., MCDONALD I
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                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred. No. 1.14e-02;
29; Mismatches 35;
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No. 8.80e-03
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Best Local
Matches
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STRAIN-CV. COLUMBIA;

ROUNSLEY S.D., LIN X., KAUL S., SHEA T.P., EUJII C.Y.,

SHEN M., RONNING C.M., FRASER C.M., SOMERVILLE C.R., VE

"Arabidopsis thaliana chromosome II BAC T18E12 genomic

SUBMITTED (SEP-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; AC005313; G3548813; -.

SEQUENCE 149 AA; 17102 MW; C0311A4F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EUPHYLLOPHYTES; SPERMATOPHYTA; MACNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE; CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
 245
                            227
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AAGAA
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                                                                      CTAATAACATAAAAGAAGATATGCTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATG N N I K E D M V V I Q G N A F A S S H E
                                                                                                  EYCKKHVVDEESDEFKTWDE
TNGARTAYTGYAARAARCAYGTNGTNGAYGARGARWSNGAYGARTTYAARACNTGGGAYG
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                            231
                                                                                                                                                                                                                                               2.4%;
larity 36.0%;
Conservative
                                                                                                                                                                                                                                              Score 162; DB 10;
Pred. No. 6.80e-02;
26; Mismatches 54
                                                                                                                                                                                                                                                                          Length 149;
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STRAIN-SUBKARYONIDE
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                         STRAIN=SUBKARYONIDE MEDLINE; 94134747.
                                                                                                                                                      "Precise excision of fallax macronuclear d
                                                                                                                                                                                                                                         STRAIN=SUBKARYONIDE 3.5;
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OXYTRICHIDAE; OXYTRICHA
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DOAK T.G., WITHERSPOON D.J.,
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nes 53; Consen
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                                                                                                                                                                                                                     WILLIAMS K.,
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MEDLINE: 98065943.
FRASER C.M., CASJENS S., HUAI
LATHIGRA R., WHITE O., KETCHI
DOUGHERTY B., TOMB J.-F., FLI
PETERSON J., KERLAVAGE A.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOAK T.G., WILLIAMS K., SUBMITTED (JAN-1994) TO EMBL; L39908; G685194; -EMBL; L23169; G438828; -
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N R., HICKEY E.K., GW
, RICHARDSON D.,
, SALZBERG S., HANSO
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STRAIN-SUBKARYONIDE MEDLINE; 90185189. HUNTER D.J., WILLIAM
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HERRICK G.,
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   WILLIAMS K.,
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                                                                                                                                                            34:429-434(1987)
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Pred. No. 2.36e-03;
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      HERRICK G
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Matches 5
                                 SEQUENCE FROM N.A.
TRANSPOSON-TBE1 FAL4;
MEDLINE; 94038943.
MILLIAMS K., DOAK T.G.,
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                                                                                                                                                                                                                                                                                                             EUKARYOTA; ALVEOLATA;
OXYTRICHIDAE; OXYTRICH
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01-MAY-1997
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                                                                                                                                                                                                                   MEDLINE; 86
HERRICK G.,
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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MEDLINE; 94134747.
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fallax ma
 telomere-bearing
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                   ILLIAMS K., DOAK T.G., HERRICK G.;
Developmental precise excision of Oxytricha trifallax
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Internal eliminated sequences interrupting the Oxytricha
                                                                                                                                                                                                                                                                                                                                                                       KDA TRANSPOSASE.
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                                                                                                                                       43:759-768(1985)
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"DNA sequence analysis of Sry alleles (subgenus Mus) misregulation as the cause of C57BL/6J-Y(POS) sex rev defines the SRY functional unit."; GENETICS 147:1267-1277(1997).
EMBL; U70651; G2623367; -
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CARDAZZO B., RINALDI T.,
SUBMITTED (FEB-1996) TO
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CARDAZZO B., PELLIZZAR
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EMBL; X57546; E31675; -.
PFAM; PF00961; Intron_maturas
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EMBL; X17484; G9845; -.
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EMBL; U68754; G1685115;
PFAM; PF00320; GATA; 1.
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01, LAST SEQUENCE UPDATE
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MEDLINE; 96346169.
WILSON T.J.M. , DENNY P.W. , PREISER
ROY A., WHYTE A., STRAIH M. , MOORE
"Complete gene, map of the plastid-
plasmodium falciparum.";
J. MOL. BIOL. , 261:155-172(1996).
EMBL; X95275; E220245; -
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Q1-NOV-1996
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RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R., RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. DR EMBL; AE000736; G2983764;  KW LIGASE. SQ SEQUENCE 454 AA; 50893 MW; 1207F9CE CRC32; Query Match Best Local Similarity 40.0%; Pred. No. 1.70e-21; Matches 114; Conservative 52; Mismatches 114; Indels 5; Gaps 5  Db H N V Y N A L A T G V A L E L G V S F Dt 831 HCAYAAYGTNYAAYGCNYINGCNGCNACNG-GNGINGCNYINGARYTNGGNGINWSNT 889 :  :	GRAHAM D.E., O'ERBEEK R., SNEAD M.A., KELLER M., AUJAY M., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; "The complete genome of the hyperthermophilic bacterium Aquae aeolicus."; NATURE 392:353-358(1998). [2] SEQUENCE FROM N.A. STRAIN-VF5;	MURC. AQUIFEX AEOLICUS. BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX. [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIM-VF5; MEDLINE; 98196666.	RESULT 1  ID 067373  AC 067373;  DT 01-AUG-1998 (TREMBLREL 07, CREATED)  DT 01-AUG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE)  DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)  DE UDP-N-ACETYLMURAVATE-ALANINE LICASE.	C 17 160 2.4 277 14 Q98460 GENOME, PARTIAL SEQUEN 1.12e-01 C 19 160 2.4 418 11 O35862 SEX DETERMINING PROTEIN C 19 161 2.4 1532 5 O77332 MAL3PS.16 PROTEIN C 20 161 2.4 1532 5 O77332 MAL3PS.16 PROTEIN C 21 165 2.4 450 5 O77338 MAL3PS.16 PROTEIN C 22 165 2.3 101 5 O77338 MAL3PS.16 PROTEIN C 23 152 2.3 101 5 O25801 SIMILAR TO GROES PROTE C 25 158 2.3 149 8 O47574 NADH DEHYNROGENASE SUB 1.84e-01 C 26 154 2.3 171 5 O446439 C 27 154 2.3 208 5 O25804 COMPLETE GENOME. C 28 154 2.3 208 5 O25804 COMPLETE GENOME. C 28 154 2.3 340 5 O17674 C49A1.2 PROTEIN C 33 152 2.3 340 5 O17674 C49A1.2 PROTEIN C 33 153 2.3 400 5 O17674 C49A1.2 PROTEIN C 33 153 2.3 534 5 O43989 HOMEDBOX CONTAINING PR 7.83e-01 C 33 153 2.3 503 5 O25873 HASTAINE RINASE C. C 39 151 2.2 3 5125 5 O15784 HISTIDINE KINASE C. C 42 150 2.2 751 5 O21672 ROAGEN AMO OF P 2.95e-01 C 42 150 2.2 2819 5 O15792 STRAIN HB3 CG2 (CG2). 1.26e+00 C 45 150 2.2 2819 5 O15792 STRAIN HB3 CG2 (CG2). 1.26e+00

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01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
CELL DIVISION CONTROL PROTEIN 27.
CDC27 OR SNB1 OR YBL084C OR YBL0718.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNCI; ASCOMYCOTA; HEMIASCOMYCETES;
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MEDILINE; 95009933.

LAMB J.R., MICHAUD W.A., SIKORSKI R.S., HIETER P.A.;

LAMB J.R., MICHAUD W.A., SIKORSKI R.S., HIETER P.A.;

"Cdc15p, Cdc23p and Cdc27p form a complex essential for mitosis.

EMBO J. 13:4321-4328(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC27_YEAST
P38042;
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                                                the
                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae chromosome YEAST 11:1103-1112(1995).
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                                                                 between
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                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                      OBERMAIER B., GASSENHUBER J., PIRAVANDI E., DOMDEY H.; "Sequence analysis of a 78.6 kb segment of the left end Saccharomyces cerevisiae chromosome II.";
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             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                             FUNCTION: EXECUTES ESSENTIAL MITOTIC FUNCTIONS NEAR THE METAPHASE/ANAPHASE TRANSITION.
SUBUNIT: CDC16, CDC23 AND CDC27 FORMS A MACROMOLECULAR COMPLEX.
SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: CONTAINS ? TPR DOMAINS.
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SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins as essential components of the yeast cell cycle."; SPRING HARB. SYMP. QUANT. BIOL. 56:663-673(1991).
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Similarity 54.5%;
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and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
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51176 MW;
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EMBL; Z35845; G536136; -.
PIR; S45825; S45825.
SGD; L0000266; CDC27.
PFAM; PF00515; TPR; 5.
CCLL DIVISION; CELL CYCLE; MITOSIS; REPEAT; TPR DOMAIN; NUCLEAR PROTEIN.
DOMAIN 358 391 ASN-RICH.
DOMAIN 358 391 G->D: IN TEMPERATURE SENSI SEQUENCE 758 AA; 85436 MM; A3C06ABO CRC32;
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Pred. No. 4.50e-03;
30; Mismatches 41
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G->D: IN TEMPERATURE SENSITIVE MUTANT
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P02381;

21-JUL-1986 (REL. (

21-JUL-1986 (REL. (

21-NOV-1997 (REL. 3)

MITOCHONDRIAL RIBOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pylori.",

NATURE 388:539-547(1997).

-i- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALA
ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

-i- PATHWAY: PEPTIOGLYCAN BIOSYNTHESIS.

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                 1004
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2
ACETYLMURAMOYL-L-ALANINE SYNTHETASE).
                                                                                                                                                                                                             1004
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MEDLINE; 97394467.
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BACTERIA; PROTEOBACTERIA;
 SACCHAROMYCES CEREVISIAE
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDOGLYCAN SYNTHESIS;
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449 AA;
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                                RIBOSOMAL
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                                PROTEIN VAR1.
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Pred. No. 1.17e-04;
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C3E4D2A CRC32;
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SUBDIVISION; HELICOBACTER GROUP;
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006225;
15-JUL-1998
15-JUL-1998
15-JUL-1998
                                                           BADCOCK K., CHURCHER SUBMITTED (MAY-1997)
                                                                                                                                                                                                                                                           15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UI
15-JUL-1998 (REL. 36, LAST ANNOTATION
UDP-N-ACCTYLMURAMATE--ALANINE LIGASE (
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EMBL; J01525; G343949; -.
PIR; A02751; R3BYM1.
SGD; L0002455; VAR1.
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HUDSPETH M.E.S., AINLEY W.M., S
"Location and structure of the nucleotide sequence of the 40.C CELL 30:617-626(1982).
                                                                                                                                                                                                                        MURC OR MTCY270.16.
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EUKARYOTA; FUNGI; A
SACCHAROMYCETACEAE;
                                                                                                     STRAIN-H37RV;
                                                                                                                                                                                   MYCOBACTERIUM TUBERCULOSIS
BACTERIA; FIRMICUTES; ACTII
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                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                              ACTINOMYCETALES;
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                    COCK K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., PARKI
MITTED (MAY-1997) TO EMBL/GENBANK/DBJ DAR BANKS.
FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
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REQUIRED FOR THE MATURATION OF SMALL RIBOSOMAL
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DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
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CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL
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EMBL; X55034; G40899; -.
EMBL; D10483; G216505; -.
EMBL; AE000118; G1786279; -.
EMBL; U67892; G2177094; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVELAND S.S., POMPLIANO D.L., ANDERSON M.S.; "Conditionally lethal Escherichia coli murein mutants contain defects that map to regions conserved among murein and folyl poly-gamma-glutamate ligases: identification of a ligase
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MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT
RILEY M., COLLADO-VIDES
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STRAIN-K12 / N
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EUR. J. BIOCHEM. 230:80-87(1995).
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MUTANT MURC3, SEG
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YURA T., MORI H., NA
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                                       ATP-BINDING.
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                                                  PEPTIDOGLYCAN SYNTHESIS;
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                                                                                                                                                                                                                                                                                           FUNCTION: CELL WALL FORMATION.

CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.

SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).

SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
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RES. 20:3305-3308(1992)
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                                                    CELL WALL; CELL DIVISION;
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            G->D: IN MURC3.
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051926;
15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                                                                                                      "Characterization of ftsZ, the cell division gene aphidicola (endosymbiont of aphids) and detection CURR. MICROBIOL. 36:85-89(1998).
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                                                                                                             modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                              the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
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CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
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MURC_ECOLI STANDARD; PRT; 491 AA.

P17952; O07099;

P17952; O07099;

P1 01-NVC-1990 (REL 16, CREATED)

P1 01-AUG-1991 (REL 19, LAST SEQUENCE UPDATE)

P1 15-UTL-1998 (REL 36, LAST ANNOTATION UPDATE)

P1 15-UTL-1998 (REL 36, LAST ANNOTATION UPDATE)

P1 15-UTL-1998 (REL 36, LAST ANNOTATION UPDATE)

P1 15-UTL-1998 (REL 36, LAST ANNOTATION UPDATE)
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-i- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: AFP + UDP-N-ACETYLMURAMOYL + L-ALA-ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

-i- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
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P95836;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE-ALANINE LIGASE (EC 6.3.2.8
ACETYLMURANOYL-L-ALANINE SYNTHETASE) (FRAGMENT).
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15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
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SEQUENCE 28
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LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R.
DOUGHERTY B., TOMB J.-F., FLEISCHWANN R.D., RI
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., S
VAN VUGT R., PALMER N., ADAMS M.D., GOCAXNE J.
UTTERRACK T., WADTHEY L., MCDONALD L., ARTIACE
GARLAND S., FUJII C., COTTON M.D., HORST K., F
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Swiss Institute of Bioinformatics and
Bioinformatics Institute. There are no
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CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

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SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., Y.
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CYANOBACTERIA; CHROOCOCCALES;
                                                                              equires a license agreement (S email to license@isb-sib.ch).
                                        SYNTHESIS;
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STRAIN-168 / MARBURG;
MEDLINE; 96310371.
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15-DEC-1998 (REL. 37, LAST ANNOTATION UP-N-ACETYLMURAMATE--ALANINE LIGASE (ECACETYLMURANOYL-L-ALANINE SYNTHETASE).

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15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE-ALANINE LIGASE (EC 6.3.2.8) (UDP-N-ACETYLMURAMOYL-L-ALANINE SYNTHETASE).
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SChreiber, L.; Deutsche, U.; Storck, T.; Mueller-Hill, D.
Submitted to the EMBL Data Library, December 1989
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##cross-references GB:AJ235271; GI
PID:g3860967
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Similarity 38.4%;
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#length
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#formal_name Rickettsia prowazekii
21-Nov-1998 #sequence_revision 21-
                                                                      host Ictalurus punctatus (channel catfish)
17-Aug-1992 #sequence_revision 17-Aug-1992
09-Sep-1997
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#title
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#accession G64597
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*Journal Virology (1992) 186:9-14

*Litle Channel cattish virus: a

*cross-references MUID:92087490
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##cross-references GB:M75136;
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##residues
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##residues 1-4.
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L I D D Y A H H P T E I S A T L K S A R THYTNATHGAYGAYTAYGCNACCAYCCAYCCAGARATHWSNGCNACNYTNAARWSNGCNM
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Similarity 42.7%;
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Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujli, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
Nature (1997) 388:539-547
The complete genome sequence of the gastric pathogen
Helicobacter pylori.
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llarity 50.8%;
Conservative
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09-Aug-1997 #sequence_revision 0
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  (strain 26695)
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                                                                                                                                                                                     preliminary; nucleic acid
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                                                                                                #molecular-weight 50793
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                                        Score 180;
Pred. No. 1.
14; Mismatc
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Pred. No. 9.19e-04;
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                                        DB 2; Lo
1.95e-03;
ches 17;
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Best Local S
Matches 7
                                                                                                                                                                                                     #authors Hardy, C.M.; Clark-Walker, G.D.
#journal Curr. Genet. (1991) 20:99-114
*title Nucleotide sequence of the COX1 gene in Kluyveromyces lactis mitochondrial DNA: evidence for recent horizontal transfer of a group II intron.
#cross-references MUID:92035081
#accession S17998
                             10 - 369
  370-763
                                                                                                           #introns
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##cross-references GB:AE0001213; GB:AE000520;
##experimental_source strain Nichols
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I F G S I R E
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K Y P H K E V V A V F Q P H T F S R T Q
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                                                                                                         mitochondrion
SGC2
69/1; 235/3; 324/2
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gene COXI intron 4 protein - yeast (Kluyveromyces marxii
var. lactis) mitochondrion (SGC2)
#formal_name mitochondrion Kluyveromyces marxianus var.
lactis, Candida sphaerica
10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change
                                                                                  mitochondrion
                                                                                           *superfamily cytochrome-c
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larity 37.4%;
Conservative
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#domain cytochrome-c oxidase chain I homology #status
atypical #label CO1\
#domain intron-encoded domain #label INT
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es EMBL:X57546
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                                                      #domain cytochrome-c
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                                           #label EXN\
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Pred. No. 4.48e-12;
36; Mismatches 91;
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                                                                                              oxidase chain
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REFERENCE
#authors
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Best Local
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                                                                                                                                                                                                                                                                                                                         #title Genomic sequence comparison of two unrelated isolates human gastric pathogen Helicobacter pylori. #cross-references MUID:99120557 #accession B71917
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##cross-references GB:AE001489; GB:AE001439;
##experimental_source strain J99
                                                                                            842
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                                                                                                                                                                                                                                                                                                            ##status
                                                                                                                                                                                                                                                                                           ##molecule_type DNA
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                                                                             TNWSNGCNYTNGAYGARYTNAAYYTNGARGARATHMGNAAYAAYYTNYTNAAYTTYAARG
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ATHAAYAAYYTNATHA
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* M F I I T P S N N T F F N I M C H F L
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   GNATHAARAARMGNTTYGAY.
                                               TTAGTTAGAGAAGCTAGATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTG S Y L E K L D V T N I K E A L E T F G G
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Similarity 37.2%;
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                                                                                                                                                        Similarity
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G.F.; Trust, T.J.
Nature (1999) 397:176-180
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#length 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B71917 #type complete udp-n-acetylmuramate--alanine ligase
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strain J99
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                                                                                                                                        Conservative
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I L Q K N N L I L I D D Y
-ATHYTNCARAARAAYAAYYTNATHYTNATHGAYGAYTAY
                                                                                                                                     Score 198; DB 2;
Pred. No. 1.90e-05;
34; Mismatches 65
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Pred. No. 3.83e-06;
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                                  R.; Aravind, L.; Mitchell, W.P.; Olinger, L.;

R.L.; Zhao, Q.; Koonin, E.V.; Davis, R.W.

#journal Science (1998) 282:754-759

#title Genome sequence of an obligate intracellular pat.

#cross-references MUID:99000809

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Fujita, N.; Isono, K.; Mizobuchi, K.; Nakata, A.
submitted to the EMBL Data Library, December 1992
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perne Burland, V.; Riley, M.; Collado-Vides, J.; Glasner Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau,
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Nucleic Acids Res. (1990) 18:4014
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The genome sequence of mitochondria. C71679
                                                               Andersson, S.G.E.; Zomorodipour, Sicheritz-Ponten, T.; Alsmark, Naeslund, A.K.; Eriksson, A.S.
                                                                                                                                                     Rickettsia prowazekii
#formal_name Rickettsia prowazekii
21-Nov-1998 #sequence_revision 21-
                                                                                                                                                                                              C71679 #type complete UDP-n-acetylmuramate--alanine ligase
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#length 491 #molecular-weight 53626 #checksum
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ATP; cell division; cell wall; ligase; P-loop; peptidoglycan
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27; Mismatches 80
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                                                                                                                         Genomic sequence of a
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Local Similarity 39.18;
hes 79; Conservation
                                                                                                                                                                                                                             ##molecule_type DNA
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Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fields, C.; Gooayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.F.; Phillips, C.A.; Sprigs, T.; Hedblom, E.; Cotton,
M.D.; Uterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.M.; Braddon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
Whole genome random sequencing and assembly of Haemorhi''.

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UDP-N-acetylmuramate--alanine ligase (EC 6.
Haemophilus influenzae (strain Rd KW20)
#formal_name Haemophilus influenzae
18-Aug-1995 #sequence_revision 18-Aug-1995
                                                         peptidoglycan biosynthesis
#superfamily UDP-N-acetylmuramate--alanine ligase
#TP; cell division; cell wall; ligase; P-loop; pe
                                                                                                                             one of the ligases responsible for the UPD-N-acetylmuramyl pentapeptide, an \ensuremath{\mathsf{UPD}}
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nucleotide-binding motif A (P-loop)
#molecular-weight 51994 #checksum 7812
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The complete genome of the hyperthermophilic bacteri
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#formal_name Aquifex aeolicus
08-May-1998 #sequence_revision 08-May-1998 #text_change
21-Aug-1998
B70418
                                                                                                                                                                                                                                                                                                                                                                        complete genome of the hyperthermophilic bacterium
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ces GB:AE000736; NID:g2983763;
source strain VF5
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Pred. No. 1.30e-19;
52; Mismatches 114;
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PID:g1653723
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                        E Y L V A E V D E S D G S L T K H H P E GNGARTAYYTNGTNGCNGARGINGAYGARWSNGAYGGNWSNYTNACNAARCAYCAYCCNG
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UDP-N-acetyImuramoylalanine--D-glutamate ligase
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DNA Res. (1996) 3:109-136
Sequence analysis of the genome
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Makamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Sh
S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.
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REFERENCE $71000
#authors Varon, D.; Brody,
#journal MO1. Microbiol. (1
#title Bacillus subtilis
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#journal Mol. Microbiol. (1996) 20:339-350
Bacillus subtilis operon under the dual control general stress transcription factor sigma(B) a sporulation transcription factor sigma(H).
#cross-references MUID:96310371
#accession $71002
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#accession C690
##status
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##cross-references EMBL:L31845; NID:g556013;
##experimental_source strain 168, substrain 1
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_ntp n.a. - n.a. Smith-Waterman search, using a protein database which has been backtranslated into n.a. using IUPAC symbols

Run on: Tabular output not generated. Wed Nov 24 01:12:22 1999; MasPar time 218.82 Seconds  $1484.328\ \mbox{Million}$  cell updates/sec

N.A. Sequence: Description: >US-09-103-287-1 (1-1351) from US09103287.seg 6755 1 ATGAGTAAGGAGTTTTATAT......TTAATATGTTTTATAATAGAG 1351
TACTCATTCCTCAAAATATA.....AATTATACAAATATTATCTC

Scoring table: TABLE bktranslate2

Gap 30

Nmatch

STD :

Dbase 0; Query 0

122810 seqs, 120205779 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60

Database:

1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 77.827; Variance 184.008; scale 0.423

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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в70220 S14577	A45600 R3BYM1	G64597 S14469	B/191/ A71699 H36789	C71338 S17998	C71679 A71475	E64185 CEECAM	B70418 S76722 H70201	C69662	ID
conserved hypothetica asparagine-rich prote	asparagine-rich blood ribosomal protein var	<pre>UDP-N-acetylmuramate- asparagine-rich prote</pre>	udp-n-acety1muramate- UDP-n-acety1muramoy1a hypothetical protein	<pre>gene COX1 intron 4 pr</pre>	<pre>UDP-n-acetylmuramate- probable muramate-Ala</pre>	<pre>UDP-N-acetylmuramate- UDP-N-acetylmuramate-</pre>	<pre>UDP-N-acetylmuramate- UDP-N-acetylmuramoyla UDP-N-acetylmuramate-</pre>	UDP-N-acetylmuramate-	Description
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collagenase - Clostri	hypothetical protein	DNA-directed RNA poly	asparagine-rich prote	major merozoite surfa	collagen alpha 1(XI)	hypothetical protein :	DNA helicase II (mutB	heme lyase yejR – Rec	asparagine-rich prote	a .	probable multiple tra	2		hemoglobin beta C(NA)	f22b7.3 protein - Cae	hypothetical protein	ത	~		sex-determining prote	ribosomal protein VAR	hemoglobin beta C(NA)	kinetochore SKP1 prot	ision	probable murC protein
1./4e+00	1.40e+00	4.62e-01	.7		w		4.62e-01			3.68e-01	7.22e-01	1.40e+00	1.12e+00	4.62e-01	4.62e-01	1.86e-01	7.35e-02	. 28e	.34€	.34e	2.34e-01	.34e-	.48e-	9e-	1.39e-02

## ALIGNMENTS

RESULT ENTRY

#authors	REFERENCE	ACCESSIONS		DATE	ORGANISM		TITLE	ENTER
Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A	A69580	C69662; S71002	17-Mar-1999	05-Dec-1997 #sequence_revision 05-Dec-1997 #text_c	#formal_name Bacillus subtilis	Bacillus subtilis	UDP-N-acetylmuramatealanine ligase (EC 6.3.2.8)	C69662 #type complete

murC -

Alloui, G.; Azeyedo, V.; Bertero, M.G.; Bessleres, P.;
Bolotin, A.; Bornchert, S.; Boriss, R.; Boursler, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Cadawil, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.;
Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Lazarevio, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Kunita, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
N.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
N.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.;
Sekowska, A.; Sacror, S.J.; Serror, P.; Shin, B.S.; Soldo,
B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
Takemaru, K.; Takeuchi, M.; Tanakoshi, A.; Tanaka, T.;
Vandenbol, M.; Vannier, F.; Vassarotti, A.; Tanaka, T.;
Wanbutt, R.; Wedler, E.; Wedler, H.; Weitzenegger, T.;
Winters, P.; Wigat, A.; Yoshida, K.; Yoshikawa, H.F.; Zumsnoto,
K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumsnoto, Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P. THIS PAGE BLANK (USPTO)

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

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Matches 41; Conser
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Patent No. 5189151

APPLICANT: BAUDRY, BERNADETTE; LEVINE, MYRON M.

TITLE OF INVENTION: HIGHLY SPECIFIC DNA PROBE FOR
ENTEROAGGREGATIVE ESCHERICHIA COLI
NUMBER OF SEQUENCES: 1
                                                                                                                                                                      SEQ ID NO:1
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 290 BP: 17 A; 34 C; 8 G
                                     509 CTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTCAAAGATATT 567
                                                             296 CTTATGAAGCAAAAATGCAGAATAATAAATTGGATATTGCTAATTATTTAAAATATATT 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 1:
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Local Similarity 12.6%;
hes 14; Conservative
                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 16-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
NAME: WILSON, MARY J.
22,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
"NDT TOARTON NUMBER. INC/NS/273.846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
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15
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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 12-JUL-1994 CLASSIFICATION: 530
                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                         776
                                                                                                                                             BP;
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 base pairs
                                                                                                                                            296 A; 109 C; 128 G; 243 T; 65 other;
                                                                                                     1.7%;
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                                                                                       Score 23; DB 5; I
Pred. No. 7.69e-01;
0; Mismatches 18
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Pred. No. 7.69e-01;
28; Mismatches 68
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Sequence 22, 1
Patent No. 57
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APPLICANT: Wallac
                                  245 TCATGGCTACTCGCGA 230
                                                       914 WYKGKAKYRVSNRSGV 929
                                                                              305 CCTAAAAAATCATTATAACTTACAACATCTAATTTCAATTGATGTGCACGTACTATTTCT 246
                                                                                                    854 YYCVRGRSYDSDGGDYWGGTTVTVSSHUVKDMTSSSSASVGDRVTTCRSSTTHGNGNTYY 913
                                                                                                                                                                                                                                       TELEPHONE: 212-688-920
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       NAME: Hanson, No. 5795961man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 54
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION UNBER: US/08/388,672A FILING DATE: 14-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Welt, Sydney
APPLICANT: Kitamura, Kunio
TITLE OF INVENTION: Recombinant Human Anti-Lewis
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 25
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TOPOLOGY: unknown
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Similarity 13.2%;
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2, Application US/08388672A
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Old, Lloyd J.
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Pred. No.
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atches 28;
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                                                                                          MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP; 6 A; 6 C; 4 G; 5 T; 60 OTHER.
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                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                       1.7%;
Local Similarity 10.1%;
es 7; Conservation
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Local Similarity 19.8%;
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MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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LENGTH: 965 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: unkno
TGTGGAGACAGGAAGTGATCATAAAACTCACCATCCACATACACATCAAAAGCAGTACCT 738
                                                                                                                    TOPOLOGY:
                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                     81 base pairs
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                                                                                                                                                                                                   : (212) 790-9090
(212) 869-9741/8864
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PC/TUS9511934
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                                           Score 23; DB 4;
Pred. No. 7.69e-0
19; Mismatches
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Pred. No. 2.46e-01
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                                              43;
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Best Local Similarity 13.2%;
Matches 10; Conservative
Sequence 1, Application US/08273846
Sequence 1, Application US/08273846
Patent no. 5641863
GENERAL INFORMATION:
APPLICANT: "SCHEBIBER, ALAN D.
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                                                                                                                                                                                                                                                                                                               939 ATTTGCAATTGTAGTT
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QUENCE 82 BP; 1
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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SOFTWARE: PatentI
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FILING DATE: 20-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leslie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Release #1.0,
                                                                                                                                                                                                                  DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT/US95/11934
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Pred. No. 7.69e-01;
19; Mismatches 47
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    STIMULATING PHAGOCYTOSIS
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RESULT
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                                                                                                                                                                                                                                               Patent No. 5668263
GENERAL INFORMATION:
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Sequence 2, Application US/08357962
Patent No. 5668263
                                                                                                                                                                                                                                                                                                              XXXXXX
                                                                                                                                                                                                                                                                                                                     US-08-357-962-2 STANDARD; DNA; UNC; 108 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 108 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                        1.8%;
Local Similarity 31.6%;
hes 18; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                       39 RTCNTWYGCHACHACHACHRTDACYGSWCCWCCWRGWRGHACYGAYWCHGTDMT 95
                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                    APPLICANT: Hoyer, Lois
APPLICANT: Livi, George
APPLICANT: Shatzman, Allan
TITLE OF INVENTION: CONSERVED YEAST NUCLEIC ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPULUE TYPE: GE
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REFERENCE/DOCKET NUMBER: P5(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5019
TPILEDRY. 2100-2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/3
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                 ZIP:
                                                                                                                                     CITY: King of Prussia
STATE: PA
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                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 3
                     FILING DATE:
                                                                                                                            COUNTRY:
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                    NUMBER: US/08/357,962
16-DEC-1994
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22; N
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Pred. No. 2.46e-01
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Best Local S
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 INFORMATION FOR
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1278 ATCACCTGCACCCATAAATAAAACAACAGCATTATCAAATTGTTCTAATACATTAAT
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Local Similarity 31.6%;
nes 18; Conservative
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APPLICANT: I
APPLICANT: (
APPLICANT: (
                           TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 579596
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Welt, Sydney APPLICANT: Kitamura, Kur
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Antibodies
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NAME: Jervis, Herbert H
                                                                                                                                               APPLICATION NUMBER: US/08/388,672A FILING DATE: 14-FEB-1995
                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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New York
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Y: U.S.A.
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Jervis, Herbert H
Jervis, Herbert H
Jervis, Herbert H
Jervis, Herbert H
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Old, Lloyd J.
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Pred. No. 2
22; Mismat
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-878-106-2 STANDARD; DNA; UNC; 108
                                        Patent No.
                                                Sequence 5, Sequence 5,
                                                                               XXXXXX
                                                                                        US-08-238-163-5 STANDARD; DNA; UNC;
                                                                                                                                                                                                               SEQUENCE 108 BP; 20 A; 23 C; 12 G; 10 T; 43 OTHER.
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Sequence 2,
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       GENERAL INFORMATION:
APPLICANT: BENNET
APPLICANT: LABAVI
                                                                                                                               324 TACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACA 366
                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hoyer Lois
APPLICANT: Livi, George
APPLICANT: Shatzman, Alla
TITLE OF INVENTION: CONSE
NUMBER OF SEQUENCES: 9
                                                                                                                                                 48 HACHACHACHRTDACYGSWCCWCCWRGWRGHACYGAYWCH 90
                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/357,962
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
 APPLICANT:
                                                                                                                                                                                                                          FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                            MOLECULE N' HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 108 base pairs
                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 610-270-5019
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P50278
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                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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Similarity 32.6%;
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                                        , Application US/08238163
, Application US/08238163
5569830
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, Application US/08878106
5817466
                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                        Conservative
POWELL, Ann
          BENNETT, Alan
LABAVITCH, Jo
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          John M.
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Pred. No. 7
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7.72e-02;
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Best Local
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Sequence 2, Application US/08878106
Patent No. 5817466
                                                                                                                                                                                                                   US-08-878-106-2 STANDARD; DNA; UNC; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                         XXXXXX
                                                                         GENERAL INFORMATION:
APPLICANT: Hoyer, Lois
APPLICANT: Livi, George
APPLICANT: Shatzman, Allan
TITLE OF INVENTION: CONSERVED YEAST NUCLEIC ACID SEQUENCES
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                        440 CCCATACCTGTGCCATCACCAATTAAAAATGAAGTCTTTTTATCACCATTCATAACATGT 381
                                                                                                                                                                                                                                                                       380 GATAATAAACCTGTTGTAGAAGTTTTACCATGTGCACCAGTTACAGCTACTGAAGTA 324
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                                                                                                                                                                                                                                                                                                70 GNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTA 126
                                                                                                                                                                                                                                                                                                                                                 11 VVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNYG- 69
                                                                                                                                                                                                                                                                                                                                                                      1.9%;
Local Similarity 18.8%;
les 22; Conservation
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LENGTH: 215 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                            CORRESPONDENCE ADDRESS:
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OTHER INFORMATION: 5
IENCE 215 BP; 15 A; 8 C
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TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: PLANT INHIBITORS AND THEIR USE TO CONTROL FUNGAL DISEA
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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         STREET: 709 Swedeland CITY: King of Prussia STATE: PA
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CLASSIFICATION:
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CITY: San Francisco
                           ADDRESSEE: Smilling
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USA
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                                                SmithKline Beecham Corporation
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Pred. No. 2.37e-02;
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T; 141 OTHER.
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Best Local Similarity 46.2%;
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Sequence 2, Application US/08357264
Patent No. 5541077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
SEQUENCE 1200 BP; 406 A; 224 C; 230 G; 323 T; 17 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-357-264-2 STANDARD; DNA; UNC; 1200 BP
                                                                                                                                                         APPLICATION NUMBER: US 08/15266
FILING DATE: 16-NOV-1993
APPLICATION UNMBER: US 663897
FILING DATE: 14-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16773
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
                                                                            TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
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TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1200 base pair
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 1200 base pair
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                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BURNIE Mr., James P.
APPLICANT: MATTHEWS Ms., Ruth C.
TITLE OF INVENTION: FUNGAL STRESS PROTEINS
 TOPOLOGY: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                         STRANDEDNESS:
                                                                                                                                            REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: PNK/5544/202253/DJP
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                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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1100 New York Avenue, N.W.
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DNA (genomic)
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Pred. No. 7.
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Best Local Similarity 46.2%;
Matches 18; Conservative
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Sequence 2, Application US/08357962
Patent No. 5668263
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324 TACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACA
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                                                             48 HACHACHACHRTDACYGSWCCWCCWRGWRGHACYGAYWCH 90
                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linea MOLECULE TYPE: Gei
                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: ORIGINAL SOURCE:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
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APPLICANT: Livi, George
APPLICANT: Shatzman, Allan
TITLE OF INVENTION: CONSERVED YEAST NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: P50278
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Pred. No. 7.
20; Mismatc
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Pred. No. 7.16e
15; Mismatches
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Best Local Similarity
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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-238-163-5 STANDARD; DNA; UNC; 215
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                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 CATTACCTTGTATAACTACCATATCTTCTTTTATGTTATTAGCACCAAATGGTAATATTT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   406 TCTTTTTATCACCATTCATAACATGTGATAATAAACCTGTTGTAGAAGTTTTTACCATGTG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 TTCCGACAAAATGATAGTGTGTCATTA 20
                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            APPLICANT: POWELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
   ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                        NUUKESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco
STATE: Californ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTACAACATCTAATTTCAATTGATGTGCACGTACTATTTCTTCATGGCTACTCGCGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: sing
                CLASSIFICATION:
                              FILING DATE:
                                        APPLICATION NUMBER:
                                                                                                                                               COUNTRY: US
ZIP: 94105-1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                           US/08/238,163
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Pred. No. 6.73e-22
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Best Local S
Matches 2
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OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08672514 Sequence 2, Application US/08672514 Patent No. 5686248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1237 CAATTTGATAATGCTGTTGTTTTATTTATGGGTGCAGGTGATAT 1280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1117 TTCTTATGTGAAATTTTTGGCTCAATTAGAGAAAATTCTGGCGCATTAACGATACAAGAT 1176
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MURNIE Mr., James P.
APPLICANT: MATCHHEWS Ms., Ruth C.
APPLICANT: MATCHEWS Ms., Ruth C.
TITLE OF INVENTION: FUNGAL STRESS PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 NNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 DKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNYGGNNVGAAKTH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 YYTHTNVSGADS-KTVTDSYNASGTSSSNGGTDGNRSGADSYGSS-KTAMTSRNRTGKTA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 15.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                       COMPUTER: . IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: . Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1
FILING DATE: 16-NOV-1993
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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                                        APPLICATION NUMBER: 16-NOV-
                                                                                                              APPLICATION NUMBER: FILING DATE: 28-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                                               COUNTRY: JUSA
ZIP: 20005-3918
                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                      STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: ": misc_feature
               FILING DATE:
                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                       1100 New York Avenue, N.W
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                                                                                                                             28-JUN-1996
               14-MAR-1991
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-1993
                            US 663897
                                                                                   08/152,669
                                                                                                                                            US/08/672,514
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Pred. No. 7.16e-03
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Sequence 14, Applicati 6.73e- 108-232- Sequence 2, Applicatio 7.16e- 108-672- Sequence 2, Applicatio 7.16e- 108-357- Sequence 2, Applicatio 7.72e- 108-357- Sequence 2, Applicatio 7.72e- 108-357- Sequence 2, Applicatio 7.72e- 108-238- Sequence 2, Applicatio 2.46e- 108-357- Sequence 2, Applicatio 2.46e- 108-357- Sequence 2, Applicatio 2.46e- 108-357- Sequence 2, Applicatio 2.46e- 108-358- Sequence 2, Applicati 2.46e- 108-368- Sequence 2, Applicati 7.69e- 17-US95-1 Sequence 97, Applicati 7.69e- 189151-1 Sequence 97, Applicati 7.69e- 108-388- Sequence 22, Applicati 7.69e- 108-388- Sequence 27, Applicati 7.69e- 108-388- Sequence 27, Applicati 7.69e- 108-388- Sequence 27, Applicati 7.69e- 108-388- Sequence 7, Applicati 7.69e- 108-388- Sequence 7, Applicati 7.69e- 108-381- Sequence 7, Applicati 7.69e-	SUMMARIES	Mean 8.554; Variance 5.055; scale 1.692  No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.	ed _COMB 2:5B_COMB 3:5C_COMB 4:PO	g: Minimum Match 0% Listing first 45 summaries	eg	Gap b  Dbase 0; Query 0	1 ATGAGTAAGGAGTTTTATATTTAATATGTTTATAATAGAG 1351 TACTCATTCCTCAAAATATAAATTATACAAATATTATCTC TABLE default	>US-09-103-287-1 (1-1351) from US09103287.seq 1351	not generated.	; MasPar time 99.13 S	elease 3.1A John F. Collins, Biocomputing Research Unit. opyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd n.a n.a. database search, using Smith-Waterman algorithm	***********************************	(Fa)	
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6049	6049	5852	4235	4235	4235	4041	1288	1265	1265	1250	1011	774	540	162	162	162	156	156	156	156	156	156	81	75
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US-08-463-	US-08-471-	US-07-867-	PCT-US94-0	US-08-082-	US-08-021-	US-08-471-	US-08-440-	US-08-182-	US-08-712-	US-08-117-	PCT-US96-0	PCT-US91-0	US-08-117-	US-08-545-	PCT-US95-0	US-08-242-	PCT-US94-0	US-08-242-	US-08-084-	US-08-545-	US-08-021-	PCT-US95-0		PCT-US95-1
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence
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Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicati	Applicatio	Applicatio	Applicatio	Applicati	<pre>l9, Applicat</pre>	Applicatio	Applicati	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	$\mathbf{-}$	Applicatio	Applicatio	ᄗ	Applicati
	6.97e+00	•	•	2.35e+00	2.35e+00			٠	•	2.35e+00	2.35e+00	2.35e+00	٠.	'n	'n	2.35e+00	2.35e+00	2.35e+00	2.35e+00	2.35e+00	ω	2.35e+00	2.35e+00	2.35e+00

## ALIGNMENTS 1 3-232-463-14 STANDARD; DNA; UNC; 7218 BP. KX

US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.

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Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
COUNTRY: USA
ZIP: 22313-0299
COMPUTER: IDEA PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE: APPLICATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELEPHONE: (703)683-4109
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

WPI; 94-279739/34. P-PSDB; R65152.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARS or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.

Sequence 114 BP; 0 A; 4 C; 4 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            970466 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)1(TGC)(NNB)10(TGC)2(NNB)4X(NNB)8(TGC)(NNB)9Y: X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in 070465-68. Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The objectides are also
This sequence represents a human or mammalian DNA replication origin consensus sequences of the invention, designated uniorsconsensus. Administration of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication in vivo or in vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-1998.
25-JUN-1998.
21-MEC-1997; CA0972.
21-MAY-1997; US-047322.
16-DEC-1996; US-033374.
(UYMC-) UNIV MCGILL.
Cossons NH, Nielsen TO, Price GB, Zannis-Hadjopoulos M; WPI; 98-362770/31.
                                                                                                                                                                                                                                                                                                                                              Human or mammalian origin of replication consensus sequences - for inhibiting DNA replication, for controlling initiation of replication, maintaining circular plasmids and in assembly of human artificial chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalian DNA replication origin consensus sequence, uniorsconsensus. DNA replication origin; human; mammal; alphaconsensus; uniorsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V44650;
06-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying proteins or peptide(s) which bind a ligand -
screening a recombinant vector library expressing fusion
                                                                                                                                                                                                                                                                                                          Claim 1; Page 42; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           976 CTCTTGGATGGTGCATAATCATCTACAATAACTTGATTTGCAATTGTAGT 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 bnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 btgcnnbnnbnnbnnbnnbnnbnnbnnbnnbtgctgcnnbnnbnnbnnbnnnnnnnn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCAACAACTTCTTTATGTGGATATTTCTTTCGTGCTGTGTCAATTGTAGCACTAATTT 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
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Pred. No. 2.37e-04;
30; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 114;
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                                                                                                                                                                                                                                         chromosomal function. The consensus sequence can be combined with cloned human telomeres and large centromeric blocks for assembly of human artificial chromosomes and maintained as bacterial plasmids, circular or linear, large or small yeast artificial chromosomes (YACs) or as episomal elements.
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                              semi-conservative replication in proliferating mammalian cells, or inserted into mammalian or human artificial chromosome vectors for gene therapy. Particularly, they are used to create shuttle vector constructs for defining the essential mammalian elements required for maintenance of
246 AGAAATAGTACGTGCACATCAATTGAAATT 275
                                                                           186 TAATAACATAAAAGAAGATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGA 245
                                  62 -kmwwtwkawsdatakwwwkdakwkmwrkt 90
                                                                                                             2 wmtwaakrawrwwkkdavwwgakrwwkwvwhrassacmdwkaaktwkggwtwarrywkgr
                                                                                                                                                      th 2.4%;
Similarity 12.2%;
11; Conservative
                                                                                                                                                                                                                                   91
                                                                                                                                                                                                                                   BP;
                                                                                                                                                                                                                                   15 A;
                                                                                                                                                      Score 33; DB 46; L
Pred. No. 6.91e-04;
53; Mismatches 25;
                                                                                                                                                                                                                                   1 C;
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                                                                                                                                                                                          Length 91
                                                                                                                                                        Indels
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Search completed: Sat Nov 27 11:49:04 1999 Job time: 316 secs.

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                                                          Disclosure; p; English.
Random point mutations were introduced into the alpha fragment E.coli beta-galactosidase. The wild type sequence was obtained it coll beta-galactosidase. The wild type sequence was hybridised it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1988.
30-MAR-1988;
03-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                           Introducing random point mutations into nucleic acods by prepn of single stranded template, annealing a prim misincorporation, completion of molecules and screenin Disclosure; p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A,
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer_bind
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08-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BECT ) BECTON DICKINSON Shank DD, Spears PA;
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26-MAY-1992; US-889651.
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.coli beta galactosidase alpha-fragment; base substitutions; ss
scherichia coli.
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42; Misma
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les and screening.
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2.98e-06;
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         WO9418318-A.
18-AUG-1994.
01-FEB-1994;
01-FEB-1993;
30-DEC-1993;
31-JAN-1994;
(UYNC-) UNIV
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070466;
070466;
05-APR-1995
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Q51746;
31-MAY-1994
                                                                                                                                                                                                                                                                                                                                  be useful as an initial screen to
see also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 (
                                                                                                                                                              Generic DNA sequence to generate a random TSAR-9 petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker;
                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleoti
(051735). It hybridized to all spp. of mycobacte
cross reacted to a few non-mycobacterial spp. Th
be useful as an initial screen for mycobacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                           (BECT ) BECTON DICKINSON Shank DD, Spears PA; WPI; 93-378844/48.
                                                                                                                        misc_feature
                                                                                                                                           Synthetic.
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24-MAY-1993;
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EP-571911-A.
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NORTH CAROL
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larity 11.7%;
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                                                                                sequence of comments)"
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The sequence is that of a Streptococcal polypeptide coding region. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleuriempyema, endocarditis or infection of the cerebrospinal fluid. Sequence 1825 BP; 550 A; 385 C; 366 G; 524 T;
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(SMIK ) SMITHKLINE BEECHAM PLC.
Black MT. Hodgson JE, Knowles DJC, Lonetto MA, Nicholas
Reid RH, Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1998.
24-NOV-1997; U21976.
27-NOV-1996; US-031879
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                                                                                                                                                                                                                                                                                                                                                                                              accaataacggctgtcgcattcatgatattgtgacgaccaaaggttggaatgtggaattg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaagtcatcaataatcactgtatcattgacaattttctcagtgaaacgacgtttaacacc 1178
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tttggcatagtcgttaaaggcattgaaaacatcctcgagacttgtgaaataatctggatg
                                                                                   agacgtaatcttacgcaattcagcatcttcaccatagacaaaaagacccatcgtaatttg
                                                                                                                                                         ATTTTGAGCATAAATGTCAT - - CCGA - ATCTTTAAATCCATAGTAATAAATTGGAACATC
                                                                                                                                                                                 atcactagctacaaagtcattgccttcagcttcaaaaccataataaattggtgcatc 1418
                                                                                                                                                                                                                                                            ATCATAAAACTCACCATCCACATACACATCAAAAGCAGTACCTTTATCCGTAATTTGAAT
                                                                                                                                                                                                                                                                                                          ccccaagttttgtccacggaaatgaacggtgaaggttgaaccagttgttgaacgaagaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggcaaatgttttcaagtgctcacgcaccaagttcaaatcaaatcctgctgtgtaaagaag 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTGGATATTTCTTTCGTGCTGTGTCAATTGTAGCACTAATTTCTCTTGGATGGTGTGC
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                                                     TGCTTCAATTTTACGTAGATGTTCATCATCACCCCCAAGCAATAATACCTTTTTTAACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATAATCATCTACAATAACTTGATTTGCAATTGTAGTTTCATTGAAACGACGTTTAACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers complement (256..423)
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Pred. No. 3.
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prophylaxis; ds.
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3.68e-72;
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                                                                                                                                                                                                                              Query Match 3.0%;
Best Local Similarity 6.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wo-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; haso colors.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and them expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1988.
30-MAR-1988: 105163.
30-MAR-1989: 105163.
03-APR-1987; US-034819.
03-SUOMEN SOKERI OY.
Lehtovaara P. Knowles J, Koivula A, Bamford J,
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                         occurred singularly in any given mutant. See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Introducing random point mutations into nucleic acods by prepn of single stranded template, annealing a primer, misincorporation, completion of molecules and screening.
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N81164 standard; DNA;
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                                                      ncccbnnhvchnvhbnnhrnwayvrhdarrdd
                                                                                                               AATGAAGTCTTTTATCACCATTCATAACATGTGATAATAAACCTGTTGTAGAAGTTTTA 354
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                                                                                                                                                                                                                                                                                                                                                 204 BP;
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coli.
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Pred. No.
53; Misma
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   밁
                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                    PT Nucleic acid encoding antigenic peptide(s) from Streptococcus
PT pneumoniae - or their epitope-containing fragments, useful in
PT protective or therapeutic vaccines, and for diagnosis
PT protective or therapeutic vaccines, and for diagnosis
PT protective or therapeutic vaccines, and for diagnosis
PT protective or therapeutic vaccines, and for diagnosis
PT protective or therapeutic vaccines from Streptococcus pneumoniae.
PT protection caid sequence encoding the Streptococcus pneumoniae protein
PT protection caid sequence encoding the Streptococcus pneumoniae.
PT protective antibodies against
PT protection can be useful in vaccines for inducing protective antibodies against
PT protection caid or meningitis. Probes based on the nucleic acid
PT protection protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, ce.g. by injection, orally or through the skin, typically at 0.01-1000
PT present seducine protein in per dose.
PT protective or their protein and for passive to purify the protein and for passive contains an expectation or passive contains an expectation or passive contains an expectation or passive contains and per dose.
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Matches 63
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Streptococcus pneumoniae; antigen; vaccine; infection;
Streptococcus pneumonia; otitis media; meningitis; ss.
Streptococcus pneumoniae.
Streptococcus pneumoniae.
Location/Qualifiers
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31-OCT-1996; US-029960.
(HUMA-) HUWAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon Kunsch CA, Rosen CA;
pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a
                                                                                                                                                 $ $ $ $ $ $
                                                                                                                                                                                                                                                                                                                                                                                                       Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays pharmaceutical compositions and vaccines for Streptococcus
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                                                                                                                                          present invention describes a computer readable medium which has nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded it, or a representative fragment or a sequence at least 95% identical SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 391 (V52134 to V52524) are genomic fragments from Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98-272225/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccaataacggctgtcgcattcatgatattgtgacgaccaaaggttggaatgtggaattgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aagtcatcgataatcactgtatcattgacaatttttctcagtgaaaacgacgtttaacaccg
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                                                                                          tattogtcagattcaaagacaaaatatttggcattggccgaaccacgacctgtcccatct 1354
                                                                                                                                                                                                                                                            tcaaagtcaatgttggtgataatagagtattctgggtggtaaggcatgaagtgacgctca
                                                                                                                                                                                                                                                                                                                                                                                                                          gacgtaatcttacgcaattcagcatcttcaccatagacaaaaagacccttggtgatttgt 1174
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                                                                CCAATTAAAAATGAAGTCTTTTATCACCATTCATAACATGTGATAATAAACCTGTTGTA
                                                                                                                                                  TATTCACATGCCTCAAAAGCGAAATAATCACTTTCAGGCAATCCCATACCTGTGCCATCA
                                                                                                                                                                                                                                    TCGAAATCAATATTTGTCATAATTGCGTAATCAGGTTTATAACTTAAAAAGTGACGTCTA
                                                                                                                                                                                                                                                                                                                                                         ttggcatagtcgttaaaggcattaaaaacatcctcgagacttgtgaaataatctggatgg 1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCATAAAACTCACCATCCACATACACATCAAAAGCAGTACCTTTATCCGTAATTTGAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAATTACAGCTAATGCATTTAAAACTGTATGGTCACCATATTGTGGAGACAGGAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAAACGTTTCTAATGCTTCTTTAATATTTGTAACATCTAGCTTCTCTAAATAACTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gcaaatgttttcaagtgctcacgcaccaagttcaaatcaaatcctgctgtgtaaagaaga
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                                                                                                                                                                                                                                                                                                                  TGTGCCATTTCTTGGAATGCATCAAAAACATCATTAATATCTTTGAAATAATCAGGATGA
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. No. 7.05e-101;
Mismatches 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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PS Claim 1; Page 1983; 2084pp; English.

Claim 1; Page 1983; 2084pp; English.

CR A computer readable medium has been developed which has recorded on it computer readable medium has been developed which has recorded on it cross an include the sequences isolated from the Enterococcus faecalis genome. CR 119319 represent these nucleotide sequences which are primary curie identify fragments of the Enterococcus faecalis genome with cross commercial importance. The products can be used to detect the presence cross faecalis in samples. They can also be used for commercial importance infection in an animal and monitoring crossing Enterococcus faecalis in samples and for identifying agents which can be used to compose the products can be used for modulate the growth or pathogenicity of Enterococcus faecalis, or can be used in various or in vitro. In particular the cross properties encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1998.
04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
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Barash SC, Dillon PJ, Kunsch CA:

WPI; 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides

used to develop products for the detection of Enterococcus and for

use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis genome contig SEQ ID NO:780. Enterococcus faecalis; contig; detection; Enterocovaccine; attenuation; computer readable medium; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecalis WO9850555-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                       gaagagggatgatatccaagcccgaaatattcaacgaacaacggaaggctcatcttttga
                                                                                                                                                           tgatgataagtatcttcgccagttagaatcagaagtgccagtttattattatggcgtcac
                                                                                                                                                                                                                               cgttttttcagcgttccaaacaatggctcatcaagtcaaaaaaggaatttttgcttatgg
                                                                                                                                                                                                                                                                                                 ttatgcgattatgacgaatatcgattttgatcatccagattactacaagagcattgagga 126
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 TGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATATGGTGACCATAC
                                                                                                                                        TGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTACTATGGATTTAA
                                                                                                                                                                                                                                                                              TTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTCAAAGATATTAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 227; DB 60;
Pred. No. 2.76e-11:
3; Mismatches 22:
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 C;
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aaaggctacaacgttcaaggatcagacgtagaagagtatttctttacacaaacgggatctt 316

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В
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# Enterococcus faecalis; contig detection; Enterococca,

# vaccine; attenuation; computer readable medium; ds.

Enterococcus faecalis.

# WO985055-A2.

12-NOV-1998.

14-NOV-1998.

# 14-NOV-1997; US-066009.

R 16-MAY-1997; US-044631.

R 16-MAY-1997; US-046655.
                                                                                          Query Match
Best Local s
                                                                                                                                                                                               Claim 1; Page 1327-1330; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcus infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barash SC, Dillon WPI; 99-045171/04.
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X13228;
19-MAR-1999 (first entry)
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taccattttgtcggaattaaaggttctggcatgagctcattagcgttggtcttacaccaa 256
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                                                                                          Similarity
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                                                                                                                                                    4956
                                                                                                                                                                                       in vaccines to prevent or attenuate an Enterococcal
                                                                         16.6%;
larity 66.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    faecalis genome contig SEQ ID NO:291. faecalis; contig; detection; Enterococcal infection;
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                                                                                                                                                  1540
                                                                         Score 224; DB 60;
Pred. No. 1.65e-111;
1; Mismatches 228;
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RESULT
ID VI
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Sequence (MurC ORF) of the MurC gene.
                                                                                                                 V53479
V53479;
          DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response induction; eye infection; respiratory infection; inhibitor; bacternial infection; cardiac infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
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antimicrobial compound therapy; ss.
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                                                                                                                                 standard;
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Similarity 100.0%;
660; Conservative
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PS Claim 1. Page 146: 390pp; English.

CC This sequence encodes a Staphylococcus aureus protein of unknown

CC function, and represents a DNA Sequence of the invention.

CC (NCIMB 40771). Host cells containing the DNA sequences are used to

CC (NCIMB 40771). Host cells containing the DNA sequences are used to

CC produce polypeptides or fragments. The proteins are used in the treatment

CC of disease, for inducing an immune response by administering them, to

CC produce antibody and/or T-cell immune response. Antagonists of the

CC proteins are used for the inhibition of bacterial polypeptides.

CC conditions which may be treated include bacterial infections, especially

CC respiratory, cardiac, gastrointestinal, central nervous, eye, kidney,

CC urinary tract, skin, bones and joints. The proteins can also be used to

CC dentify antimicrobial compounds which are boroad spectrum antibiotics,

CC especially useful in the treatment of H. pylori infection.

Sc Sequence 619 BP; 208 A; 117 C; 79 G; 215 T;
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Matches
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P-PSDB; W77686.
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24-SEP-1996; US-027032.
(SMIK ) SMITHKLINE BEECHAM CORE
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1 Similarity 99.88;
610; Conservation
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Pred. No. 0.00e+00;
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Local Similarity 94.7%;
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Pred. No. 0.00e+00;
0; Mismatches 72;
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Claim 2; Pages 4-5; 39pp; English.

The invention relates to a UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoded by the S. aureus MurC gene. Host cells containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. bacterial (especially S. aureus) infections. They are also useful against
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07-JAN-1999
26-JUN-1998; 305064.
03-JUL-1997; US-052720.
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(SMIK ) SMITHKLINE BEECHAM E
BURDHAM MKR, WAllis NG;
WPI; 99-062655/06.
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MurC gene; UDP-N-acetylmuramate:L-alanine ligas;
bacterial; infection; H. pylori; cancer; ulcer;
immunogen; drug; genetic immunisation; ds.
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V74703;
anti-S.aureus vaccines
Claim 1; Page 1287-1288; 3271pp; English.
This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention: The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus contig SEQ ID #392.
Computer readable medium; vaccine; S.aureus infection; immuno
cellulitis; eyeilid infection; food poisoning; osteomyelitis;
skin infection; surgical wound infection; scalded skin syndro
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Distribution rights by Oxford Molecular Ltd
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                                                                      Staphylococcus aureus Partial nucleotide se DNA encoding a Staphy Enterococcus faecalis Enterococcus faecalis
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## ALIGNMENTS

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Search completed: Sat Nov 27 11:49:34 1999 Job time : 13 secs.
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8537..9000

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7811..8104
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5415..5492
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5511..5758
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/gene="pol"
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57..1738
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gene="env"
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005..5295
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                                                                                      Score 19; DB 3; Length 9178; Pred. No. 3.83e+00; 0; Mismatches 20; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                AGAAGCTAGATGTTACAAATATTAAAGAAGCATTAGA 890
                                           1 (bases 1 to 9143)
Spire,B., Sire,J., Zachar,V., Rey,F., Barre-Sinoussi,F.,
Galibert,F., Hampe,A. and Chermann,J.-C.
Nucleotide sequence of HIV1-NDK a highly cytopathic stra
human immunodeficiency virus HIV1
Gene 81, 275-84 (1989)
full staff_review
                                                                                                                                                                                                              DNA.
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Kindly provided prior to publication by J.-C.
                                                                                                                                                                                                                                                            M27323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. The VI415 gag sequence clusters with HIV-1 A subtype sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1 (HIV-1), Rwandan isolate VI415.
Human immunodeficiency virus type 1
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
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Rwandan national residing in
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Human immunodeficiency virus
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Louwagie,J.J., McCut
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Similarity 75.7%;
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RALGTGATLEEMMTACQGVGGPGHKARVLAEAMSQVQHTNIMMQRGNFKGQRRIKCFN
CGKEGHLARNCRAPRKKGCWKCGKEGHQMKDCTERQANFLGKIWSSSKGRPGNFPQSR
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KIEEIKNKNKQKTQQAAAGTGNSSNVSQNYPIVQNAQGQMIHQAISPRTLNAWVKVIE
EKAFSPEVIPMFSALSEGATPQDLNMMLNIVGGHQAAMQMLKDTINEEAAEWDRLHPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sequenced_mol="DNA"
/tissue_type="blood"
278 c 366 g
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/isolate="VI415"
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Pred. No. 3.83e+00;
0; Mismatches 9
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                                                                                                                                                                                                                                                                             type 1, isolate NDK,
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  Chermann,
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Best Local Similarity 66.1%;
Matches 39; Conservative
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3307 a. 1617 c 2193
5'-terminus of 5' R repeat
                                                              Nucleotide sequence of a Ugandan HIV-1 provirus diversity from other HIV-1 isolates
                                                                                                                                                                              Human immunodeficiency virus type Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is an infectious molecular clone of an isolate estimated to 10,000 times more cytopathic in vitro than a prototypical HIV-1. [1] reports that only minor sequence differences appear to be responsible for the "acute biological effect".
Hardcopy of sequence [1] kindly provided by J.D. Oram, Location/Qualifiers
                            full staff_entry
                                                                                                Carswell, J.W.
                                                                                                              Oram, J.D., Downing, R.G., Roff, M., Clegg, J.C.S.,
                                                                                                                                            Viridae; ss-RNA enveloped viruses; Retroviridae; Lentivirinae.
                                                                                                                                                                                                                M62320
                                                                                                                                                                                                                                               HIVU455
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                                                                                                                                                                                                                          55 9178 bp ss-RNA immunodeficiency virus type 1,
                                               Hum. Retroviruses
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/codon_start=5759
7883..7928
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/codon_start=5094
5365..5579
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/note="tat protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="gag polyprotein"
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0; Mismatches 20
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	e transcriptase" ,"ttg") sequence hxb2 has ttg, a	/product="reverse transcriptase"	product="reverse transcriptase" /product="reverse transcriptase" replace(736738,"ctg") /note="reference sequence hxb2 has ctg, a phenotypically silent change"	lysine change" /product="reverse transcriptase" replace(679681,"ttc") note="reference sequence hxb2 has ttc, a phenotypically	transcriptase" "agg") sequence hxb2 has agg, an arginine to	product="reverse transcriptase"  /product="reverse transcriptase"  replace(398.600,"aca")  /note="reference sequence hxb2 has aca, a threonine to an	d change" transcriptase" "tac") sequence hxb2 has tac, a phenotypical	e transciptase" ,"gac") sequence hxb2 has qac, an	<pre>isoLeucine change" /product="reverse transcriptase" replace(\$08.510,"cct") /note="reference sequence hxb2 has cct, a phenotypically</pre>	iptase" hxb2 has aca, a	e transcri , "agt") sequence	e transcriptase"  "Tacc")  "Bacc")	iptase" hxb2 has ata, an isoleucine to	a histidine change." /product="reverse transcriptase" replace(364366,"gaa") /note="reference sequence hxb2 has gaa, a glutamic acid to	e transcriptase" ,"gat") sequence hxb2 has gat an	<pre>serine change" /product="reverse transcriptase" replace(346348,"ttt") /note="reference sequence hxb2 has ttt, a phenotypically</pre>	
Query Match 1.4%; Score 19; DB 3; Length 1302; Best Local Similarity 66.1%; Pred. No. 3.83e+00; Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;	FEATURES from to/span description  pept < 4 > 1302 pol polyprotein (AA at 4)  BASE COUNT 529 a 211 c 270 g 292 t  ORIGIN	Virolgie und Immunologie, Kellnerweg 4, W-3400 Goettingen, Germany.	smann,G. räcterization of a new German HIV-l isolate: HIV-lNH5 ublished (1992) l staff entry	oped viruses cinae. , Sauermann,	000 f 3 an immunodeficiency virus type 1 (HIV-1), clon an immunodeficiency virus type 1	HIVNH51 1302 bp ss-DNA	Db 137 aaatttcaaaaattgggcctgaaaatccatacaatactccagtatttgctataaagaaa 195 	Query Match 1.4%; Score 19; DB 3; Length 1299; Best Local Similarity 66.1%; Pred. No. 3.83e+00; Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;	/product="reverse transcriptase" BASE COUNT 531 a 217 c 263 g 288 t ORIGIN	<pre>/produc(t="reverse transcriptase"</pre>	/product="reverse transcriptase" /product="reverse transcriptase" allele /note="reference sequence hxb2 has caa, a phenotypically silent change"	/product="reverse transcriptase"  allele replace(11561158,"act")  and the product of the produ	/product="reverse transcriptase"  allele replace(10301032,"gag")  /note="reference sequence hxb2 has gag, a phenotypically silent change"	<pre>product="reverse transcriptase"  replace(991.993, "aag")  /note="reference sequence hxb2 has aag, a phenotypically silent change"</pre>	rse 91,	<pre>/product="reverse transcriptase" replace(877.879, "ata") /note="reference sequence hxb2 has ata, an isoleucine to a valine change"</pre>	<pre>/product="reverse transcriptase" replace(856858,"acc") /note="reference sequence hxb2 has acc, a threonine to a proline change"</pre>

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liele 'Prace(a) - a observative 'Product 'Preverse proline change 'Product 'Preverse replace(872.879) /note-"reference valine change 'Product 'Preverse replace(889.891, /note-"reference 'Product 'Preverse replace(1991.993, /note-"reference silent change 'Product 'Preverse replace(1030.103) /note-"reference silent change 'Product 'Preverse replace(1156.1156.1156.1156.1156.1156.1156.1156	lele replace(856858, "acc")  /product="reference sequence hxb2 has acc, a threonine to a proline change"  /product="reverse transcriptase"  replace(877879, "ata")  lele /note="reference sequence hxb2 has ata, an isoleucine to valine change"  /product="reverse transcriptase"  /product="reverse transcriptase"  lele replace(889891, "gaa")  /note="reference sequence hxb2 has gaa, a glutamic acid lysine change"  /product="reverse transcriptase"  /product="reverse transcriptase"  /product="reverse transcriptase"

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Science 261, 1179-1181 (1993)

RD full staff_review

This sample has been taken from patient M, one of the seven patients (A,M,L,F,C,V,R), in the study(1). All patients had acute, self-limited symptomatic illness with measurable viremia followed by seroconversion. Patient M was a chronically infected male who subsequently transmitted the virus to patient F. The authors report that the sequences in this study are found to be uniformly macrophage-tropic and non-syncytium-inducing. The sequence for sample M clone 2, along with other patient M clones 1, 3-9, 11, and 12, is shown in alignment following the printed text entry. These gas sequences cluster with HIV-1 B subtype sequences. See also L21224-L21591 and L24161.
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                                                                        1 (bases 1 to 309)
Zhu,T., Mo,H., Wang,N., Nam,D.S., Cao,Y.,
Genotypic and phenotypic characterization
                                                                                                                                                                            Human immunodeficiency virus type 1 (HIV-1), clone 10, ADC sample Human immunodeficiency virus type 1
                                                                                                                                                                                                                                        gag cds, p17
L21375
                                                                                                                                                                                                                                                                         HIVF10S1 309 bp ss-RNA VRL 09-SEP-1993 Human immunodeficiency virus type 1, clone 10, ADC sample F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhu, T., Mo, H., Wang, N., Nam, D.S., Cao, Y., Koup, R.A. and Ho, D.D. Genotypic and phenotypic characterization of HIV-1 in patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1 (HIV-1), clone 2, ADC sam
Human immunodeficiency virus type 1
Viridae; ss-RNA enveloped viruses; Positive strand RNA virus;
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L21492
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                                       with primary infection
Science 261, 1179-1181 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%;
Similarity 77.1%;
27; Conservati
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                                                                                                                                      Viridae; ss-RNA enveloped viruses; Retroviridae; Lentivirinae.
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Similarity 67.2%;
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  sample has been taken from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sequenced_mol="RNA"
61 c 62 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="myristylated/gene="gag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Human immunodeficiency virus type 1"
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Pred. No. 3.83e+00;
0; Mismatches 8
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Pred. No. 9.90e-01;
0; Mismatches 19
patient F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gag protein
                                                                                                                                                         Positive strand
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                                                                            Koup, R.A.
of HIV-1 i
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  of the
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                                                                                                                                                                                                                                                                           sample F, partial
                                                                                                                                                         RNA virus;
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  seven
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                                                                                               Ho, D.D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other sequences in this set are included in the Retroviruses and AIDS Compendium (see accession 231354, 231365-231367, and 231374).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurusinghe,A., Land,S., Birch,C., McGavin,C., Tachedjian,G., Doherty,R. and Deacon,N. Reverse transcriptase mutations and sequential patient with AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1 (HIV-1), isolate RET7. Human immunodeficiency virus type 1
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Human immunodeficiency virus
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                                                                /note="reference sequence
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                      replace(259..261,"ttc"
                                                                                                                                silent change"
/product="reverse transcriptase"
                                                                                                                                                                                                                                         replace(16..18 "gag")
/standard_name="polymorphism"
/note="reference sequence hxb
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/sequenced_mol="RNA"
64 c 62 g 55 t
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QNKSKKKAQQATAAADTANSSQVSQNYPIVQNIQGQMVHQPISPRTLNAWVKVVEEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="gag
                                                                                                             replace(118..120, "gag")
                                                                                                                                                                                             /product="reverse transcriptase" replace(97..99, "gca")
                                                                                                                                                                                                                                                                                                                                                /organism="Human immunodeficiency virus type
/cell_type="T-lymphocyte"
                                           /product="reverse transcriptase"
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                                                                                                                                                                         note="reference sequence hxb2 has
                                                                                                                                                                                                                                                                                                                                                                                                  ..1299
                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
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                                                                                      hxb2 has
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tat protein, exon 2 (first express tat protein, exon 3 (AA at 8598) t in 4.41; c in p q in 4.41; c in p t in 4.41; c in 1.5 c in 4.41; q in 1.5 c in 4.41; q in 1.9 a in 4.41; q in 1.9 a in 4.41; q in 1.9 a in 4.41; q in 1.9 a in 4.41; q in 1.9 q in 4.41; t in 1.9 q in 1.9 q in 4.41; t in 1.9 q in 1.9 q in 4.41; t in 1.9 q in 1.9 q in 4.41; at in 1.9 q in 4.41; at in 1.9 q in 4.41; at in 1.9 q in 4.41; at in 1.9 q in 4.41; at in 1.9 q in 4.41; at in 1.9 q in 4.41; at in 1.9 q in 4.41; at in 1.9 q in 4.41; at in 1.9 q in 4.41; at in 1.9 q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 1.5, p q in 4.41; at in 
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Simian (Sooty mangabey) immunodeficiency virus proviral DNA, clone SMH3 and SMH4. Clone H4i is infectious.

1 (bases 1 to 10276)

1 (bases 1 to 10276)

1 Hirsch, V.M., Olmstead, R.A., Murphey-Corb, M., Purcell, R.H. and Johnson, P.R.

SIV from Sooty mangabeys: An African non-human primate lentivirus closely related to HIV-2

Nature 339, 389-391 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIVSMMH4
Simian (S
                  ű
                                                                                                                                                                                                                                                                                                           The smH-4 sequence is presented in this entry with exception of the extra "a" it has at position 4529 causing a frameshift in the integrase of the pol gene. Clone smH-3 does not possess the additional "a" and has a normal pol gene. Follow-up work revealed the presence of a 36bp stretch -- coordinates 6391 to 6426 -- in the smH-4 [ref 2]. Clone H4i, without the extra 'a' in the integrase cds, is infectious.
                                                                                                                                                                                                                                                           This sequence does not possess the cds seen in other SIV sequences. I reading frame for nef.
                                                                                                                                                                                    ٨
                                                                                                                                                                                                                      The SMM sequence
12% in the gag co
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence kindly supplied in computer-readable form by V.M. Hirsch, Georgetown University, NIH, Twinbrook II, 12441 Parklawn Drive, Rockville, MD 20852 (02-FEB-1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished, January 1990 (Hirsch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 6391 to 6426; correction of [1]) Hirsch, V.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete genome.
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c in 4.41; t in 1.5, 1.9, B
c in 4.41; t in B,P
g in 4.41; t in B,P
c in 4.41; t in P
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2469 g 2227 t
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Pred. No. 9.90e-01;
0; Mismatches 13
                                                                                                                                                                                                            description
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#GQWTDYDYWQVTWIDEMGDFYCSTPPLVRLVFNLVKEDIQGAETFYUDRSCORQSREGKA
GYWTDRGRGKTKLLEOTINQAELEAFYLLALDSGPKANIIUNSGYDAGIVAGQPTES
ESRLVNQIIEKMIKKEAIYVAWPPAHKXIGENQEVDHLVSQEIRQVLFLEKIEFAQEE
HEKYHSNVKKLVFKFXLPRLVAKQIVDTCDKCHLKGEAIHGQVAXLGTWQMDCTHLE
GKIIIVAVHVGSGFIEAEVIPXETGRQTALELLKLASRWPITHLHTDNGANETSQEVK
NVAWWAGIEQTFXVPYNPQSQXYVEAMNHHLKTQIDRIREQANSIETIVLMAIHGUNF
KRRGGIODMTPAERLVNMITTEQEIQFQQSKNSKFKNFRYYYREGRDQLWKGPGELLW
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SQDINERPKQAWCWFGGEWKEAIREVKXXLVEHPRYKCTNXXXJIKLTAPGGGDPEVT
FMWTNCRGEFLYCKMNWFLLWVEXIKNGSWWFSQNYKEVYDCHIJOINTWHK
VGKNVXLPPREGDLTCONSTUTSLIAEIDWINGNKTVITMSAEVYAELYBLELGDYKLVE
ITPIGFAPTSVKRYTTTGASRNKRGVFVLGFLGFLATAGSAMGAASLTLSAQSRTLLA
GIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVTAIEKYLKDQAPXNSWGCAFRQVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MGCLGNQLLIALSLXSASGIYCVQYVTVFYGVPAWRNATVPLFC
ATRNROTWGTTQCLPDNGDYSELAINVTEAFDAWDNTVTEQALEDVWHLETSIKPCV
KLTPLCITMRCNKSEXXRWGLTGXPAPTTTQTSTTPPSPIIAKVVNUSDPDCIRSNNCT
GLEQEPWYSCKENMTGLKRDKKREVNETWYSRDLVCEQNSNGNETDSKCYMNHCNTSV
IQESCDKHYWDAIRFRYCAPPGYALLRCNDTNYSGFAPNCTKVVVSSCTRMMETQTST
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HKVGWAWWTCSRVIFblrdekhlikogcywnifblokgwistyaveltwysnatwptatp
DYADTLLHGTYFPCESEGEVRRAIERGEKLLSCCKFPKAHKNOVPSLOYLALTUVSHVX
SQGEXPTWKOWRRNXRRGXRLATQNXRRNKQGSSESFAXGANFPGLAKXLGILA"
                    YXYKAFVEHPEEFGSQSGLSKEEVQRRLTARGLLKMADKKKTS"
1785 c 2350 g 2143 t 108 others
                                                                  /translation="MGGVTSKKQRXAGGNLXERLLQARGETYGRLMEGLEGEYSQSXDASGKGLSSLSCEPQKYCEGQFMNTPWRRPPATBCAKLGYRQQNMDDVDNEDLYGCPVSPRVPWRIMTYKLAIDMSHFIKEKGFLEGVYYSIRRHKILDYLEKEEGIIPDWQNYTAE
RVPWRIMTYKLAIDMSHFIKEKGFLEGVYYSIRRHKILDYLEKEEGIIPDWQNYTAE
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DXFGNWXDLTXWIKYIQYGVLIVLGVIGLRIVIYVVQMLARLRQGYRPVFSSSPAXVX
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NYIYDRHGDTLEGAGELIRILQGALFIHFRGGCRHSRIGQSGGXNPLSTIPPXRGVL"
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/gene="vpr"
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/gene="vpx"
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                                                                                                                                                                                         /product="nef
/gene="nef"
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| FQVWRRXWEYWHDEMGMSVSYTKXRYLCLIQKALFMHCKKGCRCLGGEHGAGGWRPG
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                                                                                                                             SIVSMM (sooty mangabey) isolates bc13 and bc11. The prototype infectious 4.41 was constituted from PCR fragments 4 and 41 of bc13; for other clones, see COMMENT.

1 (bases 1 to 9996)
Kindly submitted in computer readable form prior t James Mullins, Stanford University, Palo Alto, CA.
                                                                                                                                                                                                                             SIVSMMPBJ 9996 bp ss
Simian (sooty mangabey)
                                                               SIV-smmpbj14
                                                                              Sequence analysis and acute
                                                                                                                                                                                               M31325
                                                  Nature
                                                                                                 Fultz, P:N.
                                                                                                           Dewhurst,S., Embretson,J.E., Anderson,D.C., Mullins,J.I. and
                                                                                                                                                                                                              bcl3 and
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larity 71.7%;
Conservative
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Pred.
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The PBJ virus is the most acutely pathogenic primate lentivirus reported to date. The prototype shown below is a chimera derived from two PCR fragments; other chimeric clones of bel3 are 1.9 (infectious) and 1.5 (noninfectious, possibly due to a T -> C change in the rev start codon). Of the bell isolate, the B and P clones are both nonpathogenic.

PBJ-4.41 has the second NFkappa-B element found in HIV-1's but not in HIV-2's nor in the SIV's related to the HIV-2's, including the other known sooty mangabey isolate, H4, nor in the nonpathogenic B and P clones (see annotation at position 9651 below and discussion in [1], Fig. 2).

variant variant 3264 3614 3614 3861 3904 3904 49062 49062 49062 51066 51066 51066 5578 5578 5578 57066 2108 3232 828 873 915 1115 1205 1625 1635 1742 rom to/span vpX protein g in 4.41; c g in 4.41; a a in 4.41; g c in 4.41; t taatin n coin t in 4 c in 4 c in 4 a in 4 a in 4 c in 4 tct in description in in g polyprotein 1.5 in 4.41; c in 1.5 in 1.5 in 1.5 in 1.5 in 1.5 in 4.41; g in 1.5 in 4.41; t in 1.5 in 4.41; t in 1.5 in 4.41; t in 1.5 in 4.41; ctc in ij procein 4.41; ttt ca ၁ မှာ B d td in in in in in in 'n 1.555 שמח in ď

BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                                   Recombinant clones that represent the 3' part of the genome of the human spumaretrovirus (foamy virus) were established from viral DNA (clone C55; see X05592) and cDNA (clone B52). The region common to both viral inserts comprises 817 bp (from the BamHI at bp 4548 in X05591 to the HINDIII site at bp 816 in X05592 corresondig to bp 5365 in a fusioned viral sequence. The env precursor polypeptide contains 14 pot. N-linked glycosylation sites. *source: cell.type=HSRV-infected HEL fibroblasts; clone=B52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I (bases 1 to 4549; enum. 1 to 4549)
Fluegel,R.M., Rethwilm,A., Maurer,B. and Darai,G.
Nucleotide sequence analysis of the env gene and
regions of the human spumaretrovirus reveals two
EMBO J. 6, 2077-2084 (1987)
                                                                                                                                                                                                                                                                                  Data kindly reviewed (02-SEP-1987) by Fluegel R.M. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human spumaretrovirus (HFV or foamy virus) genomic RNA with env
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ilarity 70.8%;
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gene product (343 AA)"
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galttsntpannadcawletqeeeeeevgfpvrpqvplrpmtykgafdlsfflkekgg
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LIRDGGTNSTDETFRPGGGDMRDNWRSELYKYKVVEIKPLGLAPTKAKRRVVEREKR
AALAAVELGELCAAAGSTWAASAITLTVQARQLLSGIVQQOSNLLKAIEVHQHMQLTV
VWGIKQLQTRVLAIERYLKDQQLLGIWGCSGKLICTTAVPWNSSWSNKSQEEIWDNM
TWMQWDREINNYTETIYRLEVSOTQQEQNEKDLLALDKWQNLWSWFDIFKMLWYIK
IFIMIVGGLIGLRIIFAVLSIVURVRQGYSPLESTQTLIWBYRGPDRPRGIIEBEGGG
DKGRSTRLVSGFLALAMDDLRSLFLFSYHRLRDLIILIVARVVELLGQRGWETLKYLG
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ENLTNNAKIIIVQLNQSVEINCTRPNNNTRQSIRIGPGQTFYATGDIIGDIRQAHCN
ISRQKMKETLQQVKGKLKEHFNKTIKFAPSSGGDIEITTHSFNCGGEFFYCNTSALF
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/translation="MIDLLAKVDYRLAVAAFIIAFIIAIVVWTIAYIEYRKLLRQRK
IDRLIERIERAEDSGNESDGDTDELSTMVDRGNLRLLDAVDV
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DQMHQDIISLWDEGLKPCVKLTPLCVTLNCSNKVTATGNGSVTYNSTEKDMRNCSFN
                                                                                                                         note="env glycoprotein precursor
                                                                                                                                                                                                                              /note≖"3′ domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Virol. 66, 41, full staff_entry
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Simian immunodeficiency virus
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Simian immunodeficiency virus,
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Courgnaud, V., Laure, F., Fultz, P.N., Montagnier, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unclassified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MGVRNSVLSGKKADELEKIRLRPGGKKKYMLKHIVWAANELDRF
GLAESLLENKEGCQKILSVLAPLVPTGSENLKSLYNTVRVLWCIHAEEKVKHTEEAKQ
IVQRHLVVETGTADKWPATSRPTAPPSGRGGNYPVQQVGGNYTHLPLSPRTLNAWVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARNCQPKKEKKETVEXEVATDLGLXR"

join(6002..6065,8295..8533)

/product="rev protein"
RLIRGKMTLTEEVQWTEMAEAEYEENKIIPSQEPEGCYYQEGKPLEAPVIKSQDNQWS
                                                  TVLDVGDAYFSIPLDEEFRQYTAFTLPSVNNAEPGKRYIYKVLPQGWKGSPAIFQHTX
RNVLEPFRKANPDVTLIQYMDDILIASDRTDLEHDRVVLQLKELLNSIGFSTPEEKFQ
                                                                                                                           /translation="MPRKTGGFFRAMPMGKEAPQFPHGPDASGADTNCSXRGSSCGST
EELHEGGQKABGEQRETLQGGNGGFAAPQFSLWRRPVVTAYIEGQPIEVILDTGADDS
IVAGIELGPRYPKIVGGIGGFINFXEYKDVKIKVLGKVIKGTIMTGDTPINIFGRNL
LTAMGMSLNLPIAKVEPIKVTLKPGKDGPKLRQWPLSKEKIIALREICEKMEKDGQLE
                                                                                                                                                                                                                                                                                                                                                                                                                    VEEKKFGAEVVPGFQALSEGCTPYDINQMLNCVGEHQAAMQIIREIINEEAADWDLQH
PQPGPIPAGQLREPRGSDIAGTTSTXDEQIQWMYRQQNPIPVGNIYRRWIQLGLQKCV
RMYNPTNILDVKQGPKESFQSYVDRFYKSLRAEQTDPAXKNWMTQTLLIQNANPDCKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"METPLKEQESSLESSREHSSSISEVDADTPESASLEEEILSQLY
RPVEACYNKCYCKKCCYHCQHCFLKKGLGICYEQQRRRTPKKTKANTFSASDKSLSXR
                                                                                                     XAPPTNPYNTPTFALKXXDGNKWRMLIDFRELNKVTQDFTEVQLGIPHPXGLAKRRRI
                                                                                                                                                                                                                                                                                                                                      XCXNCXKEGHSARQFRAPRRQGCWKCGKAGHVMAKCPERQAGFLGLGPWGKKPRNFPM
AQMPQGLTPTAPPEDPAVDLLKNYMKVGRRQRENRERPYKEVTEDLLHLNSLFGEDQ"
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WQQILALADRIYSFPDPPADTPLDLAIQQLQGLAIEXLPNPPASAPEPLKDAAESP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(5776..6065,8295..8391)
/product="tat protein"
                                                                                                                                                                                                                                                              /product="reverse transcriptase"
/gene="pol"
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                                                                                                                                                                                                                                                                                                                                                                                            /LKGLGINPTLEEMLTACQGVGGPGQKXRLMAEALKDALTQGPLPFAAVQQKGQXKII
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                                                                                                   agaacag in [6]; gaca in a in [6]; g in [1] c in [6]; at in [1] c in [6]; at in [1] c in [6]; at in [1] ttc in [6]; att in [1] at in [6]; att in [1] at in [6]; at in [1] aaa in [6]; gg in [1] caca in [6]; ttag in [1] acacac in [6]; ttag in [1] acacac in [6]; ttag in [1] acacac in [6]; ttag in [1] acacac in [6]; ta in [1] acacac in [6]; ta in [1] tin [6]; tat in [1] ga in [6]; tat in [1] ga in [6]; a in [1] c in [6]; a in [1] c in [6]; a in [1] ga in [6]; a in [1] c in [6]; a in [1]
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  EPVPFQLPPIERLNLDCSESGGTSGTEGVGN'
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numbered 1 in [3]
a in [1], [4], [6]; g in [3]
tg in [1], [4], [6]; aa in [3]
g in [1], [4], [6]; a in [3]
g in [1], [4], [6]; a in [3]
g in [4], [6]; g in [1], [3]
g in [2], [3], [6]; g in [4]
numbered 1 in [2]
c in [4], [6]; t in [2], [3]
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                                                                            annotations
                                               1.6%;
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                                      Score 21; DB 3; Length 10277; Pred. No. 2.31e-01; 0; Mismatches 10; Indels
                                       0
                                      Gaps
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HIVDJ373A 3340 bp ds-DNA VRL 31-DEC-1993 Human immunodeficiency virus type 1, DJ373 from Djibouti, proviral DNA encoding env, tat, vpU, rev, and nef genes. L23065 Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D. Genetic diversity of the HIV-1 envelope glycoprotein Unpublished (1993) full automatic Human immunodeficiency virus type 1 (HIV-1), DJ273 from Djibouti, PCR amplification of proviral DNA from cocultivated PBMC's Human immunodeficiency virus type 1 Viridae; ss-RNA enveloped viruses; Positive strand RNA virus; env gene; envelope glycoprotein; nef gene; rev gene; tat gene; Retroviridae; (bases 1 to 3340) Hegerich, P.A., by Dr. h Laboratory

These sequences were kindly provided prior to publication by Dr. Joost Louwagie of the Henry M. Jackson Foundation Research Laborator; Rockville; Maryland. Twenty-one full length gp160 coding sequences from eight African countries (Djibouti, Gabon, Kenya, Senegal, Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with thirty-two previously published full-length gp160 env sequences. Sequences Du258, Du259, K124, Sm365, Sm145, UG266, UG268, UG274, VI191, and VI525 have corresponding gag sequences published by Louwagie et. al. in ALDS 7, 769-780 (1993) and in the 1993 compendium. This sequence clusters with C subtype env sequences. See also accession numbers L22939-L22957 and L23064. /tissue\_type="blood"
join(87..>302,2619..>2707)
join(87..>302,2619..>2707)
/note="tat protein, exon 2 (first expressed exon)"
/translation="MEPVDPNLEFWNHPGSQPKTACTKCYCKKCSYHCLVCFQTKGL
GISYGRKKRRQRRSAPSSSEDHQNLISKQ" /note="tat protein, exon 3 (AA at 2620)"
/translation="PLSRTQGDPTGPEESKKKVESKTKADPLD"
/oin(226.>302,2619.>2838)
/note="rev protein, exon 2 (first expressed exon)"
/translation="MAGRSGDSDEALLQAVRIIKILYQS"
/note="rev protein, exon 3 (AA at 2621)"
/translation="SyyeppKGTRQAQRNRRRWRARQRQIHSISERILSTCLGRPA /proviral /organism="Human immunodeficiency virus type 'sequenced\_mol="DNA" /isolate="Djibouti" /cell\_type="lymphocyte" Location/Qualifiers

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Hirsch, V., Riedel, N. and Mullins, J.I.
The genome organization of STLV-3 is similar to that of the virus except for a truncated transmembrane protein Cell 49, 307-319 (1987)
Kestler et al.(Nature 331, 619-622 (1988)) present strong evidence that the isolates previously referred to as STLV-III AGM ([1], [2], [3]) and HTLV-IV ([4]) are not authentic, but were derived from cell cultures infected with SIV MAC-251. The reference sequence
                                                                                                                Unpublished
Unpublished
                                                                                                                                               6 (bases 1 to 10249)
Donahue, P.R., Kornfeld, H.,
                                                                                                                                                                                                                                                                                                                                           full staff_review
4 (bases 809 to 1677; 5731 to 10249)
Hahn,B.H., Kumar,P., Taylor,M.E., Arya,S.K. and Shaw,
Human retroviruses, cancer and AIDS: approach to prev
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1 (bases 506 to 5975; 6319 to 10125)

Franchini,G., Gurgo,C., Guo,H.-G., Gallo,R.C., Collati,E.,
Fargnoli,K.A., Hall,L.F., Wong-Staal,F. and Reitz,M.S.Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simian (macaque) immunodeficiency virus, complete genome; isolate Mm251, proviral DNA. M19499 M15897 M16125 Y00283 X06879 Y00294 Y00295 X06391 X06393
                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                           Unpublished (1987) UCLA Symposia on Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the human immunodeficiency viruses Nature 328, 539-543 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of simian immunodeficiency virus and its relationship the human immunodeficiency viruses
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|10127.10132
|/note="670..675 for the 5'LTR'"
| 1931 c 2559 g 2309 t
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ELDKGLSSLSCEGOKYNOEQYNNTPWRNPAEEREKLAYKRQNNDDIDEEDDDLYGYSV
RPKVPLRTMSYKLAIDMSHFIKEKGGLEGIYYSARRHRILDIYLEKEEGIIPDMODFT
SGPGIRYPKTEGWLWKLVPVNVSDEAQEDEEHYLMHPAQTSQWDDPWGEVPAWKFDPT
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9073..9864
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/note="'premature stop 1 @ 8801 (SIVmm142)'"
/note="'premature stop 2 @ 9158'"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAYTYEAYVRYPEEFGSKSGLSEEEVRRRLTARGLLNMADKKETR"
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for this entry is from [6], with exception of bases 10250-10277 which are from [3].

See also entries <SIVMM32H> and <SIVMM1A11>, independent molecu-clones from virus isolated from the same rhesus macaque that provided the virus for SIVMM251. In addition, entry <SIVMM239> shows greater than 98% homology to entry <SIVMM1A11> at the nucleotide level molecular

SIVMM251 sequence results in the coding sequence ending 4 amino acids earlier than it does in SIVMM142. Also, the variation marked at position 6377 ('aa' in K6W, 'aga' in K78) implies different amino acid sequences for those isolates from that point onward in The vpR coding region has been annotated to end near where the gene ends in the SIVMM142 sequence. A base change from 'a' at position 6443 in SIVMM142 to 't' at corresponding position 6418 in the

The tat start is annotated in agreement with the site in [4] agrees with HIV2ROD) sequence rather than at the site marked for the K78 sequence. (also in [2]

with reference [2] for the K78 sequence. This position also agrees with the rev start in the SIVMM142 sequence. However, [4] annotates the rev start at position 6354. Both of these sites are in the same frame. The sequence annotation shows two alternate 3' splice junction sites at 8743 and 8785. See reference [2]. The start codon for rev is marked at position 6504 in accordance

Clean copy of sequence [5] kindly provided by H.W. Kestler to the EMBL data library (25-FEB-1988). Computer-readable copy of sequence [6] kindly provided by J.Mullins (12-SEP-1988).

An internal stop codon is present in the env cds at positions and 8785-8787 in [1], [2], [3], [4], [6].

rhesus monkeys 17 months after infection. BK28 was originally called HTLV-4 (Nature 326, 610-613 (1997)), but it has since been found to correspond to SIVMM251. The K6W sequence [1], which was derived from isolate Mm251, contains about 25 frame shifts in gag-pol relative to this sequence. causing persistent lymphadenopathy and death [6] has shown proviral clone BK28 to be biologically active, in one out of four

protein about 36 A single base insertion at e base insertion at position 9678 results in coding region. The nef coding region in [1] about 36 residues longer than that produced n a frameshift in ] would produce a d by the other

This entry 1990 HUMAN replaces pages I-B-81 RETROVIRUSES AND AIDS through I-B-85 (APR 90) in the

binding	rpt	rpt	LTR	LTR	pept			pept.ps	pept		pept		pept	pept	pept	pept		pept	pept	FEATURES
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primer (Lys-tRNA) binding site	R repeat 3' copy	R repeat 5' copy	3' LTR	5' LTR	nef protein	[5])	[2],[3],[4],[6];	envelope polyprotein (in-frame stop at 8785,	<pre>envelope polyprotein (premature termination)</pre>	rev protein, exon 3 (AA at 8790)	rev protein, exon 2 (first expressed exon)	tat protein, exon 3 (AA at 8789)	tat protein, exon 2 (first expressed exon)	vpR protein	vpX protein	vif protein	2216)	pol polyprotein (NH2-terminus uncertain; AA at	gag polyprotein	description

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAAATGGCACATAATGTTAAAAAAAGGTATTATTGCTTGGG 631
                                        the nucleotide level. Analysis in differences in SIVMMIA11 and SIVMM2 differences in biologic properties.

Location/Qualifiers
                                                                                              Kindly provided to GenBank in computer readable form prior to publication by K.E. Shaw. See also <SIVMM239> (accession number M33262); SIVMM1A11 and SIVMM239 show greater than 98% homology at the nucleotide level. Analysis in [1] largely focuses on sequence differences in SIVMM1A11 and SIVMM239 which may account for
                                                                                                                                                                                                                                               AIDS
                                                                                                                                                                                                                                                                 Luciw P.A., Shaw,K.E., Unger,R.E., Planelles,V., Stout,M.W., Pratt-Lowe,E., Leung,N.J., Banapour,B. and Marthas,M.L. Genetic and biologic comparisons of pathogenic and non-pathogenic molecular clones of simian immunodeficiency virus (SIVmac)
                                                                                                                                                                                                                                                                                                                                                                                                          M76764
Simian immunodeficiency virus from the same rhesus macaque that provided the virus for the clone SIVMM251; independent molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIVMM1A11 10274 bp ss-RNA VRL 18-OCT-1991 Simian immunodeficiency virus from the same rhesus macaque that provided the virus for the clone SIVMM251; independent molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cap site of genomic RNA.
                                                                                                                                                                                                                                                                                                                                                                                                clone 1Al1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 1.6%;
Similarity 75.6%;
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one 1A11, complete
                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 10274)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3290 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8298..8300
  join(6301..6596,8799..8898)
/note="'for splice patterns,
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5298..5636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="env polyprotein (in-frame stop codon at 8298)"
/codon_start=6090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="R repeat 3/
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'note="3' LTR"
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                                                                                                                                                                                                                                               Hum.
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Pred. No. 2.31e-01
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  see Unger, R.E. et al.'"
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SNRTRHCQPEKAKKETVEKAVATAPGLGR"
join(6527..6596,8799..9055)
/note="'for splice patterns, see Unger,R.E. et al.'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALKPGKVGPKLKQWPLSKEKIVALREICEKMEKDGQLEEAPPTNPYNTPTFAIKKKOK
KKRKHLIDFRELNRVTQDFTEVQLGIPHPAGLAKKRBITVLDIGDAVESIPLDEEFRO
YTAFTLPSVNNAEPGKRYIYKVLPQGWKGSPAIFQYTMKYLEPFRKANDDVTLVQYM
DDILIASDRINLEHDRVVLQLKELLNSIGFSTPEEKFQKDPPPQWMGYELWPTKWKLQ
KIELPGRETWTVNDIQKLVGVLNWAAQIYPGIKTKHLCRLIRGKMTLTEEVQWTEMAE
AEYEBKKIILSQEGECYYQEGKPLEATVIKWQDWGSYKHHQEDKILKVGKEAKIKN
THTNGVELLAHVIQKIGKEAIVINGQVPKFHLPVKDWSYKHHQEDKTLKVGKDTNO
THTNGVELLAHVIQKIGKEAIVINGQCYPKFHLYWKDLWTDYMQVTWIPEWNFI
STPPLVRLVFWLUKDDIEGEETYYTDGSCNKOSKEGKAGYTDRGKDKWVLEQTTNO
QAELEAFLMALTDSGPKANIIVDSGYVMGIITGCPTESESRLVNVKELVFKEGLPRI
ANVPAKKGIGGNQEVDHLYGGGTQVLFLEKLEPAGDEHDKVISHVKELVFKGLFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MGARNSULSGKRADELEKIRLRÞNGKKKYMLKHVWAANELDRF
GLAESLLENKEGCQKILSVLAPLVPTGSENLKSILVNTVCVITCHHAEEKKFIEBAKQ
IVQRHLVVETGTAEIMENTSRFTAPSSGRGRINFDVOJGGVNYVHLPLSBRTLNAWKLL
IEEKKEGAEVVPGFQALSEGCTPYDINQMLNCVGDHQAAMQIIRDIINEEAADWDLQH
PQPAPQOGLKEBFGSDIAGTTSSVDEDIQWMKRQDHPLPVGNIYRWIQLGLQKCVR
MYNPTNILDVKOGFKEBFCSYVDRFYKSLAABOTDAAVKNWMTOTLLJONANDPOKLV
LKGLGVNPTLEEMLTACOGVGGPGQKARLMAEALKEALAPVPIFFAAAQQRGPRKPIK
/note="'Accession Number M74144(1 to 1572 = SU)'"
                                                                                                                                                                                                                /translation="MSDPRERIPPGNSGEETIGEAFEWLNRTVEEINREAVNHLPRELIFQVWQRSWEYWHDEQGMSPSYVKYRYLCLIQKALFMHCKKGCRCLGEGHGAGGWRPGPPPPPPGLA"
                                                                                                                                                                                                                                                                                                                                                                                      /translation="MEEEKRWIAVPTWRIPERLERWHSLIKYLKYKTKDLQKVCYVPH
FKVGWAWWTCSRVIFPLQEGSHLEVQGYWHLTPEKGWLSTYAVRVTWYSKNFWTDVTP
NYADILLHSTYFPCFTAGEVRRAIRGEQLLSCCRFPRAHKYQVPSLQYLALKVVSDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MLELWERGTLCKAMQSPKKTGMLEMWKNGPCYGQMPRQTGGFFRPWSMGKEAPQFPHGSSASGADANCSPRGPSCGSAKELHAVGQAAERKTERKQREALQGDDRGFAAPQFSLWRRPVVTAHIEGQPVEVLLDTGADDSIVTGIELGPHYTPKIVGGIG
                                                                         6603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAKIIKDYGGGKEMDSSSHMEDTGEAREVA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARQIVDTCDKCHQKGEAIHGQVNSDLGTWQMDCTHLEGKIIIVAVHVASGFIEAEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CWNCGKEGHSARQCRAPRRQGCWKCGKMDHVMAKCPDRQAGFLGLGPWGKKPRNFPMA
QVHQGLTPTAPPEDPAVDLLKNYMQLGKQQREKQRESREKPYKEMTEDLLHLNSLFGG
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487..492
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RRRWQQLLALADRIYSFPDPPTDTPLDLAIQQLQNLAIESIPDPPTNTPEALCDPTKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGVVEAMNHHLKNQIDRIREQANSVETIVLMAVHSMNFKRRGGTGDMTPAERLINMIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFINTKEYKNVEIEVLGKRIRGTIMTGDTPINIFGRNLLTALGMSLNLPIAKVEPVKV
                                                                                                                                                                                                                                                                                                                                                                    SQGENPTWKQWRRDNRRGLRMAKQNSRGDKQRGGKPPTKGANFPGLAKVLGILA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEQEIQFQQSKNSKFKNFRVYYREGRDQLWKGPGELLWKGEGAVILKVGTDIKVVPRF
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/codon_start=1
                                                /pseudo
                                                                    /codon_start=1
5603..9239
                                                                                                                     /note="'premature
/product="'vpr'"
                                                                                                                                                                       /pseudo
                                                                                                                                                                                                                                                                                             codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="'vif'"
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                                                                                                                                              stop
                      6603 to 8174;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Statistics: Mean 12.787; Variance 3.591; scale 3.561	Database: HIV-NA8 1:H_PRI 2:H_UNA 3:H_VIR	Post-processing: Minimum Match 0% Listing first 45 summaries	Searched: 1052 seqs, 1486975 bases x 2	STD : Dbase 0; Query 0	g table: TABLE default Gap 6 STD : Dhase 0: Onerv	Title: >US-09-103-287-1  Description: (1-1351) from US09103287.seq  Perfect Score: 1351  N.A. Sequence: 1 ATGAGTAAGGAGTTTTATATATTTAATATGTTTATAATAGAG 1351  Comp: TACTCATTCCTCAAAATATAAATTATACAAATATTATCTC	Run on: Sat Nov 27 11:49:21 1999; MasPar time 8.79 Seconds 457.159 Million cell updates/sec Tabular output not generated.	Release 3.1A John F. Collins, Bioc Copyright (c) 1993-1998 Universit Distribution rights by Oxf nn n.a n.a. database search, us	**************************************
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## SUMMARIES

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CODE F. COLLINS, Biocomputing Research Unit. 1993-1998 University of Edinburgh, U.X. button rights by Oxford Molecular Ltd Smith-Naterman search, using a protein database en backtranslated into n.a. using IUPAC symbols 24 01:07:08 1999; MasPar time 2.75 Seconds ated. 103-287-1 103-287-1 103-287-1 20 from US09103287.seq ARGAGTARGGAGTTTTATAT	1 137 2.0 2 137 2.0 3 135 2.0 4 137 2.0 5 137 2.0 6 127 1.9 7 126 1.9 9 127 1.9 10 127 1.9 11 127 1.9 11 127 1.9 127 1.9 13 121 1.8 14 121 1.8 15 122 1.8 16 122 1.8 17 122 1.8 18 122 1.8 19 120 1.8	Result Query	Statistics: Mean 77 Pred. No. is the n score greater than and is derived by	abase: HIV-AA 1:AL	Post-processing: Minimum Listing	Searched: 1479 se	Nmatch STD : Dbase 0	Scoring table: TABLE b	Title: >US-09- Description: (1-1351 Perfect Score: 6755 N.A. Sequence: 1 Comp:	Run on: Wed Nov	rch_ntp n.a n. which has	Release 3.1A J Copyright (c) Distri	
ω η * *	GAGSW2S1 GAGSW2S1 GAGSF10S1 HIVF10S1, GAG GAGSF10S1 GAGSF10S1 GAGSF10S1 GAGSF10S1 GAGSF10S1 GAGSP1136 GAGSP1136 GAGSP1136 GAGSCAM1 GAG POLYPRO GAGSCAM1 GAG POLYPRO GAGSST200 HIVF157, GAG POLYPRO GAGSW157 HIVF157, GAG POLYPRO GAGSW11321 HIVF151321, GAG GAGSW11321 HIVF151321, GAG GAGSW110 GAGSW1205 GAGSW1205 GAGSW1205 GAGSW1205 GAGSW1205 HIVF1505 GAGSW1205 GAGSW1205 HIVF1505 GAGSW1205 GAGSW1205 HIVSF2, GAG POLYPROT GAGSW145 HIVSF2, GAG POLYPROT SENVS2GH1 HIVSF2, GAG POLYPROT SENVS2GH1 HIVSF2, GAG POLYPROT SENVS2GH1 HIVSF2, GAG POLYPROT SENVS2GH1 HIVSF2, GAG POLYPROT SENVS2GH1 HIVSF2, GAG POLYPROT SENVS2GH1 HIVSF2, GAG POLYPROT SENVS2GH1 HIVSF2, GAG POLYPROT SENVS2GH1 HIVSF2, GAG POLYPROT SENVS2GH1 HIVSF2, GAG POLYPROT SENVS2GH1 HIVSF2, GAG POLYPROT SENVS2GH1 HIVSF2, GAG POLYPROT SENVS2GH1	SUMMARIES  ngth DB ID Description Pred.	7.190; Variance 217.128; scale 0.356 number of results predicted by chance to have no regual to the score of the result being analysis of the total score distribution.		Match 0% first 45 summarie	eqs, 1162203 bases x		_ 0	-103-287-1 1) from US09103287.seq ATGAGTAAGGAGTTTTATATTTAATATGTTTATAATAGAG 1 TACTCATTCCTCAAAATATATAAATTATACAAATATTATCTC	24 01:07:08 1999; MasPar time 2.75 Seconds 1143.653 Million cell updates ted.	Smith-Waterman search, using a protein databas en backtranslated into n.a. using IUPAC symbols	. Collins, Biocomputing Research Uni 1998 University of Edinburgh, U.K. n rights by Oxford Molecular Ltd	

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AF015636
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Mustela vison GT dinucleotide repeat, chromosome 1q.
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Epacris impressa.
Chloroplast Epacris impressa
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1 (bases 1 to 1056)
Brusgaard, K., Shukri, N.M., Malchenko, S., Koroleva, I. and Lohi, O.
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Submitted (22-JUL-1997) Biology, Wake Forest University,
Road, Winston-Salem, NC 27109, USA
On Oct 2, 1998 this sequence version replaced gi:3676317,
Location/Qualifiers
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Kron,K.A., Fuller,R., Crayn,D.M., Gadek,P.A. and Quinn,C.J.
Phylogenetic relationships of epacrids and vaccinioids (Ericaceae
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                                     27 11:04:25 1999
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Pred. No. 1.09e+00;
0; Mismatches 19
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/gene="F
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                                                                                                                                                                                                                                                                                                                                                                7010. .....
/gene="HII145"
/note="similar to SP:Q02286
/note="similar to identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mikortikosikvtgyglhsgekvtitirpampntgyvyyrtdl
NPAVAFPADPNSVRDTMLCTALINEQGVRISTVEHLNAALAGLGIDNIIIEVDAPEIP
IMDGSASPFIYLLLDAGIEEQNAAKKFIRIKQYVRVEDGDKWAEFKPYNGFRLDFTID
FDHPAIGKDVRNYEMMFSAQAFVHQISRARTFGFMKDIEYLOSOGLVLGGSLDNAIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deacetylase (lpxC)"
/protein_id="AAC22799.1"
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PID:216510 PID:40864 percent identity: 77.30; identity: 97.30; identity: 77.30; identity: 97.30;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="HI1144"
5966. .6883
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GGTFVGESSLTSEEHGRIVFYAVNTDAQALRKSGVGQTVGGGGGTTYKGLGAGANPNIG
RKAAEDDQDEERKMLEGADMYFIAAGWGGGTGTGAAPVVAKIAKELGILTVAVVTRHF
TFEGKKRMGFAELGIKDLSQYVDSMIIIPNQOIQKVLFKNAKLIDAFAAANDVLRNSV
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evtqeeidsalhtassiklpeglsllhvipqeyavdromniknplglqgvrlkaqvhl
iAcHODWQNNLKKAVERGGLQVDKVVFSGFAATHSVLTEDEKDLGVCLLDFGAGTMNV
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EVASIGGRAPRSITKSDLSLTTSARYTELLGVVKDELDKIKAELEAKHIKFELLAGVV
ITGGGAQIEDLKECASNVFHQQVRIASPLNITGLTDYVNRPQYSTVVGLLQYNYSNSD
                                                                                                                                                                                                                                                                                                                                                 similarity;
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LEKIDLSNAQGILVNITAGMDLVFEEFNIIGETIGSFASEEATVVVGTSLVPEMSDEI
RVTIVATGLGEIAGNEPIQVVRQGLSTQNIEGEGRVNIVPELHRRESVEVSRTASEEY
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/db_xref="GI:1574701"
                                                                                                                                        /product="chorismate mutase (pheA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANQEAWEFVTFEDKAQVPQGYVAPVQVLI"
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/protein_id="AAC22798.1"
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/translation="MALELSDIRQQITQIDRSLLKLLSERHRLAFDVVRSKEISQKSL RDVEREQLLQELVQFAENENYQLEAQYITSITQKIIEDSVLIQQYYLQNKLNEDRUN REDVEREQQLLQELVQFAENENYQLEAQYITSITQKIIEDSVLIQQVYLQNKLNEDRUN RITAFLGKRGSYSNLAARNYAARYOKOFVELGCQSFBQVFEKVQTGEADAGVLPKDYNTGQCSQ TTSGALNEVYDLLQHTDLSLVCELAYPIKHCVLVNDKTDLNQIDTLYSHPQVIQQCSQ FIHSLDRVHIEYCESSSHAMQLVASLNKPNIAALGNEDGGKLYGLSVLKTNIANQENN
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Gaps

JOURNAL REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE REFERENCE AUTHORS RESULT LOCUS SOURCE ORGANISM Note: remainder FEATURES DEFINITION KEYWORDS VERSION ACCESSION Query Match Best Local JOURNAL Matches TITLE CDS 1069 1185 1125 GTTGATGATTATGGTCATCATCCAACAGAAGTAGGCGTAACCATTAAAAGCGGCGCGGAGAA 1184 source 1009 949 GGCTGGGGAGATAAACGTATTGTAATGATTTTCCAACCGCATCGTTATTCTCGCACTCGT 1244 GCATTTTAAATGAATTTGCAGAA GATTTGTTTGATGATTTTGTACAA 1268 AAATATCCACATAAAGAAGTTGTTGCAGTATTTCAACCACACACTTTCTCTAGAACACAA 1068 GTAGATGATTATGCACACCATCCAAGAGAAATTAGTGCTACAATTGACACAGCACGAAAG 1008 g1881675 U89259.1 Submitted (11-FEB-1997) Oncological Science, School of Med. Rm5C334, USA, UT 84132, USA Witherspoon,D.J., Doak,T.G., Williams,K., Seger,J. and Herrick,G. Selection on the protein-coding genes of the TBE1 family of transposable elements in the ciliates Oxytricha fallax and O. l (bases 1 to 354)
Doak, T.G., Doerder, F.D., Jahn, C.L. and Herrick, G.
Doak, T.G., Doerder, F.D., Jahn, C.L. and Herrick, G.
A proposed superfamily of transposase genes: transposon-like
elements in ciliated protozoa and a common 'D35E' motif
Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994) Oxytricha fallax Oxytricha Doak, T.G., Williams, K., Direct Submission Eukaryotae; mitochondrial eukaryotes; Alveolata; Ciliophora; hypotrichs; Stichotrichida; Oxytricha. 2.2%; Similarity 60.4%; 87; Conservet Unpublished Oxytricha U89259 OFU89259 (bases 1 (bases 1 to 354) of. annotations omitted /translation="htrdlxkhllkahkkxxexexxxxxlkxlxkkkarexxxxxxxx QaxexxxvxxxrnxlxsextkimikiQykkipvlaQidldtslQsyliledsfdkkvi XDHQYAYKVYpFNYL" /transposon="TBE1"
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Medical Center Dr. Rockville, MD 20850, USA
The H. influenzae sequence has been updated by R. Fleischmann. New
database matches have been assigned, product names have been
improved, and a number of frame shifts have been corrected. We
gratefully acknowledge the work of Tatusov et. al. We have
incorporated their annotation into the /notes fields of the
corresponding H. influenzae genes
5 (bases 1 to 12085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merrick, J.M., McKenney, K., Sutton, G.G., FitzHugh, W., Fields, C.A., Gocayne, J.D., Scott, J.D., Shirley, R., Liu, L.I., Glodek, A., Kelley, J.M., Weidman, J.F., Phillips, C.A., Spriggs, T., Hedblom, E., Cotton, M.D., Utterback, T., Hanna, M.C., Nguyen, D.T., Saudek, D.M., Brandon, R.C., Fihe, L.D., Fritchman, J.L., Fuhrmann, J.L., Geoghagen, N.S., Gnehm, C.L., McDonald, L.A., Small, K.V., Fraser, C.M., Smith, H.O., and Venter, J.C.
                                                                                                                                                                 White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D Direct Submission
Submitted (27-SEP-1997) The Institute for Genomic Research.
                                                                                                                                                                                                                              Submitted (25-JUL-1995) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA 4 (bases 1 to 12085)
                                                                                                                                                                                                                                                                                                                                                                                                                     Tatusov,R.L., Mushegian,A.R., Bork,P., Brown,N.P., Borodovsky,M., Rudd,K.E. and Koonin,E.V. Metabolism and evolution of Haemophilus influenzae
                                                                                                                                                                                                                                                                                               White, O., Clayton, R.A., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                            whole-genome comparison with Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 269
95350630
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U32794.1 GI:1574694
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Haemophilus influenzae Rd
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Similarity 63.7%;
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Rd S
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of 163
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The whole genome was shifted by 588 nucleotides for a new start on Oct.1, 1996 this sequence version replaced gi:1221895.
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DNTQYFCPAGLTPEREQALSTLVKRAYDAVGCRGWSRIDVMCDAKGNFRLVEVNTNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"similar to GB:D10483 SP:P07862 GB:K02668 PID:145724 PID:146030 percent identity: 59.93; identified by sequence similarity; putative"
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PID:42056 percent identity:
similarity: putative"
                                                                                         ERFVTIYPQIDVPENKKIDY IDLRYTAGAAVGMVDR'
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WVKGAIVRKMWPNRLSIWVSEYQPVAFWNQNQFVTLDGIVFQLPSVRLTAKNLPYLGG
                                                                                                                                                                                                                                                                                                                                                                                                                           similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GB:D10483 SP:P06136 GB:K02668 GB:X02821
PID:145725 percent identity: 40.62; identified by sequence
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Dodson, R. and Gwinn, M.
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68.16; identified by
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	CDS	gene		( )	gene			CDS	gene		CDS	gene	CDS
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gene CDS			CDS	gene		gene CDS				gene CDS		gene CDS	
ITEESIPPTWIFFWSLROUP GLEVAL TO THE FOUND SET OF THE FOUND	A1fAFFLESVFLGKDKVSFKF1AFSTWYA1GINJALWILVANSWQJTFKOF YLEGGKAYLASFEDAVVNYSTPYRFVHMFLAGVITGAIFVAGISAYYILKKKHLDVAK ESFRIAVTIGMIASLLQIIAGDLHGYQVARTQPLKLAMMEDKWETESGAGLEIVPGIE IDKII,STI,XYHDDAKVVGTKDIJOOTEOKYAKCEFVGEDELDFF,WI.DDAGEAGROSI,V	/product="cytochrome oxidase d subunit I" /protein_id="AAC07328.1" /protein_id="AAC07328.1" /db_xref="rID:g2983769" /db_xref="rID:2983769" /db_xref="rID:2983769" /translation="MDAVLLARIQFALTAMYHFLFVPITLGLSLLLAIWTKWAREED /translation="MDAVLLARIQFALTAMYHFLFVPITLGLSLLLAIWTKWAREED /translation="MDAVLLARIQFALTAMYHFLFVPITLGLSLLLAIWTKWAREED /translation="MDAVLLARIQFALTAMYHFLFVPITLGLSLLLAIWTKWAREED /translation="MDAVLLARIQFALTAMYHFLFVPITLGLSLLLAIWTKWAREED /translation="MDAVLLARIQFALTAMYHFLFVPITLGLSLLLAIWTKWAREED	/note= ag_135/" /gene="cydA" 7056 . 8462 /gene="cydA" /codon_start=1	//db_xref="61:298377" //db_xref="61:2983777" //db_xref="61:2983777" /translation="MGKVIQPFGEEPEKKEEKTEPLTEEDFNQVIEVFKKDLKT LYPSQVKDILGVIGLGEKYGDEKFVVGLLMWEHYKHSHPLVSSFVAVLKGDKLEKISF LEAKNNYWWMKLMVKTYKDKFHTEELMRGLFELKERFEKGEI" 7056. 8462	/codon_start=1 /transl_table=11 /product="putative protein" /protein_id="AACO7336.1"	65056939 /gene="aq_1356" 65056939 /gene="aq_1356"	/translation="MMKPVLHFSKLYEVKKLLHKSRLYEVGESRCPNISECFGNKTA  TFMILGNRCTRRCAFCNVEKGFPKGVDEEBYRLLEAVKTLGLKYVVTTSVTRDDLPD  GGASHFAKCIRVLKENIEDIKVEVLIPDFRGNKKALEVVLKEKPVVLNHNVETVPRLY  PSVRIGANYKRSLNILKWSKEIDKSVYTKSALILGFGERKEEVIKVMEDLRSVDCDFL  VLGQYYQPSLKHHPVVKYYSEEEFKEFEBIGYENGFKFVVSKPNARSSYKAFESLLST	/db_xref="PID:g2983766" /db_xref="G1:2983766"	/geneipn /codon_start=1 /transl_table=11 /product="Lipoic acid synthetase" /protein_id="AACO7325.1"	VYIPODGEIRELNKTYRKKDRPTDVLSEPMGEDEGGYKILGDVVISQDTAERQARELG HSLEEEVKRLIVHGIVHLLGYDHEKGGEEEKKFRELENYVLSKLSKAL" complement(56496479) /note="aq_1355" /gene="lipA" complement(56496479)	/db_xref="gli:g2983//9" /db_xref="gI:2983779" /translation="msstkroknrvlvklkkrkvrkdkiekwaelalsalglnnvels	QIDLPKKKESGLIEAMEVLKNIEGIEFIFFKQTDVVRHPIVAKIINAYEQYEKAKEQS SGKTEEEESKEGQD 52305682 /gene="aq_1354" 52305682 /gene="aq_1354" /codon_start=1 /trans1_table=11 /product="hypothetical protein" /protein_id="AACO7338.1"	GTELJIKGEEDKVREFVNFLKAVLKRLEHERLTAEEVKEYAKQFLKSVEAYKIEEQPG REEKELEEEVILJITHRKKAIVPKTETQKKYVEAIKKNDIVFGIGPAGTGKTYLAMAMA LQHLKEGKVNKIILTRPAVEAGEKLGFLPGTIAEKVḤPYLTPLYDALYDMVDYDKAVI MLERNIIEIAPLAFMRGRTLNDAFIILDEAQNAFRDQMKNFLTRIGFGSKAVITGDVT

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                                                                                                                                                                                                                                                                                                    GenBank
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AUTHORS
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AUTHORS
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KEYWORDS
SOURCE
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ORIGIN
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LOCUS
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MEDLINE
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ESKQKLEELKKRLGLS" 939. .1469

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1171 TAAATGATTATGGACATCATCCTACTGAATTATCTGAAACTATTAAAACAATACGAAAAA 1230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1291 ATCTATATTTCGATTTTATTAAAATTTTATCTCAAGTAGACTCTTTATT 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  950 TAGATGATTATGCACACCATCCAAGAGAAATTAGTGCTACAATTGACACAGCACGAAAGA 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGGCCTAAAAAAATTTAATAATGATATTTCAACCTCATCGATATACAAGAACCCGAA 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTTTTAAATGAATTTGCAGAAAGTTTATGTAAAGCAGATCGTGTATT 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98196666
2 (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aguifex aeolicus section
AE000736 AE000657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Similarity
100; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M., Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L., Graham,D.E., Overbeek,R., Snead,M.A., Schler,M., Aujay,M., Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V. The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aquifex aeolicus
Aquifex aeolicus
Eubacteria; Aquif
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative indicates no similarity to known proteins Hypothetical indicates similarity to a protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA 92121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-JUL-1997) Diversa Corporation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aeolicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 15862)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pacteria; Aquificales; Aquificaceae; Aquifex.
(bases 1 to 15862)
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larity 59.2%;
Conservative
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LILSGIGKVSASMSTTISIULFQPDIINSGSAGSLNACLKIGDIIIPKKTCYYDVDL
TNEGYSKGQIPEYPQJFKTUKKULFEILKEIAVEFKFKFLJGLLVVTGDSFTRKSNCIKK
IKNQFSSAIGVDMESTAIGQVCHNFKIPFIIIKSISDLSDNNATSHFEKNIPIASLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKLVKLLKKISSQNSI"
1 750 c 957 g
                                                                                     /transl_table=11
/product="putative protein"
/protein_id="ARC07332.1"
/db_xref="PID:92983773"
/db_xref="GI:2983773"
                    /translation="mmGllkRllrvvraeahsvvekleDpIkITeEGLrELRKQlkEA
MEALAQvkasQIRFEREARNEKERAKALvKKAESLLLQAQEGKISPEEAEKLAAELIQ
KAELHEKNARRLEEEAKRQREMAVKLQAKIDELKVQIAKYEAELKTLKARLATARAVK
KVNKQIAKVDPSDTIAMLERMKEKVEEEETLAQAYEELAKQEVALDVESEAEKKLKEV
                                                                                                                                                                                                                                                               /gene="aq_1345"
233. .937
                                                                                                                                                                                                                                                                                                                                                      /organism="Aquifex aeolicus"
/strain⇒"VF5"
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:63363"
                                                                                                                                                                                                               codon_start=1/
                                                                                                                                                                                                                                   gene-"aq_1345"
                                                                                                                                                                                                                                                                                                                                                                                                        .15862
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Pred. No. 3.84e-02;
0; Mismatches 69
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n 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        of unknown function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Swanson, R.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lenox, A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              San Diego,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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REFERENCE
AUTHORS
TITLE
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
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LOCUS
                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                   VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.4%;
Best Local Similarity 63.6%;
Matches 77; Conservative
                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4083 CCAATGTTGACTACGAGCATGTTGATTTTTTTAAAAATTATGAGGCTCTTGAAGAGGCTT 4142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4023 TTGAAACTTGTGAATATAAGAAACATTTTTTGAATTTTTAGCCCTAATATGCTTATTTTAA 4082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGAGGCATGTGAATATAGACGTCACTTTTTAAGTTATAAACCTGATTACGCAATTATGA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 587
                                                                                                                                                                                                                                                                                                                                                               94099442
U87256.1
                                                                                                                                                                                                                       Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Carnivora; Fissipedia; Mustelidae; Mustela.

1 (bases 1 to 1056)
Brusgaard, K., Shukri, N.M., Malchenko, S., Koroleva, I.
                                                                                                                                                                           Animal
                                                                                                                                                                                                                                                                                                                                                                                                       Mustela vison
U87256
                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                          Mustela vison
                                                                                                                                                                                                                                                                                                                            American mink.
                                                                                                                                                                                                                                                                                                                                                                                                                                            MVU87256
                                                                                                                                                                 ted (27-JAN-1997) Breeding and Genetics, Science, Blichersalle K25, Tjele 8830, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          annotations omitted.
/note="primers: 1167F: agcccctgcatatctacttctt, gaggatcttaccgctgttgag" 98. .119
                                                                                            /organism="Mustela vison"
/db_xref="taxon:9667"
                                                                             /chromosome="1"
                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MKEDRVVFIFGPTAVGKSNILFHFPKNKAEIINVDSIQVYKEFN
IASSKPSKNLMKHIKHHLVDFLDPEKDYTIGIFYEQALKIVKEIRQKKKIPIFVGGTA
FYFKHLKDGFPSTPLVTSKIRIYVNNLLELKGKSYLLKELKNVDPIRFNMLNKNDIYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA)" /protein_id="AAC67163.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="BB0821"
6563. .7483
                                                                                                                                                                                                                                                                                                                                                                   GI:4099442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKRSLEVYYQTGIPISQFQKKQSSEFKNIVIIGLKRSFEDLKTRISIRINEMLNSGLL
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kilgqafndvltgkfrysiegr"
6563. .7483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hypothetical protein; identified
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="B. burgdorferi
/protein_id="AAC67174.1"
/db_xref="PID:g2688769"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="PID:g2688758"
/db_xref="GI:2688758"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="similar to GP:216567 percent identity:
dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="BB0821"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:2688769"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                1056 bp DNA MAM
1 GT dinucleotide repeat, chromosome
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Pred. No. 3.77e-03;
0; Mismatches 44
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                                                                                                                                                                                                                             and Lohi,0
                                                                                                                                                                                                                                                                                    Eutheria;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1087 CAAATTCATTTAAAAATGCTTGTGTTCTAGAGAAAGTGTGTGGTTGAAATACTGCAACAA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              706 YARRKMYGTGAAWASATAYSTGAGTTBWRVTSWKMBKYKKTGMMHHCAWKYGKGTCGCCY 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BUChnera aphidicola UDP-N-acetylmuramate: L-alanine ligase (murC157), D-alanine: D-alanine ligase (ddlB), cell division protein (ftsA), cell septation protein (ftsZ), and pfs genes, AF012886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-JUL-1997) Microbiology, University of California, Davis, CA 95616-8665, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baumann,L. and Baumann,P. Characterization of ftsZ, the cell division gene of Buchnera aphidicola (endosymbiont of aphids) and detection of the procurr. Microbiol. 36 (2), 85-89 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98087557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eubacteria; Proteobacteria; 1 (bases 1 to 6757)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buchnera aphidicola
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AF012886.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 34.5%;
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/gene="ddlB"
1577. .2497
/gene="ddlB"
                                                                                         /translation="MNINKIKKNNFFKEKKILKIHLIGIAGSGMSGIALILFNLGYKI
SGSDLLENIFMTKKLKNNGINITFGHSEENIKYADFIIISSAIPSDNBEIKAAKKKNIH
ILLRAEMQJE HØGFKGIAVGGTHGKTTLLAHIFDILMONKLDPTVINGGLIKSINSH
AKLGFSKYFIAEADESDGSFLCLNPTTAIITNIEPDHJDNYNGEFKLLKKTFLDFLNK
LPSYGIAILCTDNKAILNILFRIKCKVITYGENKSABFRITSYKOSDDFISNTTLIRKK
QLNNLEIILNLPGEHHALNATAAIATAYTQH IPDEXIYQSLKNFKGTSRRFEDVGKLF
IKKKSIQNKSVMLINDYGHHPTELSETIKTIRKSWPKKNLIMLFQPHRYTRTHNLYFD
FIKILSQVDSLLILNYYSANESFISGADSFSLYSDIKKIKNVILVTNRNLILNYLLP
                                                            HLNGNDIILIQGAGDIDTIINKIFILKNKKVII"
1577. .2497
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Buchnera aphidicola is a prokaryotic endosymbiont
of the aphid Schizaphis graminum"
                                                                                                                                                                                                                                                                                                                                                                                                         /gene="muro
129. .1580
                                                                                                                                                                                                                                                         /product="UDP-N-acetylmuramate: L-alanine ligase"
/protein_id="AAC46066.1"
/db_xref="pID:92738586"
/db_xref="GI:2738586"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name="1167F"
complement(300. .320)
/standard_name="1167R"
a 221 c 210 g
                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /specific_host="Schizaphis graminum"
/db_xref="taxon:9"
                                                                                                                                                                                                                                                                                                                                                                                    'gene="murC157"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Buchnera aphidicola"
                                                                                                                                                                                                                                                                                                                                                                                                                     murc157"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 23;
Pred. No. 3.84e-02;
29; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gwinn,M., Dougherty,B., Tomb,J.-F., Fleischmann,R.D.,
Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J.,
Salzberg,S., Hanson,M., van-Vugt,Ramer,N., Adams,M.D.,
Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L.,
Artiach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Horst,K.,
Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-DEC-1997) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="hypothetical protein; identified by Glimmer;
putative"
                                                                                                                                                                                                                                /transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAC67167.1"
/db_xref="piD:g2688762"
/db_xref="g1:2688762"
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PID:1045895 percent identity: 31.20; identified by
sequence similarity; putative"
//codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="BB0813"
68. .244
/note="hypothetical protein; putative"
                                                        /gene="BB0816"
2578. .3528
                                                                                                                                      TARKLSEAFSGGSIIKKYFAILLGEVKSPVVYKNHLFRNKRLRKTFVLEDKNFVNAIT
KVNPILSCKRATLVEIVIETGFTHQIRSQCSFNNHPLINDKKYCNKFKKSDYFLHAFL
                                                                                                                                                                            /translation="MRLDKYIFLEVLANDNGKRLDSILIKILNFSKASIIKHIRKGDI
RLNGLKSHFSCRVCKGDKIYLYKSLAQNLNLTTDKCFKSNIDFQYIRKRIIYEDSDLL
VLDKQKGILVHGGKNSLDFLVNSYLLSQNLRSLSFKPSAVHRLDRNTSGIIIFAKNIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identity: 33.64; identified by sequence similarity;
putative"
                                     /gene="BB0816"
                                                                                                                     VKFNGTFFKKNEFCSKPSLDF"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="BB0815"
1666. .2559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FASMFLGLIFYLSILFFGLNIWFFHPVFPSFFVSIFTFLVVNFFCKKNSKVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
/product="B. burgdorferi
/protein_id="AAC67176.1"
                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="BB0815"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="BB0814"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'FPSIIFFWFVFLF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MRNGILYAILLYVFMFVLWFCFAYFIDTSTTIFNIPLWFFLSGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="BB0813"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ∕organism="Borrelia burgdorferi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref="PID:g2688771"
'db_xref="GI:2688771"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="similar to PID:606198 GB:U00096 PID:1789656 percent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "BB0814"
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              identified by Glimmer;
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CDS
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                                       gene
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/note="similar to GB:L77117 SP:Q58071 PID:1591369 percent identity: 38.76; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTDEILSNNKISYYDNIYEFSLKQLDRSFDLIVYSSAYNKDGLQVLLEAKELNIPILS
YPEALGELSRKYYSIGIAGSHGKTTTTAFLGVLFNKLGLNPNVIVGSSVKDFKDNSAI
AGISNIFIVETCEYKKHFLNFSPNMLILTNVDYEHVDFFKNYEALEEAFLQYINNLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MKSMTGFFYLEXIIGNYMFSVNLKSYNGKELEFKERLPEIFSGY
DLDIRNLISKYISRGNVFLNVGYELYSVNFTIPNYIEAISKURDSLAHTNLNIK
ELSLODFLSLKGALIILDEDSEHGEITYGLFKGYLEEALLHYNNGRSFEGENTKSDIVS
TLVLIERDLKIVKDACSDINVKLFASIKENISKLMDEFRDLNIAEEAAKMAIRLDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="BB0818"
/note="similar to GB:L10328 SP:P23839 GB:X14235 PID:290494
PID:42721 percent identity: 29.96; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4935
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NYELKTYLFHNYLMFSAALLALNLFLESNGKSIFDFEBAIKRIAKNYSGIKRFVETVK
EENGVIYMDDYAHHPREIKNTLFGIKNFYKNEKBIILDEMPHTFTRTKEFFADFVEVLS
AADILLLHNIYLSNRENFNPDELSYKLFLNIKKINKNTYFFKDVKDSINFIKSLLISG
                                                                                                                         /db_xref="g1:2688759"
/translation="mktalsgksgcgnttvsgmiakhyglefinytfhdiarehnipf
/translation="mktalsgksgcgnttvsgmiakhyglefinytfhdiarehnipf
SEFYEKEIIGRNDYYMDKYLDNRLSVLSRKNNTVLASRLAIWISKSADLKIYLYAKME
VRAERIMTREGGMYSDVLSSTFIRDENDKKRYLAIYNIDIDDYFSETDLVIDVTNINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEKIKEQIRNVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="BB0817"
3518. .4924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTGKSFRSHLVADKYSIPLIIDDGVLIKNMKIIAGSSAKFEDNVFKAVRRSVFEDDA
HCREMLEVLAKEEFNKILIIGTSLKMLDKIISKILFNVFKIIJITDVSTRQEIEKAR
ISROMGEHVVPAAAFEITSIRPNLLNSIKVFEKSGMFFARKKNYIRSVVRPHFYEE
VLSISKRAVRQIIEHCVSEYDRNYIVYDLKIKKDGNNYLFKLFLNIPLGNNLLNNTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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/protein_id="AAC67175.1"
/db_xref="pID:92688770"
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/translation="MMSMNFQNFSSDFFLKKILSKVKDFAISIKHKFVRVKVYALVGS
/gene="BB0820"
6376. .6576
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                                                                                                                                                                                                                                            /product="cytidylate kinase
/protein_id="AAC67164.1"
/db_xref="piD:92688759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="BB0819"
5798. .6340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIMRLDSHIETFYKNLEYEICGKALEFISQEMHREITTMSNKAVDLDIKNLILNMKLN
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/protein_id="AAC67166.1"
/db_xref="PID:92688761"
/db_xref="GI:2688761"
/translation="MKVDFDDLNNIFFVGIKGSGACSLACFLNSKGYCVEGVDVSDKF
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PID:1221261 PID:1205384 percent identity: 28.70;
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/protein_id="AAC67165.1
/db_xref="PID:g2688760"
/db_xref="GI:2688760"
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Gray, Y.H.M., Sved, J.A.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-JUN-1997) School of Biological Sciences, of Sydney, Biology Al2, Sydney University, NSW 2006, Au Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.

1 (bases 4546 to 4553)
Gray,Y.H., Tanaka,M.M. and Sved,J.A.
P-element induced recombination in Drosophila melanogaster: hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF012089 10772 bp UNA Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished 3 (bases 1
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2310
    2427. .6475
/genee"CP1"
4546. .4553
/gene="CP1"
/note="insertion site of P{CaSpeR}(50C)"
/citation=[1]
                                                                                                                                                                                              /translation="mrtavllpliallavaqavsfadvvmeemhteklehrknyqdet
/erfrlkifydehtytespackvsfklavnkyadllhegolmgenytlhk
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/db_xref="GI:2305221"
                                                                                                                                    ASSYPLV
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/db_xref="taxon:7227"
join(872. .1000,2310. .2426,6476. .6690,6751. .7707)
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Best Local Similarity 15.6%;
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                                                                                                              burgdorferi group.

1 (bases 1 to 15079)

1 (bases, Ca, Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A., Fraser,C.M., Casjens,S., Ketchum,K.A., Dodson,R., Hickey,E.K., Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B., Tomb,J.-F., Fleischmann,R.D., Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van-Vugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L., Artiach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Horst,K., Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C.

Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia
AE001180
g2688755
    Fraser,C.M.,
Lathigra,R.,
                                                                    98065943
                                                                                                                                                                                                                                                                                                                                                                                            Borrelia burgdorferi
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                                                                                                            burgdorferi
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                                                                                        Nature 390 (6660), 580-586 (1997)
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SSWTK NISPATERAVKLMEHEMKHVLVGLTKOLFGPR IXY KWOTYYF PFTQPSWELEI
YFKDIWLEVLGCGIMKHEILORSGVHOSIGYARFGVGLERLAMVLFDIPDITLFTWSNDS
GFLSQFSEKDLHNLPKYKPISHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
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TDGWTNVTPKILSYVGANKHLQTDHPLSIIRQRIVNYFYGAYRNQRGNPLFSVYDQMN
PVVTVQQNFDNLLIPADHVSRQKSDCYYINQQHLLRAHTTAHQVELISGGLDNFLVVG
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/protein_id="AAB65750.1"
/db_xref="PID:g2305222"
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    Casjens,S.,
White,O., K
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Pred. No. 8.76e-06;
72; Mismatches 51
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    Ketchum, K.A.,
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Sutton, G.G., Clayton, R. Dodson, R., Hickey, E.K.,
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Clayton, R.A.,

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	containing an expression system comprising the Murc gene can be used for the recombinant production of the polypeptide. Agonists or the Murc polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide are useful for inhibiting the polypeptide e.g. bacterial (especially S. aureus) infections. They are also useful against Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The Murc polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to identify modulators or specific receptors; in rational	eic acid - useful in diagnosis, treatment and prevention of erial infections m 1; Page 4; 39pp; English. present sequence represents a UDP-N-acetylmuramate:L-alanin present sequence represents a UDP-N-acetylmuramate.	lococcus aure	17-MAR-1999 (first entry)  10P-N-acetylmuramate:L-alanine ligase (MurC polypeptide).  MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide.  bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine  immunogen; drug; genetic immunisation.  Staphylococcus aureus.  EP-889123-A2.  07-JAN-1999. 305064.			ce bacteríal	diled 5-enol ssica napus sin nisT qene	Staphylococcus entero Staphylococcus entero Staphylococcus entero Staphylococcus entero Staphylococcus entero Staphylococcus entero	aphylococcus	reptococcus periode v	quence transc quence transc b-lipoproteir	EPV Spheroidi EPV spheroidi quence of fil	Human lutropin-chorio SalF20.5R. Pool #1. AmEDV entomonoxvirus	Amphiphilic peptide t Sequence of amphiphil Sequence of amphiphil Amphiphilic peptide t	Sequence of amp Amphiphilic per Amino acid sequ
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                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The Murc polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to identify modulators or specific receptors; in rational drug design and as an immunogen for vaccines. The Murc gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant Murc gene; for chromosomal mapping; to determine bacterial serotype; and for genetic immunisation. The present sequence represents a partial sequence of the Murc polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MurC gene;
bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. bacterial (especially S. aureus) infections. They are also useful against Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in dwelling devices for the number of the polypeptide are useful to treat in dwelling devices for the actions.
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The invention relates to a UI
(MurC polypeptide) encoded by
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03-JUL-1997; US-052720
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UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide; infection; H. pylori; cancer; ulcer; gastritis; vaccine; drug; genetic immunisation.
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31-OCT-1996; US-0299
31-OCT-1996; US-0299
(HUMA-) HUMAN GENOMI
Choi GH, Hromockyj MPI; 98-272224/24.
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W55120;
02-OCT-1998
                                The present sequence represents a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000
                                                                                                                                                                                                                                                                                     pneumoniae or their epit
protective or therapeutic
Claim 11; Page 73; 118pp;
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                    e.g. by injection,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PT New nucleic acid sequences from Staphylococcus aureus WCHU29 -
PT useful in vaccines and for treatment of bacterial infections of e.g.
PT respiratory tract and central nervous system
PS Claim 11; Page 329; 390pp; English.

CC This sequence represents a Staphylococcus aureus protein of unknown
CC The DNA sequences were isolated from Staphylococcus aureus WCHU29
CC (NCIMB 40771). Host cells containing the DNA sequences are used to
CC produce polypeptides or fragments. The proteins are used in the treatment
CC of disease, for inducing an immune response by administering them, to
CC produce antibody and/or T-cell immune response. Antagonists of the
CC proteins are used for the inhibition of bacterial polypeptides.
CC conditions which may be treated include bacterial infections, especially
CC respiratory, cardiac, gastrointestinal, central nervous, eye, kidney,
CC respiratory, cardiac, gastrointestinal, central nervous, eye, kidney,
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Matches 8
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W55117 standard;
W55117;
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                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae;
                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM (SMIK ) SMITHKLINE BEECHAM Black MT, Burnham MKR, Hodg
Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                           Choi GH, Hromockyj A, WPI; 98-272224/24.
                                                                                                                                                            WO9818930-A2.
07-MAY-1998.
30-OCT-1997; U19422.
31-OCT-1996; US-029960.
                                                                                                                                                                                                                                                                                                                              Streptococcus
                                                                                                                                                                                                                                                                                                                                                 detection; pneumonia; otitis media; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-1998
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24-SEP-1996;
                                                                                                                                       HUMA-) HUMAN GENOME
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                                                                                                                                         SCI INC.
                                                                                                                   Johnson
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                                                                                                                                                                                                                                                      "encoded by
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.63e-24;
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Query Match Best Local

2.7%; Similarity 34.9%;

Score Pred. 54; M

180; DB 18; No. 9.99e-01;

Length 395;

Mismatches

101;

Indels k q

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Gaps

0,

Conservative

Matches

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PS Claim 11; Page 72; 118pp; English.

CC The present sequence represents a protein from Streptococcus pneumoniae.

CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein

CC can be useful in vaccines for inducing protective antibodies against

CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.

CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid

CC are used to detect streptococcus infection (by usual hybridisation or

CC amplification methods), also for isolating Streptococcus genes or their

CC allelic variants. The protein can be used similarly to detect specific

CC antibodies in standard immunoassays, especially for diagnosing or

CC monitoring infections. Antibodies which bind the protein are used to

CC detect corresponding antigens, to purify the protein and for passive

CC immunisation (optionally coupled to a toxin). Vaccines are administered,

"" injection, orally or through the skin, typically at 0.01-1000
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                    This is the amino acid sequence of a mouse SRY-related protein. The gen was isolated from a mouse genomic library using a CDNA fragment amplifie by primers T33009-10 as a probe. The screen isolated 4 EcoRI fragments of 2.3, 2.8, 3.5 and 1.5 kb covering the gene. Sequence analysis reveale a 240 bp HMG box sequence between bases 7154-7393. Similarity with the human SRY HMG box sequence resulted in primers being generated to amplif the human SRY HMG box sequence for use as a probe to isolate the bovine SRY-related gene (T33008). The mouse and bovine genes are useful for determining the sex of an animal prior to birth.
                                                                                                                                                                                                                                                                                                                                                                                                                  JU-NOV-1994; JP-319525.
(KACH-) KACHIKU JUSEIRAN ISHOKU GIKUTSU KENKYUKU.
WPI: 96-336575/34.
N-PSDB; T33007.
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W03474;
23-OCT-1996 (fi
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                                                                                                                                                                                                                                                                                                                                                               of unborn animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
J08154685-A.
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Mouse; SRY; primer; PCR; polymerase chain reaction; amplification; probe; HMG box; human; bovine; sex; animal; birth.
      sequence
                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                              Bovine and mouse Sry-related DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-1996.
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                                                                                                                                                                                                                                                                                                                             Page 10-14; 21pp; Japanese.
      395
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10-NOV-1998.

14-APR-1997; 843309.

14-APR-1997; US-665435.

14-APR-1997; US-843309.

(ELIL ) LILLY & CO ELI.

HOSKING JA, Peery RB, Ska

WPI; 99-008720/01.
    W29454
W29454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Column 13-16; 14pp; English.

This is the amino acid sequence of the Streptococcus pneumoniae murb biosynthesis protein. The murb gene encodes the enzyme uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligase. The nucleic acid can be used for the production of recombinant Murb protein and the implementation of large scale screens to identify new antibacterial compounds targeted at the stem peptide biosynthetic pathway involved in the synthesis of the bacterial cell wall. Structural analysis of the Murb protein will enable structure-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae mur D biosynthetic gene - which encodes uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligauseful for identifying antibacterial compounds
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Biosynthesis; recombinant; antibacterial; bacterial cell waluridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate
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S. pneumonia
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Pred. No. 7.75e-01
18; Mismatches 4
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US5681694-A.
28-OCT-1997.
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07-JUN-1995; US-487032
01-APR-1996; US-630405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic; vaccine; identification; bindir
       infection,
Claim 61;
                                           Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevo
                                                                                 WPI; 97-052306/05.
N-PSDB; T67723.
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19-DEC-1996.
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29-JUL-1997
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The present sequence represents Streptococcus pneumoniae MurD protein (uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligase). (uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate ligase). The MurD protein is useful in a method for identifying compounds that inhibit Streptococcus pneumoniae MurD activity. Compounds identified are potentially useful as antibacterial agents.
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Hoskins JA, Peery RB,
WPI; 97-535046/49.
N-PSDB; T89154.
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MurD gene; antibacterial agent; drug screening;
uridine-diphosphate-N-acetylmuramyl-L-alanyl-D-isoglutamate
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Claim 2; Columns 21-22;
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18-JUN-1996;
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    useful for vaccines
to detect Helicobacter
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No. 7.75e-01;
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life cycle; activato
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                                                                                                                                                     Helicobacter pylori nucleic acid sequences and used for diagnostics and therapeutics Claim 18; Page 131; 235pp; English.
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Helicobacter pylori has been strongly linked to chronic
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Best Local S
Matches
Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. py infection, and to detect Helicobacter Claim 61; Pages 1035-1036; 1481pp; English.

The present sequence is a Helicobacter pylori cytoplasmic prote involved in outer membrane or cell wall biosynthesis. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide bindin compounds, useful as potential H. pylori life cycle activators inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berglindh
WPI; 97-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pMPX vectors to construct a series of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; cytoplasmic; outer membrane; cell wall; biosynthesis.
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19-DEC-1996.
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Helicobacter
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25-OCT-1995; U14364.
31-OCT-1994; US-332312.
(AMCY) AMERICAN CYANAMID C
Pausch MH, Price LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     R97985 stand
R97985;
26-OCT-1996
                                                                                                                                            Potassium channel genes from Drosophila melanogaster and Caenorhabditis elegans - useful in assaying substances to determine effects on cell growth, and in inhibiting nematode and insect pests Claim 13; Page 49-53; 79pp; English.

This sequence is presented as a potassium channel sequence encoded by the CORK gene from Caenorhabditis elegans. An alternative sequence is given in R92315. The protein may be expressed in a heterologous host cell to assay substances to determine effects on cell growth. Potassium-agonists or potassium-antagonists identified by this method may be used as nematocides, anthelminthics or in therapy of cardiac
                                                                                                                                                                                                                                                                                                                                                                               CORK potassium channel protein alternative sequence.

CORK: potassium channel; nematode; pore-forming domain;

transmembrane helix; N-glycosylation site; potassium-agonist;

potassium-antagonist; drug screening; nematocide; anthelminthic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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                   ayrayraygcncaygcngaycaycaygayraycaycayrayraygcngaygcncayc 3235
                                                                                                                                                                                                                                                                        ch MH, Price LA;
96-239450/24.
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S Y L E K L D V T N I K E A L E T F G G
                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                         Similarity
61; Conser
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63; Conser
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larity 38.0%;
Conservative
                                                                         Conservative
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                                                                      Score 175;
Pred. No. 1.
75; Mismatc
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Pred. No. 1.29e+00;
34; Mismatches 67
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                                                                         Mismatches 118;
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                                                                                    DB 18;
!.88e+00;
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RESULT 13
ID R21398;
AC R21398;
AC R21398;
DT 16-MAY-
DE Sequence
DE acetyla
KW Amphiph
KW Spermic
PM W092014
PD 06-FEB-
PF 17-UUL-
PR 19-UUL-
PA (SCRI-)
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                                                                                                                                                                                      DE Sequence of amphiphilic peptide SEQ ID No. 61 with DE acetylated N-terminus, may be a C-terminal amide. WA Amphiphilic peptide; anti-microbial; anti-viral; anti-tumour; spermicide; wound healing; sterilant.

WA Amphiphilic peptide; anti-microbial; anti-viral; anti-tumour; spermicide; wound healing; sterilant.

WO 9201462-A. PO 65-EB-1992.

PO 65-EB-1992.

PO 65-EB-1992.

PO 65-EB-1993.

PO 10-JUL-1990; US-554422.

PO 10-JUL-1990; US-54422.

PO 10-JUL-1991; US-191;   Query Match
Best Local S
Matches 2
                                                                                                                                                                               Haighten
1987.
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                                                                                                                                           Sequence
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F Y D H
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K I E A D V P I Y Y Y G F K D S D D I Y
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Score 155; DB 4;
Pred. No. 2.18e+01;
20; Mismatches 21
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                                                                                                                                                                                                            published in
2, page 80-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amphiphilic peptide(s) and analogues - for use in e.g. antimiorobial, antifungal or antitumour compositions, having increased biological activity.

The amphiphilic peptide (SEQ ID NO 61) was prepd. by standard solid phase methods. The peptide is an analogue of the peptide chaving SEQ ID NO 3 (R2824), with an N-terminal extension of 8 amino acids. Substitution and deletion analogues of this peptide chaving SEQ ID NO 3 (R2826), with an are effective as pharmacceuticals e.g. antibiotics for bacterial, fungal or viral infections, or in spermicides or antitumour or antiparasitic agents. Additionally the peptides can be used in wound healing compsns. or for treating burns or other skin or eye infections. See also R22822-89.

Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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18-JUL-1991; 024317.
19-JUL-1990; US-554442.
08-JUL-1991; US-725331.
(SCRI-) SCRIPPS RES INST.
                                                                                                                                           19-MAR-1990 (first entry)
Amino acid sequence of Shiva-5.
Shiva-5; lytic peptide; antimicrobial peptide; disease-resistant trichophyte; Shiva-2; Shiva-3; Shiva-4; Shiva-6; Shiva-7.
W08904371-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-1992 (first entry)
Amphiphilic peptide to inhibit growth of a target cell.
Antimicrobial; antifungal; antitumour; pharmaceuticals; antibiotics; antiparasitic; spermicides; burns; wound healing.
Synthetic.
Table I; 56pp; English.

agent, or polypeptide high in essential amino acids
Amino acid sequence of Shiva-5 as an exemplary lytic peptide for
use as an antimicrobial peptide contemplated for use in plant
                                                                  2-NOV-1988; U03908.
02-NOV-1987; US-115941.
(LOUU) Louisiana State Univ.
Jaynes JM, Derrick KS;
WPI; 89-165650/22.
                                                    wPI; 89-165650/22.
Transformed plants contg. heterolgous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 92-114943/15
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_ntp n.a. - n.a. Smith-Waterman search, using a protein database which has been backtranslated into n.a. using IUPAC symbols

Tabular output not generated. Run on: Wed Nov 24 01:07:37 1999; MasPar time 75.15 Seconds 1285.007 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence: Title: >US-09-103-287-1 (1-1351) from US09103287.seq 6755

1 ATGAGTAAGGAGTTTTATATA......TTAATATGTTTATAATAGAG 1351
TACTCATTCCTCAAAATATA......AATTATACAAATATTATCTC

Scoring table: TABLE bktranslate2 Gap 30

Comp:

Searched: 122461 seqs, 35738955 bases x 2 Nmatch

STD:

Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 55.325; Variance 346.966; scale 0.159

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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147 2.2 225 1 147 2.2 225 1 147 2.2 225 2 148 2.2 416 1 149 2.2 416 1 149 2.2 3169 2 143 2.1 444 1	11	148		60	μ,	US-08-117-	Sequer		20,
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 450 AA; 48579 MW;
        SEQUENCE
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US-08-665-435A-2
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                   TELEFAX: 317-276-3861 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
TYPE: am.__ in TOPOLOGY: lin MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                            SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Biosynthetic Gene MurD of Streptococcus TITLE OF INVENTION: pneumoniae NUMBER OF SEQUENCES: 3
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T N I K E A L E T F G G V K R R
                                                                                                                    NAME: Webster, Thomas REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                CITY: Indianapolis
STATE: Indiana
                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                       COUNTRY:
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Lilly Corporate Center
       PE: protein AA; 48579 MW
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Peery, Robert
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      MW; 1010380
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7.82e-01;
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Best Local
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                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                               NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                               SEQUENCE CHARACTERISTICS LENGTH: 267 amino acid
                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wallis, Nichola G.
APPLICANT: Fueyo, Joanna L.
APPLICANT: Lonetto, Michael A.
TITLE OF INVENTION: NOVEL MUTD
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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H T V L. N A L A V I A I S Y L E K L D V
                                                          TYPE: amino a
                                                                                                                                                                                                                                                                          COMPUTER: IBM CONCERNING SYSTEM:
                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dechert Price & STREET: 4000 Bell Atlantic CITY: Philadelphia
                                                                                                                         TELEFAX: 215-994-2222
                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                   TOPOLOGY:
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                                         267 AA; 29079 MW; 348410 CN;
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Score 177; DB 2;
Pred. No. 1.41e+00;
18; Mismatches 47
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Pred. No. 7.82e-01;
18; Mismatches 46
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Best Local Similarity 40.9%;
Matches 45; Conservative
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                                                                   SEQUENCE
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        820 CAYAAYGTNGARAAYGCNYTNGCNACNATHGCNGTNGCNAARYTNMGNGGNGTNGAYAAY 879
                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Wallis
                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fueyo, Joanna L. APPLICANT: Lonetto, Michael A. TITLE OF INVENTION: NOVEL MURI
                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 215-994-2252
                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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CATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTAGATGTT 867
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ZIP: 19:
                                                                                       TYPE:
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Fueyo, Joanna L.
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                                           Score 177; DB 2;
Pred. No. 1.41e+00;
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                                                                                                SEQUENCE
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 3126165418
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PRIOR APPLICATION DATA:
                                                                                                                                             FEATURE:
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                                                                                              OTHER INFORMATION: acetylate OTHER INFORMATION: a C-termi NCE 26 AA; 3155 MW; 4041 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                Similarity
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                                                                2.3%;
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Analogues Thereof
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                                                                                                             acetylated at N-terminus, a C-terminal amide.
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                                Pred.
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                                                Score 155;
Pred. No. 1
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                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US91/0504
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                      MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                     FILING DATE: 19-JUL-1990 ATTORNEY/AGENT INFORMATION:
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                                                                                          OTHER INFORMATION: acetylated at N-terminus, may OTHER INFORMATION: a C-terminal amide.

NCE 26 AA; 3155 MW; 4041 CN;
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CITY: C
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TOPOLOGY: li
                                                                                                                                                                                                                                   NAME: Gamson, Edward P. REGISTRATION NUMBER: 29
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Similarity 34.9%;
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APPLICATION NUMBER: US 07,
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: '30 amino acids
AAAGATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGT 618 K I L M M F L M H S K K W H I M L K K V
                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:
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CTTY: Chicago
                                                                                                                                                                                                                     OTHER INFORMATION: acetylated at N-terminus, may be OTHER INFORMATION: a C-terminal amide.
NCE 30 AA; 3638 MW; 5354 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 3126165460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dressler, Goldsmith, Sutker, ADDRESSEE: & Milnamow
                                                                                                                                  Similarity
22; Conser
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                                                                                                                                  Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                              Score 155;
Pred. No. 1.
20; Mismatc
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                                                                                                                                  Mismatches
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.75e+01;
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Query Match
Best Local Similarity
Matches 22; Conser
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SEQUENCE CHARATERSTICS:
LENGTH: 30 amino acids
TYPE: AMINO ACID
                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 62, Application PC/TUS9105047
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            559
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FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith,
ADDRESSEE: & Milnamow
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                            REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
                                                                                                                       FEATURE:
                                                                                                                              MOLECULE TYPE:
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COUNTRY:
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                                                                                          OTHER INFORMATION: acetylated at N-terminus, may OTHER INFORMATION: a C-terminal amide.

NCE 30 AA; 3638 MW; 5354 CN;
                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
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TOPOLOGY: 1:
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CLASSIFICATION:
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ilarity 34.9%;
Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        linear
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                                                                                                                                                                                                      3126165418
                                                                                                                             peptide
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                                                                                                                                                                                                                                        Edward P
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                                                        20;
                                                                Score 155;
Pred. No. 1.
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                                                                                                                                                                                                                        421250-80
                                                        Mismatches
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Best Local Similarity 34.9%;
Matches 22; Conservative
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                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 4212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126,65418
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Amphiphilic Peptide Compositions TITLE OF INVENTION: Analogues Thereof
ATT
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                                                                                                                                                     OTHER INFORMATION: acetylated at N-terminus, OTHER INFORMATION: a C-terminatal amide NCE 36 AA; 4362 MW; 7668 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.24
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STATE: IL
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ZIP: 60601
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                                                                                                                                                                                                                                                                             36 amino acids
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Blondelle, Sylvie
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                                                                                         Score 155; DB 1;
Pred. No. 1.75e+01;
20; Mismatches 21
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Best Local S
Matches 2
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INFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/0504
FILING DATE: 19910717
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
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CORRESPONDENCE ADDRESSEE: Dressler, Goldsmith, Sutker, Shore ADDRESSEE: 6 Milnamow
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K L L K K L L K L L K K L L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K K L K 
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                                                                                                                                                                                                                       OTHER INFORMATION: acetylated at N-terminus, may be OTHER INFORMATION: a C-terminatal amide NCE 36 AA; 4362 MW; 7668 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
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                                                                                                                                     Similarity
22; Conser
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20; 1
                                                                                                                                                       Score 155; DB 3;
Pred. No. 1.75e+01;
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Best Local Similarity 47.1%;
Matches 33; Conservative
                                                                                                              SEQUENCE
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                                      58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                            TELEFAX: 415-398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
                                                                                                                                                                   MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/01 FILING DATE: 10-SEP-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins NUMBER OF SEQUENCES: 70
TACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTCAAAGATATTAATGAT 573
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APPLICANT: Inglis, Stephen
APPLICANT: Munro, Alan J
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                                    TAYGTNATHATHGAYYTNATHCAYTTYYTNCAYGCNAAYTAYYTNAAYGTNATHAAYTAY 117
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                                                                                                           NAME/KEY: Protein
LOCATION: 1.60
OTHER INFORMATION: /note= "xa:
OTHER INFORMATION: the open r
OTHER INFORMATION: the open r
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TOPOLOGY: lin
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OPERATING SYSTEM:
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STATE: CA
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Embarcadero Center,
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                                                                   Score 148; DB 1;
Pred. No. 3.79e+01;
15; Mismatches 22
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                                                                       SEQUENCE
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                                                                                                                  TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,68
FILING DATE: 30-JAN-1992
                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781e1 Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                      MOLECULE TYPE:
MENCE 225 AA;
                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acid
                                                                                                                                                                    APPLICATION NUMBER: US 0
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
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     TELEPHONE: 904-375-8100
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                                                                                     TYPE: amino acid
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: UF114.C3
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                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
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                                         Score 147; DB 1;
Pred. No. 4.23e+01;
25; Mismatches 42
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 19-FEB-1991
                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 225 AA; 26008 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Salivanchik, David R.
REGISTRATION NUMBER: 31,794
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PRIOR APPLICATION DATA:
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APPLICANT: Hall, Richard L.
APPLICANT: Gruddl, Michael E.
TITLE OF INVENTION: NO. 5721352el Entomopoxyirus Expression
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (904) 375-8100
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                                                                  S I N I L N N E A I L N S I HWSNATHAYAAYATHYTNAAYAAYTTYGCNATHATHACNAAYGTNMGNYTNATHGAYAA 614
                                                ATGCATCAAAAACATCATTAATATCTTTGAAATAATCAGGATGATCGAAATCAATATTTG C I K N I I N I F E I I R M I E I N I C
Y N S I I S F L N I N V G T L F
RTAYAAYWSNATHATHWSNTTYYTNAAYATHAAYGTNGGNACNYTNTTY
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Conservative
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2421 N.W. 41st Street,
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2 ID NO: 3:
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Pred. No. 4.23e+01;
25; Mismatches 4;
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Matches 42; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             526
                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                          TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Moyer, Richard W. APPLICANT: Hall, Richard L. APPLICANT: Gruidl, Michael E. TITLE OF INVENTION: No. 5935777el NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  APPLICATION NUMBER: 1
FILING DATE: 30-JAN-PRIOR APPLICATION DATA:
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 07-DEC-1992
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                      MOLECULE TYPE:
                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                                                                                                                      APPLICATION NUMBER: US 0: FILING DATE: 19-FEB-1991 ATTORNEY/AGENT INFORMATION: NAME: Bencen, Gerard H.
                                                                                                                                                                                         PRIOR APPLICATION DATA:
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H N C V I R F I T * K V T S I F
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                                                                                                                        REFERENCE/DOCKET NUMBER: 35
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OPERATING SYSTEM: PC-DOS/MS-DOS
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2421 N.W. 41st Street, Suite A-1
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26008 MW;
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12-FEB-1992
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                Score 147; DB 2;
Pred. No. 4.23e+01;
25; Mismatches 42
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US-08-117-083-62
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                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PROCESS US11-F H
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APPLICANT: Munro, Alan J.

TITLE OF INVENTION: Recombinant Virus Vectors Encoding
TITLE OF INVENTION: Papilloma Virus Proteins
                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
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MEDIUM TYPE: Floppy disk
                                                                                                                                                          MOLECULE TYPE:
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LOCATION: 1.416
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OTHER INFORMATION: the open reading frame.
NCE 416 AA; 48611 MW; 1008609 CN;
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CITY: San Francisco
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STRANDEDNESS: si
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                                                                                                                        NAME/KEY:
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## RESULT 1 LOCUS DEFINITION NID VERSION KEYWORDS SOURCE ORGANISM JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE FEATURES ACCESSION gene CDS source Staphylococcus aureus. Staphylococcus aureus Eubacteria; Firmicutes; Low G+C gram-positive bacteria; Bacillaceae; Staphylococcus. Bacillaceae; Staphylococcus. E (bases 1 to 1314) S Lowe, A.M. and Deresiewicz, R.L. Cloning and sequencing of Staphylococcus aureus murC, a gene involved in cell wall biosynthesis Unpublished E (bases 1 to 1314) E (bases 1 to 1314) S Lowe, A.M. and Deresiewicz, R.L. Direct Submission L Submitted (11-NOV-1997) Channing Laboratory, Brigham and Women's buspittal and Harvard Medical School, 181 Longwood Ave, Boston, MA 02115, USA AF034076 1314 bp DNA BCT 26-NOV-1997 Staphylococcus aureus UDP-N-acetylmuramoyl-L-alanine synthetase (murC) gene, complete cds. AF034076 872642658 AF034076.1 GI:2642658 /gene="murc" /function="cell wall biosynthesis" /functe="murc; UDP-N-acetylmuramate-alanine ligase" /codon\_start=1 /transl\_table=11 /product="UDP-N-acetylmuramoyl-L-alanine synthetase" /protein\_id="AAB87090.1" Location/Qualifiers /gene-"murc" .1314

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SVAVTGAHGKTSTTGLLSHVMNGDKKTSFLIGDGTGMGLLESDVVFAFEACEYRHEFLS
YKPDYAIMTNIDFDHDDYFKDLNDVFDHFAFQEMAHNVKGGIIAWGDDEHLRKIEADVPI
YYYGFKDSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSQYGDHTVLNALAVIALSY
LEKLDVTNIKEALETFGGVKRRRUETTJANQVIYUDYAHHPREISATIETARKKYPHK
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Azevedo, V. Bertero, M.G. Bessleres, P., Bolotin, A. Borchert, S. Bouriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, V., Fuma, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, G., Guseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Kilerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Kilerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Kilerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Masuda, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Porrelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Scoffone, F., Sekiguchi, J., Schoeter, R., Scoffone, F., Sekiguchi, J., Sekowska, A., Tacconi, E., Tanaka, T., Tarakahashi, H., Takemaru, K., Ognoni, A., Tanakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Tosato, V., Uchiyama, S., Vandenbol, M., Vannier, F., Vassarotti, A., Viari, A., Wedler, E., Wedler, H., Weitzenegger, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAACCACACACTTTCTCTAGAACACAAGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT
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to 3213410.
Z99119 AL009126
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MEDLINE
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de 1'Expression Genetique, 28 rue du Docteur Roux, 757; Paris Cedex 15, FRANCE. E-mail: moszerépasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 215640)
Kunst,F., Ogasawara,N., Yoshikawa,H. and Danchin,A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The complete genome sequence of the gram-positive bacterium Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Winters,P., Wipat,A., Yamamoto,H., Yamane,K., Yasumoto,K., Yoshida,K., Yoshikawa,H.F., Zumstein,E., Yoshikawa,H. and
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                                                                                                                                                                                             complement
                                                                                                                                                                                                                                     complement(2288. .2980)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFVLSKIGNRNIVKTAVDVHLKEK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB14906.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(8..24)
                                                                                                                  /note="alternate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="hipO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APIAAWLVQKFHPQLMGVLVGGFIILVNARTLINEWIANTAVHPLIYTAIGAIWLSAV
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/strain="168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EC_number="3.5.1.32"
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                                                                        transl_table=11/
                                                                                              codon_start=1
                                                                                                                                              function="regulation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "ytnM"
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                                                                                                                                                                                        2288. .2980)
                                                                                                                  gene
                                                                                                                     of riboflavin biosynthesis genes" name: ytnK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFTISRQLMSLDHISGGRAGWNLVTSPQEGAARNHSKSNLPEHTERYEIAQEHLDVVR
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SSETGRQFAAKNADAIFTHSNSLEETKAFYADVKSRAADEGRDPSSVRIFPGISFIVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3027. .4355)
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SYVEESEENILG"
                                                            protein)"
                                                                                                                                                                                                      complement(5649. .6428)
                                                                                                                                                                                                                                 complement(5649.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MTRADEIQFGAMIHGVGGTTDGWRHPDVDPSASTNIEFYMKKAQ
TAEKGLFSFIFIADGLFISEKSIPHFLNRFEPITILSALASVTKNIGLVGTFSTSFTE
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/db_xref="PID:e1185804"
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/db_xref="PID:e1185807"
                                                                                     /product="histidine transport protein (ATP-binding
                                                                                                                                                                          /gene="hisp"
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                                                                                                                   transl_table=11/
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CGGCGCCCCCCAGGCTTTCTGCAAATTCGTCAAGGAACTGCTGCGTCCGGGTAAATGTAT 49761
                                           CAATGCTTGAGAAGTAATCAGGGTGATCAAAATCAATATTCGTCATAATCGCATAATCTG
                                                                                    ATCCATAGTAATAAATTGGAACATCTGCTTCAATTTTACGTAGATGTTCATCATCACCCC
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                                                                                                                                                                                                                                                                   AAGCAGTACCTTTATCCGTAATTTGAATATTTTGAGCATAAATGTCATCCGAATCTTTAA
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Similarity 62.1%;
789; Conservative
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EGLTIARKMRKQDAYAVAENELRKVGLQDKLNAYPSQLSGGQKGRVGIARALAIHPDV
LLFDEPTAALDPELVGEVLEVMLEIVKTGATMIVVTHEMEFARRVSDQVVFMDEGVIV
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Pred. No. 6.77e-191;
0; Mismatches 481;
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Bacillus
                Seki,T., Yoshikawa,H., Takahashi,H. and Saito,H. Cloning and nucleotide sequence of phoP, the regulatory gene for alkaline phosphatase and phosphodiesterase in Bacillus subtilis J. Bacteriol. 169 (7), 2913-2916 (1987)
J. Bacteriol.
87250247
                                                                                                                  Ogasawara, N., Moriya, S., Mazza, P.G. and Yoshikawa
Nucleotide sequence and organization of dnaB gene
genes on the Bacillus subtilis chromosome
Nucleic Acids Res. 14 (24), 9989-9999 (1986)
                                                                                                                                                                                                                        Connors; M.J., Mason, J.M. and Setlow, P. Cloning; and nucleotide sequencing of genes for three acid-soluble proteins from Bacillus subtilis spores J. Bacteriol. 166 (2), 417-425 (1986)
                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 7430)
Green,C.J., Stewart,G.C., Hollis,M.A., Vold,B.S. and Bott,K.F.
Nucleotide sequence of the Bacillus subtilis ribosomal RNA operon,
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REFERENCE AUTHORS TITLE JOURNAL MEDLINE	TITLE JOURNAL MEDLINE	REFERENCE	AUTHORS TITLE JOURNAL MEDIINE	REFERENCE	JOURNAL	AUTHORS TITLE	MEDLINE	TOTANAT	TITLE	REFERENCE	JOURNAL MEDLINE	REFERENCE AUTHORS	JOURNAL MEDLINE	AUTHORS	JOURNAL MEDLINE	TITLE	REFERENCE AUTHORS	JOURNAL MEDLINE	AUTHORS	JOURNAL MEDLINE REFERENCE		AUTHORS	MEDLINE	AUTHORS TITLE	MEDLINE REFERENCE	REFERENCE AUTHORS TITLE
16 (bases 25258 to 31212) Rowland,B., Hill,K., Miller,P., Driscoll,J. and Taber,H. Structural organization of a Bacillus subtilis operon encoding menaquinone biosynthetic enzymes Gene 167 (1-2), 105-109 (1995) 96144257	Identical amino acid sequence of the aroA(G) gene products of Bacillus subtilis 168 and B. subtilis Marburg strain Microbiology 141 (Pt 9), 2219-2222 (1995) 96118703	15 (bases 131934 to 133970) Bolotin,A., Khazak,V., Stoynova,N., Ratmanova,K., Yomantas,Y. and	Abe, A., Kolde, H., Kohno, T. and Watabe, K.  A Bacillus subtilis spore coat polypeptide gene, cots Microbiology 141 (Pt 6), 1433-1442 (1995)  Q54,00496	94331340 14 (bases 16985 to 19588)	579 (1994)	Jin S. and Sonenshein, A.L. Identification of two distinct Bacillus subtilis citrate synthase	94195107 94195107 13 (bases 196487 to 200620)	(0 in 91) coyon xicojiciicoio	Glycogen in Bacilly. Detailed, G. and remember. G. Glycogen in Bacille subtilis: molecular characterization of an operon encoding enzymes involved in glycogen biogenthesis and	12 (bases 7009 to 15526)	J. Bacteriol. 175 (22), 7348-7355 (1993) 94042910		Mol. Microbiol. 10 (2), 259-271 (1993) 95020526	Grundy, F.J., Waters, D.A., Takova, T.Y. and Henkin, T.M. Identification of genes involved in utilization of acetate and	EMBO J. 11 (8), 3117-3127 (1992) 92347349 10 (bases 134990 to 141290)	Co-ordinate expression of the two threonyl-tRNA synthetase genes in Bacillus subtilis: control by transcriptional antitermination involving a conserved regulatory sequence		regulatory sequence in multiple tRNA synthetase genes J. Bacteriol. 174 (4), 1299-1306 (1992) 92138624	Henkin,T.M., Glass,B.L. and Grundy,F.J.  Analysis of the Bacillus subtilis tyrS gene: conservation of a	MO1. Microbiol. 5 (3), 575-584 (1991) 91260441 8 (bases 140810 to 142610)	Escherichia coli lacl and galk repressors	Henkin, T.M., Grundy, F.J., Nicholson, W.L. and Chambliss, G.H. Catabolite repression of alpha-amylase gene expression in Bacillus	J. Bacterioi. 1/2 (11), 63/2-63/9 (1990) 91035248 7 (hassa 133624 to 13400)	J. and Henkin,T.M.  Ind analysis of the Bacill  protein S4	J. BACTETIOI. 1/0 (12), 3935-3938 (1988) 89053932 6 (bases 142232 to 144147)	5 (bases 201234 to 203212) Seki,T., Yoshikawa,H., Takahashi,H. and Saito,H. Nucleotide sequence of the Bacillus subtilis phoR gene
trna trna	trna	trna	trna	tRNA	trna	rRNA	rRNA	rRNA	8041	FEATURES	JOURNAL	REFERENCE	JOURNAL	AUTHORS	JOURNAL MEDLINE	AUTHORS TITLE	REFERENCE	JOURNAL	REFERENCE	JOURNAL	TITLE	REFERENCE	JOURNAL	AUTHORS TITLE	JOURNAL MEDLINE REFERENCE	REFERENCE AUTHORS TITLE
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                                          GCGCACACGGCAAAAACGTCGACTACGGGTCTGCTGGCTCACGTGATCCAAAAACGCAAAAAC 132
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                                                                                  TACGTTATCATAAGTTTTTAGGCGACTACATGAAAAAATTCACGAGTGTTGCCGTTACGG
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ANQHEDVPAYYL"
1 464 c 549 q 557 +
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DKTDSSTAMQDMREEAMQAADETKDQVLQTKEDVKDELKDAQKQAEQLNR"
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EGQMKGITTETAELLHKTNRLAEDIQEKSEKLNTVVHAVQGVGASVQQFNTSMKQAAG
SVSASVRENQDKINQVVGRSTWSQAAMEIWEKWKQKKKSAL"
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/db_xref="GI:556017"
                                                                                                                                                                                                                                                                                     reported by Bo
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                                                                                                                                                                                                                                                                                                   /note="open reading frame extends an additional 53 codons
(including the TGA stop) into the overlapping sequence
reported by Bolotin et"
                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAB40045.1"
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/db_xref="PID:g556015"
/db_xref="GI:556015"
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1123. .1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTACCTTGTATAACTACCATATCTTCTTTTATGTTATTAGCACCAAATGGTAATATTT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCCGACAAAATGATAGTGTGTCATTA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTATCCCCTTATTTCTAAGAGCAACTTCTGTAAATACGTAGTTCTCAATATCCGATCCTT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1371
                                                       Direct Submission
Submitted (30-JUN-1997) School of Biological Sciences,
of Sydney, Biology A12, Sydney University, NSW 2006, AV
                                                                                                                                                                                       Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects
                                                                                                                                                                                                                                                                                                                 1 (bases 4546 to 4553)
Gray, Y.H., Tanaka, M.M. and Sved, J.A.
P-element-induced recombination in Drosophila element insertion
                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
Eukaryotae: mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachyce
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF012089 10772 bp DNA INV 05-AUG-1
Drosophila melanogaster cysteine proteinase-1 (CP1) gene,
cds, and phenylalanyl tRNA synthetase gene, partial cds.
                                                                                                                         Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                              Genetics 144 (4), 1601-1610 (1996)
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Patent: US !
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                                          , Biology A12, Sydno
Location/Qualifiers
  /organism≃"Drosophila melanogaster"
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1491 c 1486 g
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3.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59; DB 25;
Pred. No. 5.17e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Brachycera;
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Best Local
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                                                             RWWYWAWTTTMWKWMWTTWKWAMMKTYRTWWMWKMYWTSRTTTTSAMWMWYTWSTWTKYW 1752
                                                                                                                                             h 3.0%;
Similarity 18.8%;
25; Conservative
                                                                                                                                                                                                                                                     2929
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/gene="CP1"
4546. .4553
/gene="CP1"
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6476. .6690
/gene="CP1"
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/gene="CP1"
6751. .7707
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/translation="MLITLRVGARHWLKSTRCLASSAAPAKSPSSPPOLEVSGSTYA
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PVVTVQQNFDNLLIFADHVSRQKSDCYYINQOHLLRAHTTAHQYELISGGLDNFLVVAV
PVYTVQQNFDNLLIFADHVSRQKSDCYYINQOHLLRAHTTAHQYELISGGLDNFLVVAV
EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFERRIXYRWDTYFFFTQFSMELEI
SWTKPNSPATRRAVKLMEHEMKHVLVGLTKDLFGFRIXYRWDTYFFFTQFSMELEI
SWTKPNSPATRRAVKLMEHEMKHVLVGLTKDLFGFRIXYRWDTYFFFTQFSMELEI
                                                                                                                                                                                                                                                                                                             YFKDNWLEVLGCGIMRHEILQRSGVHQSIGYAFGVGLERLAMVLFDIPDIRLFWSNDS
GFLSQFSEKDLHNLPKYKPISHYPQCINDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mrtavllpllallavaqavsfadvvmeemhteklehrknyddet
eerfelkifenenthekaklakhnorfaegkysklavnkyadlhebergolmngfnytlhk
olraadesfrovtfispahytlhksvdwrtkokodhoggiogschaesstoklego
hfrksgylyslseqnlydcstkygnngcngglmdnafryikdnggidteksypyeaid
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/gene="CP1"
                                                                                                                                                                                                                                                                                          DMVEQISLVDKFKHPKTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFNVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="phenylalanyl tRNA synthetase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGF1KMLRNKENQCG1AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="phenylalany1 tRNA sy
join(8110 .9300,9370 .>9532)
/note="potential orf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="cysteine proteinase-1"
/protein_id="AAB65749.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(2328. .2426,6476. .6690,6751.
/gene="CP1"
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/gene="CP1"
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join(872. .1000,2310.
/gene="CP1"
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172. .1000
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                                                                                                                                             Score 41; DB 21;
Pred. No. 1.98e-07;
67; Mismatches 39
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